GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein

Run on:

April 12, 2004, 10:18:37; Search time 21 Seconds (without alignments) 1543.645 Million cell updates/sec

1704 1 MKKMPLFSKSHKNPAEIVKI.....FADEKNYLIKQIRDLKKTAP 337 Title: Perfect score: Sequence:

US-10-025-730-1

283366 seqs, 96191526 residues Gapop 10.0 , Gapext 0.5

Searched:

BLOSUM62

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:* pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		_		b	_	_	_	hypothetical prote	ē.	hypothetical prote	hypothetical prote	NMDA receptor-bind		hypothetical prote	m.	ĽΩ.	hypothetical prote	hypothetical prote	hyaluronan recepto	rhoptry protein -	hypothetical prote	conserved hypothet	hypothetical prote	conserved hypothet	hyp.	hypothetical prote	0	prot	hypothetical colle
Б	I57997	T16651	T27129	T50117	G71441	B84448	S34681	T33477	H64574	H64709	B71685	T08880	B72420	F64489	T00246	871322	T43446	855123	JC5016	T28676	G70163	A90551	C82911	A70387	E82909	T07283	S11527	T18507	T50451
DB	2	7	7	~	7	~	~	N	7	N	7	7	N	N	7	0	~	N									7		
Length	341	377	338	329	305	348	399	339	677	430	298	1642	1285	1175	959	474	833	1411	725	2401	2166	2819	457	978	1830	695	1401		952
당성	80.08	62.4	6	49.0	0	7	28.5		7.9	7.5	7.4	7.4	7.2	7.0	7.0		6.7	9.9	6.5	6.5	•				6.4	6.4		6.4	6.4
H		1063.5	1006.5	834.5	685	632	485	143.5	134.5	128	125.5	125.5	123.5	120	118.5	115	113.5	112.5	111.5	111.5	111	111	109.5	109.5	109.5	109	109	108.5	108.5
Result No.		2	n	4	ı Cı	9	7	no.	ď	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

type I restriction replication helica nositive trans-act	importin beta-1 SU type I restriction	major merozoite su major merozoite su	phosphoprotein pho ang protein - fiss	myosin-like coiled	hypotherical prote	protein kinase nom GTPase-activating	hypothetical prote	nypotmeticat proce
D64315 S73254	140033 E90106 G64514	SAZQGM A45948	\$68686	T50073	S56748 T24587	T00456	T34107	T18499
000	100	-10	N	4 (7)	2 74	0 0	10	0
1163	855 855 855 855	1726	570	1727	474 1295	781	1001	1619
4.6.	 	999	900	6.3	6.2	6.2	9 9	6.2
108.5	107.5	107.5	107	107	106 106	105.5	105.5	105.5
30	3 8 8 2 8 8	33.5	37	39	4 4 1	47	4 4 0 4	45

ALIGNMENTS

hypothetical calcium-binding protein - mouse

C;Species: Mus sp. (mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 19-May-2000
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 19-May-2000
C;Accession: 157997
R;Miyamoto, H; Matsushiro, A; Nozaki, M.
Mol. Reprod. Dev. 34, 1-7, 1993
Mol. Reprod. Dev. 34, 1993
Mol. Reprod. Dev. 34, 1993
Mol. Reprod. Dev. 34, 19 A; Molecule type: mRNA A; Residues: 1-341 <RES> A; Residues: 1-341 <RES> C; Superfamily: Saccharomyces hypothetical protein YKL189w C; Superfamily: Saccharomyces hypothetical protein types of Symposium binding

2 59 4 MPL-FSKSHKNPAEIVKILKDNLAILEKO---DKKTDKASEEVSKSLQAMKEILCGTNEK 4; Gaps Query Match

80.8%; Score 1376; DB 2; Length 341;
Best Local Similarity 80.7%; Pred. No. 7.9e-85;
Matches 272; Conservative 32; Mismatches 29; Indele

60 EPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI 119 120 61 EPQTEAVAQLAQELYNSGLLGTLVADLQLIDFBGKKDVAQIFNNILRRQIGTRTPTVEYI g ð

180 120 SAHPHILFMLLKGYBAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDI 179 121 CTQONILFMLLKGYESPEJALNCGIMLRECIRHEPLAKIILWSEGFYDFFRYVEMSTFDI à g

g

ð

239 180 ASDAFATFKOLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDR ð

q

HNFAIMTKYISKPENLKLAMALLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP 299 240 à q

KLIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTA 336

300 301

Š g RESULT 2

T16651 hypothetical protein R02E12.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000

```
185/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Map position: 1
A,Introns: 34/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Simi
hes 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                               ö
                                                                                                  d
                                                                                                                                                                 à
                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                        요
                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                              A;Accession: T16651
A;Accession: T177
A;Accession: T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Y53C12A.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Date: 127129
R;Rershaw, J.; Lennard, N.
R;Rershaw, J.; Lennard, N.
R;Reference number: Z20315
A;Reference number: Z20315
A;Accession: T27129
A;Accession: T27129
A;Accession: T27129
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T338 cML>
A;Residues: 1-338 cML>
A;Residues: 1-338 cML>
A;Residues: clone Y53C12A.4
A;Gene: CESP:Y53C12A.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 QSLKILGELILDRHNFNIMIKKISNPONIRIMMELLRDKSRNIQYEAFHVFKVFVANPNK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 PLFSKSHKNPAEIVKILKDNLAILEK-----ODKKTDKASEEVSKSLQAMKEILCGTNEK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEILCGTNEKEPPTE---AVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 KSFIYGNDSAEPSSEHVVQVAQLAQEVYNANILPMLIKMLFKFEFEKKKDVGQIFNNLLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSLKLLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 RQIGTRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 MP-LFSKSHKNPAEIVKILKDNLAILEK-------QDKKTDKASEEVSKSLQAM 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 DFFKYVELSTFDIASDAFATFKOLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 PKPISDILNRNREKLVEFLSEFHNDRTDDEQFNDEKAYLIKQIQEMKSS 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 TQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKKT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.1%; Score 1006.5; DB 2; Length ilarity 57.2%; Pred. No. 4e-60; Conservative 60; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             introns: 29/3; 103/3; 136/2; 215/1; 282/3
Superfamily: Saccharomyces hypothetical protein YKL189w
                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: X
A;Introns: 37/3; 146/2; 225/1; 315/3
C;Superfamily: Saccharomyces hypothetical protein YKL189w
                                                     submitted to the EMBL Data Library, April 1996
A, Description: The sequence of C. elegans cosmid R02E12.
A, Reference number: Z18554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 1063.5; DE; Pred. No. 7e-64; 53; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.5'
Matches 211; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 191; Conserv
C; Accession: T16651
R; Leimbach, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 2
A; Introns: 29/3; 1
C; Superfamily: Sac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
A;Molecule type: DNA A;Rebidues: 1-329 <SEE> A;Rebidues: 1-329 <SEE> A;Cross-references: EMBL:AL157734; PIDN:CAB75774.1; GSPDB:GN00066; SPDB:SPAC1834.06c A;Experimental gource: strain 972h(-); cosmid c1834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 ILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDIASDAF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 ATEKOLLIRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHNFAI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245 MTKYISKPENLKIMMNILRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPKLIEF 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 AVAQLAQELYSSGLLVTLIADLQLIDFECKKDVTQIFNNILRRQIGTRSPTVEYISAHPH 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 HNFAIMTKYISKPENLKLMMALLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP 299
                                                                                                                                                                                                                                                                                                                                                                                              244 HNFSTMNKYITSPENLKTVMELLRDKRRNIQYEAFHVFKIFVANPNKPRPITDILTRNRD 303
                                                 EPPTEAVAQLAQBLYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI 119
                                                                                  64 EPNNEQYTQLAQEVYNANVLPMLIKHLHKPEFECKKDVASVFNNLLRRQIGTRSPTVEYL 123
                                                                                                                                                                                    180 ASDAFATEKDLITRHKVLVADFILEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDR 239
                                                                                                                                                                                                                                                                                               61
4 PLFGKADKTPADVVKNLRDALLVIDRHGTNTSERKVEKAIEETAKMLALAKTFIYGSDAN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mo25 homolog [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 LFSKSHKNPAEIVKILKDNLAILE-KQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LFNKRPKSTQDVVRCLCDNLPKLEINNDKK--KSFEEVSKCLQNLRVSLCGTABVEPDAD
                                                                                                                                                         120 SAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ب.
۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T50117
R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. abumitted to the EMBL bata Library, February 2000
A;Reference number: Z25039
A;Accession: T50117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: Saccharomyces hypothetical protein YKL189w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.0%; Score 834.5; DB 2, 51.5%; Pred. No. 1.2e-48; tive 63; Mismatches 93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 KLVEFLTAFHNDRTNDEQFNDEKAYLIKQIQELR 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 KLIEFLSSFOKERTDDEQFADEKNYLIKQIRDLK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSSFOKERTDDEQFADEKNYLIKQIRDL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSAFHTDRKNDEOFNDERAFVIKOIERL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: SPDB:SPAC1834.06c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
```

.,

14; Gaps

63

```
A; Cross-references: EMBL: Z28189; NID: 9486334; PIDN: CAA82032.1; PID: 9486335; MIPS: YKL189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: 228189; NID: 9486334; PIDN: CAA82032.1; PID: 9486335; MIPS: YKL189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast 9, 661-667, 1993
A,Title: DNA sequence analysis of the YCN2 region of chromosome XI in Saccharomyces cer
A,Reference number: S33960; MUID:93348778; PMID:8394042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein YK1189w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Species: 30.5ep-1993 #sequence revision 30.5ep-1993 #text_change 19-Apr-2002
C;Accession: 534681, 533963; 538021; 338026
R;Wieman, S.; Voes, H.; Schwagaer, C.; Rupp, T.; Stegemann, J.; Zimmermann, J.; Grothue Simbnitted to the BMBL Data Library, July 1993
A;Description: Sequencing and analysis of 51.5 kilobases on the left arm of chromosome A;Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T.; Stegemann, J.; Zimmermann, J.; Grothue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Mala e Silva, A.; Bossier, P.; Vilela, C.; Fernandes, L.; Soares, H.; Guerreiro, P.; submitted to the Protein Sequence Database, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:X69765; NID:g296985; PIDN:CAA49422.1; PID:g296989
R;W.temann, S.; Voss, H.; Schwager, C.; Rupp, T.; Grothues, D.; Sensen, C.; Stegemann, submitted to the Protein Sequence Database, March 1994
A;Reference number: S37825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 LDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 MDRSNSGVMVKYVSSLDNLRIMMNLLREPTKNIQLEAFHIFKLFVANENKPEDIVALLVA 303
                                                                                                                                                                                                                                                                        DIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYE-KLLQSENYVTKRQSLKLLGELI 236
                                                                                                                                                                                                                             59 KEPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEY 118
                                                                                                                                                                                                                                                                                                                                                                119 ISAHPHILFMLLKGYEAP-QIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTF 177
                                                                                                                                     -- EVSKSLQAMKEILCGTNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL:X74151; NID:9450365; PIDN:CAA52249.1; PID:9395236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 NQPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLK----KTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 11L
C;Superfamily: Saccharomyces hypothetical protein YKL189w
38.7%; Pred. No. 4.5e-35; ive 80; Mismatches 117;
                                                                                               6 LFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ĺτ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Experimental source: strain S288C
R, Cheret, G.; Mattheakis, L.C.; Sor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Experimental source: strain S289C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: SGD:S0001672
                                   Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: S38024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: S34681
A,Molecule type: DNA
A,Residues: 1-399 <WIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-399 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-399 < CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Residues: 1-399 <MAI>
   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S38026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S33963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S3802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: SGD: HYM1
       Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                     g
                                                                                                                                                                                                                                    \delta
                                                                                                                                                                                                                                                                                             쉽
                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                 hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: Columbia
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 0.3-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 18-Aug-2000
C;Accession: G71441
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Millor, T.; Pohl, T.M.; Terryn, N.; Gial
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A;Reference number: A71400; MUID:99121113; PMID:9461215
A;Accession: G71441
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-305 < ABEV>
A;Cross-references: G8:297343; NID:92245073; PID:92245086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein At2g03410 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: B84448
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Accession: B84448
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 FSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDY-EKLLQS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENYVTKROSLKLLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIOFEAFHVFKV 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 FINILRROIGTRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIIL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 VANLOROOVNSRLIAADYLESNIDLMDFLVDGFENTDMALHYGTMFRECIRHQIVAKYVL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: AE002093; NID: 94335759; PIDN: AAD17435.1; GSPDB: GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 EVSKSLOAMKEILCGINEKEPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 DSEHVKKFFYYIQLPNFDIAADAATFKELLTRHKSTVAEFLIKNEDWFFADYNSKLLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FVASPHKTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
40.2%; Score 685; DB 2; Length 305;
Best Local Similarity 45.9%; Pred. No. 1.1e-38;
Matches 135; Conservative 68; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: At2g03410
A;Map position: 2
C;Superfamily: Saccharomyces hypothetical protein YKL189w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Map position: 4COP9-4G3845
C;Superfamily: Saccharomyces hypothetical protein YKL189w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.1%; Score 632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-348 <STO>
```

Db

ŏ qq 280

à

qq

d

ð

g

ò

Query Match

C.Genetics:

ט

```
hypothetical protein T27C10.3 - Caenorhabditis elegans
hypothetical protein T27C10.3 - Caenorhabditis elegans
c;Species: Caenorhabditis elegans
c;Species: Caenorhabditis elegans
c;Date: 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T33477
R;Zhu, H.J.; Graves, T.; Hawkins, M.
submitted to the RBLD Data Library, October 1998
A;Description: The sequence of C. elegans cosmid T27C10.
A;Accession: T33477
A;Accession: T3347
A;Accession: T3347
A;Accession: DAA
A;Molecule type: DNA
A;Residues: 1-339 < ZHU>
A;Residues: 1-339 < ZHU>
A;Residues: 1-339 < ZHU>
A;Residues: Lass cosmid T27C10.
                                             6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 ILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQ 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 LMNTNKFRD------FDVIQGTFDTLQIIFFTNHESANNFIKNNLPRFMQTLHKLIA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 SENYVTKRQSLKLLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 CSNFFIQAKSFKFLNELFTAQTNYETRSLWMAEPAFIKLVVLAIQSNKHAVRSRAVSILE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 VFVASPHKTQPIVEILLKNQPKLIEFL------SSFQKERTDDEQFAD----- 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 TEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISAH 122
                                                                                                                                                                                                            PHILFMLLKGYE-----APQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELS 175
                                                                                                                                                                                                                                                                                                             135 PKTISLMLRTABVALQOKGCODIFLTVGNMIIECIKYEQLCRIILKDPQLWKFFEFAKLG 194
                                                                                                                                                                                                                                                                                                                                                                    176 TFDIASDAFATFKOLLTRHKVLVA-DFL--EQNYDTIFEDYEKLLQSENYVTKRQSLKLL 232
                                                                                                                                                                                                                                                                                                                                                                                                             195 NFEISTESLOILSAAFTAHPKLVSKEFFSNEINIIRFIKCINKLMAHGSYVTKROSTKLL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 GELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVE 292
                                                                                           7 FSKSHKNPAEIVKILKDNLAILEK----QDKKTDKASEEVSKSLQAMKEILCGTNEKEPP 62
                                                                                                                                    74
                                                                                                                                      16 WKKNPKTPSDYARLIIEQLNKFSSPSLTQDNKR-KVQEECTKYLIGTKHFIVGDTDPHPT
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 339;
Length 399;
  28.5%; Score 485; DB 2; Length 399
33.0%; Pred. No. 3.6e-25;
tive 75; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 8.4%; Score 143.5; DB 2; Length 3 Local Similarity 19.3%; Pred. No. 0.02; Pred. No. 0.08; Albert 38; Conservative 50; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 ILVKONRDKLLTYFKTFGLD-SQDSTFLDEREFIVQEIDSLPR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C'Genetics:
A;Gene: CESP:T27C10.3
A;Map position: 1
A;Introns: 72/3; 120/3; 233/3; 295/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---EKNYLIKQIRDLKK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :: :|::| ::
268 WDMQRPFTQEQLQDFEE 284
  Query Match
Best Local Similarity 33.0%
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321
                                                                                                                                                                                                                                                                                123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                         g
                                                                                                8
                                                                                                                               g
                                                                                                                                                                                       ò
                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
```

```
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Date: 09-Aug-1997
C;Accession: H64574
C;Accession: M.D.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn Sen, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Accession: H64574
A;Acce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 EDYEKLIQSENYVTKRQSLKLIGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQ 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 -- PSVYQYREYKAGKNSQAEAHEAIRITHPHALKDLEKVCSDAKISEELALKLYQLIYTN 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 PL---AKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIF 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 TICSQSRNALY-NQYDCIFK-----IKSESFKLSFKLLKEKGFLEIEELIQGKEEIN 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432 RE-EQESEIENFSLKENDSVPLKEVFIKK----IEKPSPKPYKESAFIPLLESEG---- 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 ILCGINEKEPPTEAVAQIAQELYSSGLLVTLIADIQLIDFEGKKDVTQIFNNILRRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 RSPTV----EYIS-----AHPHILFMLLKGYEAPQIALRCGIMLRECIRHE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 FSKSHKNPA-EIVKILKDNL------AILEKQDKK---TDKASBEVSKSLQAMKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 FKFKDKNEASQFLKDLKDGLGSMSVLVSLKESLSNKEPKKPFTTSKLLSQASKSLKI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----IGRPSTYASFLDLLLKRKYISIDTKTNAITPTSQGLEVISFFKKDKEVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 7.9%; Score 134.5; DB 2; Length 677; Local Similarity 21.6%; Pred. No. 0.19; tes 88; Conservative 58; Mismatches 134; Indels 127; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---EOF-----ADEKNYLIKQIRDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 532 IALTSKDKSKLGNTTKQFEBCLDLIMRGBASYBKFMLEVISKLKSTA 578
topoisomerase I - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 FEAFHVFKVFVASPHKTQPIVEILLKNQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

hypothetical protein HP1520 - Helicobacter pylori (strain 26695)

Cypate: O's-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999 Cypate: O's-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999 CyAccession: H64709

RyTomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D Feterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn son, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997

A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Rarpk, P.D.; Smith, H.O.; Fraser, C. A.; Reference number: A64520; MUID:97394467; PMID:9252185

A,Cross-references: GB:AE000650; GB:AE000511; NID:g2314700; PIDN:AAD08565.1; PID:g23147 C,Superfamily: Helicobacter pylori hypothetical protein HP1520 A;Status: preliminary, nucleic acid sequence not shown, translation not shown A;Molecule type: DNA A; Residues: 1-430 < TOM>

7.5%; Score 128; DB 2; Length 430; 20.9%; Pred. No. 0.29; Query Match Best Local Similarity

RESULT 9 H64574

QY 330 RDLKKTAP 337 :	RESULT 12 T08880 NWDA receptor-binding protein yotiao - human C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 C.Accession: T08800 R.Lin, J.W.; Wyszynski, M.; Madhavan, R.; Sealock, R.; Kim, J.U.; Sheng, M. J. Neurosci. 18, 2017-2027, 1998 A.Title: Yotiao, a novel protein of neuromuscular junction and brain that interacts wit A;Mclecule Type: mmuber: 216511; MUID:98151389; PMID:9482789 A;Accession: T08800 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Mclecule Type: mRNA A;Mclecule Typ	Query Match 7.4%; Score 125.5; DB 2; Length 1642; Best Local Similarity 20.2%; Pred. No. 2.4; Matches 77; Conservative 73; Mismatches 117; Indels 115; Gaps 15; Qy 18 VKILKDNIALIENCOKKTOKASEDSKSLQAMKEHLGCTHERPPTERAVQLAGELYSSG 77	RESULT 13 B725 SEQLKPKPGEISFINEEVKSLK 996 RESULT 13 B726 Dispecies: Thermotoga maritima (strain MSB8) C;Species: Thermotoga maritima C;Species: Thermotoga
Matches 82; Conservative 73; Mismatches 135; Indels 102; Gaps 20; Qy 7 FSKSHKNPABIVKILKDNLAILEKODKKTDKASEBVSKSLQAMKEILCGTNBKEPP 62 :	Oy 63 TEAVAQLAQELYSSGLLVTLIADLQLIDFECKKDVTOIFNNILR 106 112 DNILLELEKEKKALLKSLRDIASGFDVEEEIKTIKNEKNKSFYEILDNHLTEESSEK 169 OY 107RQIGTRSPTV-EYISAHPHILFMLLKGYBAPQIALRCGIMLRECIRHEPLAKII 159 170 HYSFKYRDIFDGSKKVKDFVNKHHDLIEQYPNKYQ	Db 328 IQNVKSLVNLYREKKPEIEEIIKQASKDQKEWESVIEIFNQRFLVPFKVELONQ 381 Qy 312 RTDDEQFADEKNYLIKQIRDLKK 413 RESULT 11 B71685 ENGLATE PROTECTED PROPAZERIJ C, Species: Ricketteia prowazekij C, Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000 C, Accession. R, Andersson, S. G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U RA, Andersson, S. G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U RA, Andersson, B71685 A, Tele: The genome sequence of Rickettsia prowazekij and the origin of mitochondria. A, Reference number: A71630; MUID:99039499; PMID:9823893 A, Accession: B71685 A, Residues: 1-298 <and> A, Residues: 1-298 <and> A, Residues: 1-298 <and> A, Residues: 1-298 <and> A, Generics: C, Generics: A, Generics:</and></and></and></and>	

: : : : : :	DD 371 IKEQYEKEFINLDNIIKNPYILVED-LKENDSFERIIFEELDSWEER QY 230KLLGELILDRHNPAIMTKYISKDENLKLMMNLLEDKSPNIC	RESULT 15 T00246 DNA polymerase V - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 31 C;Accession: T00246; T39442 R;Shimizu, K. submitted to the EMBL Data Library, March 1998 A;Description: S;pombe homolog of S.cerevisiae DNA polymerase V.	A;Reference number: 214129 A;Accession: T00246 A;Accession: T00246 A;Accession: T00246 A;Residues: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-959 cSHI> A;Cross-references: EMBL:AB012696; NID:d1224325; PIDN:BAA32046.1; R;Xiang, Z.; Aves, S.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Submitted to the EMBL Data Library, March 1998 A;Reference number: 221854 A;Accession: T19442 A;Accession: T19442 A;Accession: DBJ A;Molecule type: DBA A;Accession: DBJ A;Accession: DBJ A;Accession: DBJ A;Accession: DBJ A;Accession: DBJ A;Accession: DBJ	A; Krestudes: 1-755 cliffs. AL022305; PIDN:CAA18436.1; GSPDB:GN00067, A; Experimental source: strain 972h-; cosmid c14C8 A; Experimental source: strain 972h-; cosmid c14C8 C; Genetics: C; Genetics: A; Gene: pol5+; SPBC14C8.14c A; Map position: 2 A; Introns: 66/3 A; Introns: 66/3 Query Match Best Local Similarity 20.5%; Pred: No. 3.5; Matches 80; Conservative 63; Mismatches 135; Indels 11:	OY SERKALPAEIVKILKDNIAILEKODKKTDKASEEVSKSLQAMKEILA SEZ KSPKANILISMDESVIEIVQKSLSVLHKVTKKIDKKAQHL-QQLAB OY SERVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTI DS SESQLLYSLVLLQVYAGDTDSIDVLEDIDNCYSKVFNKKSKRESTSI OY 120SAHPHILFMLLKGYEAPQIALRC	250 151 680 211 731 263
A;Residues: 1-1285 <arn> A;Cross-references: GB.AE001695; GB:AE000512; NID:g4980569; PIDN:AAD35182.1; PID:g498057 A;Experimental source: strain MSB8 C;Genetics: A;Genetics:</arn>	Query Match Query Match Best Local Similarity 21.5%; Pred. No. 2.4; Matches 86; Conservative 78; Mismatches 129; Indels 107; Gaps 23; Qy I MKKMPLFSKSHKNPABIVKILKDNIAILEKQDKKTDKASEBYSKS 45	Qy 46 LQAMKEILCGTNEKEPPTEAVAQLAQELYSSGLLVTLIAD 85 :::	QY 177 PDIASDAPATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLG 233 Db 781 FDRLMLEVPSGFSFBEFKTFLEVLVPEVKQVVYLDKLNLLLVEVPVSQSERVKSLL 836 QY 234 ELILDRHNFAIMTKYISKPENL-KLMMNLLRDKSPNIQFBAF-HVFKVFVAS 283 Db 837 DTFLKKEBAVSEKKAVKSVTIPSGVNPDELSSYLKKLIRNVEITVFPNMGQMIVBG 892 QY 284 P-HKTQPIVBILLKNQPKLIBFLSSFQKERTDDEQFADEK 322 Db 893 PENEVEKAVELVBAREKKIVLKERKDYVKVSDGK 926	RESULT 14 F64489 F64489 F64489 F64489 C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C;Accession: F64489 F;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.Bult, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Freich, C.I.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.	A.Authors: Kaine, B.P.; Bordovsky, M.; Klenk, H.P.; Framer, C.M.; Smith, H.O.; Woese, G.A.Authors: Kaine, B.P.; Bordovsky, M.; Klenk, H.P.; Framer, C.M.; Smith, H.O.; Woese, G.A.Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A.Reference number: A64300; MUID:96337999; PMID:8688087 A.Recession: F64489 A.Recession: F64489 A.Recibering pre-liminary; nucleic acid sequence not shown; translation not shown A.Residues: 1-1175 <buld. 1-1175="" <buld.="" a.map="" a.recibering="" a.residues:="" b.="" for1494096-1497623<="" gb:l77117;="" gb:u67593;="" nid:g2826427;="" pid:g1500409;="" pidn:aab99538.1;="" position:="" tc:genetics:="" td=""><td>Query Match Pest Local Similarity 21.5%; Pred. No. 3.6; Best Local Similarity 21.5%; Pred. No. 3.6; Matches 76; Conservative 58; Mismatches 131; Indels 88; Gaps 15; Qy 7 FSKSHKNPAEIVKILKD-NLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPTEA 65 Db 232 FNKFREENQDFDKYLTDENIAFRPHWKKFDEFAENIKKVIAELEGSKYKKYPGLPG 287 Qy 66 VAQLAQELYSGLLVTLIADLQIIDFEGKKDVTOFNNILRRQIGTRSPTVEXISAHPHI 125 Db 288 VLYFLGMEDAYSRYIELWKNEGEKGEEKLYNALI-ESLENRKENLEF 333</td></buld.>	Query Match Pest Local Similarity 21.5%; Pred. No. 3.6; Best Local Similarity 21.5%; Pred. No. 3.6; Matches 76; Conservative 58; Mismatches 131; Indels 88; Gaps 15; Qy 7 FSKSHKNPAEIVKILKD-NLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPTEA 65 Db 232 FNKFREENQDFDKYLTDENIAFRPHWKKFDEFAENIKKVIAELEGSKYKKYPGLPG 287 Qy 66 VAQLAQELYSGLLVTLIADLQIIDFEGKKDVTOFNNILRRQIGTRSPTVEXISAHPHI 125 Db 288 VLYFLGMEDAYSRYIELWKNEGEKGEEKLYNALI-ESLENRKENLEF 333

```
7; SPDB:SPBC14C8.14c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFLEQNYDTIF 210
: ||: | :
EELERKLDKVL 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PENLKLMMNLL 262
| : |
| CASNKEKKKNAQ 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKLIB----- 303
| |::|
GHKVLEEKGQAV 836
                                                            NIQFEAF--- 274
| |: |
KITFDEFLRII 477
                                                                                                                                                                                                                                                                      ; PID:d1033008
                                                                                                                                                                                                                                                                                                                                                                                                                           .13; Gaps 19;
                                      |: |
BRRELGDKFNP 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----- 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRSPTVEYI- 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --GIMLRECI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEGMFAGEEV 679
                         ROSL---- 229
|||| :
YELSAFKLEK 370
                                                                                                                                                                                                                                                                                                                                                                                                                                             LCGTNEKEPP 62
                                                                                                                                                                                31-Jan-2000
                                                                                                TLIK 327
|:|
TLLK 528
```

Qy

Search completed: April 12, 2004, 10:27:41 Job time: 23 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

April 12, 2004, 09:49:37 ; Search time 18 Seconds (without alignments) 974.869 Million cell updates/sec Run on:

US-10-025-730-1 1704 1 MKKMPLFSKSHKNPAEIVKI......FADEKNYLIKQIRDLKKTAP 337

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 141681 segs, 52070155 residues Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Description	Q9h9s4 homo sapien	mus m	Q9y376 homo sapien		_							Q9zq77 arabidopsis		Q9tzm2 caenorhabdi	Q99996 h a-kinase	Q9zdn2 rickettsia	-	O60094 schizosacch	075330 homo sapien					la la	0	Q14738 h serine/th	_	_	m	S	-#	LO.	10
SUMMARIES	ď	TD	MO2L_HUMAN		MO25 HUMAN	MO25 MOUSE	MO25_DROME	MO2M CAEEL	YFV6_SCHPO	DE76 CHLPR	MO2N ARATH	MO2M_ARATH	HYMA EMENI	MO2L ARATH		MO2L CAEEL	AKA9 HUMAN	Y295 RICPR	YF19 METJA	DPO5_SCHPO	HMMR HUMAN	GSHB_MOUSE	YM42 YEAST	RASO_AQUAE	YCX7_CHLVU	LATA_LATMA	2A5D_RABIT	2ASD_HUMAN	- 1	DNAB_PORPU		TIRH METJA	MSP1 PLAFC	۵,	ALM1_SCHPO
	6	9	н	н	7	٦	н	н	Н	Н	Н	Н	Н					•	ч				Н				Н								
	t t	rengen	334	334	341	341	339	338	329	321	343	343	384	348	399	339	3911	298	1175	959	724	474	1411	978	695	1401	586	602	1075	268	483	1042	1726	1726	1727
de	Query	Marcin		97	81	80	9	D O	49	S	OI.	'n	6		æ.		7.5						9.9						٠	٠	•	•	6.3	٠	٠
	9	2000	1685	1669	1381	1376	1111	1006.5	834.5	116	728	716.5	999	632	485	143.5	128.5	125.5	120	118.5	116.5	115	112.5	109.5	109	109	108.5	108.5	108.5	108	107.5	107.5	107.5	107.5	107
	Result		Н	~	m	4	ιΩ	φ	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

q à

P48637 homo sapien	Q23917 dictyosteli	Q63713 rattus norv	Q92805 homo sapien	Q59068 methanococc	P13819 plasmodium	P08569 plasmodium	O66652 aquifex aeo	Q9utj8 schizosacch	P19598 plasmodium	Q9ppz6 ureaplasma	Q02224 homo sapien
GSHB_HUMAN	REGA DICDI	RSG2_RAT	GOA1 HUMAN	YG74 METUA	MSP1_PLAFF	MSP1_PLAFM	MUTS AQUAE	RASO_SCHPO	MSP1_PLAF3	PRIM_UREPA	CENE_HUMAN
٠	Н	ч	М	Н	-	Н	н	٦	Н	Н	1
474	793	847	767	634	1701	1701	859	1290	1682	641	2663
6.2	6.2	6.2	6.2	6.1	6.1	6.1	6.1	6.1	6.1	6.1	6.0
106	105.5	105.5	105	104.5	104.5	104.5	104	104	104	103.5	103
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT	0.7.1
MO2L	
O F	MOZL HUMAN STANDARD; PRT; 334 AA. Obugga obbyss.
ב ב	
I I	(Rel. 40, Last
DŢ	41, Last
DE.	MO25-like protein.
S C). Ghordata
3 6	bukariyota; merezoa; Cinotacta; transara; betrestata; betrestata; Mammalia; Bitheria: Primates: Catarrhin; Hominidae; Homo.
ŏ	
RN	[1]
RP	
Z.	Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
R.	Shiratori A., Sudo H.,
¥ 6	Wagatsuma M., Hosoiri T., Katu Y., Kodaira H., Kondo H., Sugawara M., Tababachi M. Chiba v. Tabida s. Mirabasa Y. Con V. Tabidanis s.
Z Z	Tahii S. Kawai V. Saito K.
2	J., Wakamatsu 7
RA	Ninomiya K., Iwayanagi T.;
RT	υ
RL	
N.	[2]
RP	SEQUENCE OF 276-334 FROM N.A.
%	Pearce A.;
E.	Submitted (Jak-2001) to the EMBL/GenBank/DDBJ databases.
3 5	-:- SIMILAKII: BELONGS TO THE MOZS IMMILY.
9 8	This SWISS-PROT entry is copyright. It is produced through a collaboration
ပ္ပ	between the Swiss Institute of Bioinformatics and the EMBL outstation
ព	the European Bioinformatics Institute. There are no restrictions on its
ပ္ပ	profit institu
ပ္ပ	modified and this statement is not removed. Usage by and for commercial
ဗ္ဗ	requires a license
ខ្លួ	or send an email to license@isb-sib.ch).
2 2	639: BAB14147.1: ALT INIT
R	EMBL: AL138875; CAC28084.1;
DR	InterPro; IPR008938; ARM.
DR	InterPro, IPR004892; Mo25.
ద	
S	SEQUENCE 334 AA; 38728 MW; 97702273D8548432 CRC64;
g g	Query Match 98.9%; Score 1685; DB 1; Length 334; Best Local Similarity 99.7%; Pred. No. 1.38-100;
Ma	les 333; Conservative 0; Mi
ò	4 MPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPT 63
Ę	MDI RSKSHKNDDETVXTTXTNIL BITERODKKTDKBSERVSKSTODMKETT GTINEKEDDT 60
3	

```
124 HILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIASDA 183
                                                                     HILFMLLKGYEAPQIALRCGIMLRECIRHEPLVKIILFSNQFRDFFKYVELSTFDIASDA 180
                                                                                                                                                            184 FATFKOLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHNFA 243
                                                                                                                                                                                                                                                                                                                         244 IMIKYISKPENLKLMMNLLRDKSPNIQPEAFHVFKVFVASPHKTQPIVEILLKNOPKLIE 303
                                                                                                                                                                                                                                                                                                                                                                                      241 IMTKYISKPENLIKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPKLIE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Nakaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Parado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Baladarelli R., Tenaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T., Baldarelli R., Hall D.P., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Brada D., Brusic V., Chothia C., Corbani L.B., Cousins S., Dalla B., Dragani T.A., Fletcher C.F., Forrest A., Farzer K.S., Grimmond S., Gustholdi M., Gissi C., Godzik A., Gough J., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Kanai A., Kawaji H., Massawa Y., Kedzierski R.M., King B.L., Nonagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Nonagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pescole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Sandelin A., Schneider C., Sengle C., Sengle C., Sangle C., Satou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wanner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wang I., Yang I., Kanai T., Wahlestedt C., Wang Y., Watanabe Y., Walana A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Yasunishi A., Yaoshino M., Waterston R., Iander E.S., Rogers J., Birney B., Malayarishi Y., Walalyarishi Y., Salbazuk R., Shinagawa A., Hannayarishi Y., Walalyarishi Y., Malayarishi Y., Walalyarishi Y., Malayarishi Y., Malayarishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birney E., Hayashizaki Y., "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=FVB/N; IISSUE-Mammary gland, and Salivary gland;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 FLSSFQKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 FLSSFQKERTDDEGFADEKNYLIKQIRDLKKTAP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUB-Cerebellum, Eye, Pituitary, and Testis, MEDLINE-22384683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MO2L_MOUSE STANDARD; PRT; 334 AA. Q9DB16; Q8B652; Q91WB9; Q91XL0; 10-OCT-2001 (Rel. 40, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MO25-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
MO2L MOUSE
MO2L MOUSE
MO2L MOUSE
DT 16-0CT-
DT 10-0CT-
DE MO25-1:
OS MUSS MUSS MUSS
OC BUKATYON
OC BUKATY
                                                                     qq
                                                                                                                                                            à
                                                                                                                                                                                                                         임
                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 IMTKYISKPENLKLAMMALLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPKLIE 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Hellon E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mitting M., Madan A., Young A.C., Shevchenko Y. Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Gener than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFVASPHKTQPIVEILLK -> NSVFITNRIHGLKRWLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 BAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISAHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 FATEKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHNFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 MPLFSKSHKNPAEIVKILKDNIAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 HILFMILKGYBAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVBLSTFDIASDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 FATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHNFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH16546).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missing (In isoform 2).
/FIId=VSP 007418.
S -> P (IN REF. 1; BAB23953).
L -> R (IN REF. 2; AAH16546).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                           007418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               822F04A87FB4EB6F CRC64;
                                                                                                                                                                                                                        U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                       Note=No experimental confirmation available;
-!- SIMILARITY: Belongs to the Mo25 family.
                                                                                                                                                                                                                                                         Svent=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; DB 1;
1.4e-99;
                                                                                                                                                                                                                                                                                                                      Isoid=09DB16-2; Sequence=VSP_007417, VSP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in isoform 2).
FTId=VSP 007417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                      IsoId=Q9DB16-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.9%; Score 1669; 98.5%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AK006323, BAB23953.2, ALT INIT.
EMBL, AK030442, BAC26978.1, ALT_INIT.
EMBL, AK03642, BAC3647.1, ALT_INIT.
EMBL, AK076789, BAC36470.1, ALT_INIT.
EMBL, AK076687; BAC364313.1,
EMBL, BC016129, AAH16128.1,
EMBL, BC016128, AAH16464.1,
EMBL, BC016289, 1500031K13Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38718 MW;
                                                                                                                                                                                                        and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 329; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03204; Mo25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternative splicing VARSPLIC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                     .
U
                                                                                                                                                                                                                                                                                                                                                          Yu Y., Fu
                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                               MEDIINE=20272150; PubMed=10810093;
Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
"Identification of novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics.";
Genome Res. 10:703-713(2000).
                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                           н.
                                                                                                                                                                                                                                                                                                                                             TISSUE=Hypothalamus;
Jin W., Shi J., Ren S., Gu J., Fu S., Huang Q., Dong H.,
Wang Y., Chen Z., Han Z.,
"A novel gene expressed in the human hypothalamus.";
Submitted (DEC=1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sci. U.S.A. 99:16899-16903(2002).
                                                  301 FLSSFQKERTDDEQFADEKNYLIKQIRDLKKAAP 334
                                   FLSSFQKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
MO25 protein (CGI-66).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the Mo25 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF151824; AAD34061.1; -.
EMBL; AF113536; AAF14873.1; -.
EMBL; BC020570; AAH20570.1; -.
                                                                                                                 STANDARD;
                                                                                                                                                                                              (Human)
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acad.
                                                                                                                                                                                                                                NCBI TaxID=9606;
                                                                                                                                                                                              Homo sapiens
                                                                                                                 HUMAN
                                   304
                                                                                                      HUMAN
             g
                                                                                                                 ò
```

InterPro; IPR008938; ARM.

```
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               179
                                                                                                                                                                                                                                                60 EPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI 119
                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                239
                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CTQONILFMLLKGYESPEIALNCGIMLIRECIEHEPLAKIILWSBOFYDFFRYVEMSTFDI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 HNFTIMTKYISKPENLKLMMMLLRDKSRNIQFEAFHVFKVFVANPNKTQPILDILLKNQA 300
                                                                                                                                                              4 MPL-FSKSHKNPAEIVKILKDNLAILEKQ----DKKTDKASEEVSKSLQAMKEILCGTNEK 59
                                                                                                                                                                                                         09
                                                                                                                                                                                        1 MPFPFGKSHKSPADIVKNLKESMAVLEKQDISDKKAEKATEEVSKNLVAMKEILYGTNEK
                                                                                                                                                                                                                                                                         61 BPQTEAVAQLAQELYNSGLLSTLVADLQLIDFEGKKDVAQIFNNILRRQIGTRTPTVEYI
                                                                                                                                                                                                                                                                                                                             .20 SAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDI
                                                                                                                                                                                                                                                                                                                                                                                                              180 ASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYYTKRQSLKLLGELILDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Reprod. Dev. 34:1-7(1993).

-!- FUNCTION: ONE OF THE FIRST GENES TO BE TRANSCRIBED DURING MOUSE DEVELOPMENT, MAY PLAY SOME GENERAL FUNCTION.

-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

-!- DEVELOPMENTAL STAGE: TRANSCRIBED DURING EARLY MOUSE DEVELOPMENT.

-!- DEVELOPMENTAL STAGE: TRANSCRIBED DURING EARLY MOUSE DEVELOPMENT.

-!- DEVELOPMENTAL STAGES FROM THE BGG THROUGH THE BLASTOCYT, MOST ABUNDANT AT THE 2-CELL STAGES.

-!- SIMILARITY: Belongs to the Mo25 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miyamoto H., Marsushiro A., Nozaki M.;
"Molecular cloning of a novel mRNA sequence expressed in cleavage
stage mouse embryos.";
                                                                                                                          4
                                                                               81.0%; Score 1381; DB 1; Length 341; 81.0%; Pred. No. 3.2e-81;
                                                                                                                          Indels
                   Pfam; PF03204; Mo25; 1.
SEQUENCE 341 AA; 39869 MW; EC710A528B6F9811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 KLIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 KLIEFLSKFQNDRTEDEQFNDEKTYLVKQIRDLKRPA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEE-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last Bequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 AA.
                                                                                                                        31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93119656; PubMed=8418809;
InterPro; IPR004892; Mo25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:107438; Cab39.
InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; S51858; AAB24801.1;
                                                                                              Local Similarity 81.0 es 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MO25 protein.
MO25 OR CAB39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE
                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            006138
                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
MO25 MOUS
  8 8 8
8
                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                     임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽
```

1

```
MEDIINE-20196066; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
Adamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
Adamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,
A Sutton G.G., Wortman J.R., Yachards S., Ashburner M., Henderson S.N.,
A Button G.G., Mortman J.R., Yalang Q., Chen L.X.,
A Brandon R.C., Bazer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.W., Dong Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                  60 EPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 SAHPHILFMLLKGYBAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 ASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 HNFTIMTKYISKPENLKLMMNLLRDKSRNIQFEAFHVFKVFVANPNKTQPILDILLKNQT 300
                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                        1 MPFPFGKSHKSPADIVKNLKESMAVLEKQDISDKKAEKATEEVSKNLVAMKEILYGTNEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ASDAFATFKDLITRHKLLSAEFLEQHYDRFFSEYEKLLHSENYYTKRQSLKLLGELLLDR
                                                                                                                                                                                                                                                                 4 MPL-FSKSHKNPAEIVKILKDNLAILEKQ---DKKTDKASEEVSKSLQAMKEILCGTNEK
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96268479; PubMed=8672247;
Nozaki M., Onishi Y., Togashi S., Miyamoto H.;
Nolecular characterization of the Drosophila Mo25 gene, which is conserved among Drosophila, mouse, and yeast.";
DNA Cell Biol. 15:505-509(1996).
                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidaa, Drosophilidae, Drosophila.
                                                                                                                     Length 341;
                                                                                                                                                                                               29; Indels
Pfam; PF03204; Mo25; 1.
SEQUENCE 341 AA; 39842 MW; E7F668529D6FE811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 KLIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 KLIEFLSKFQNDRTEDEQFNDEKTYLVKQIRNLKRAA 337
                                                                                                                 DB 1;
                                                                                                                 ; Score 1376; DB 1;
; Pred. No. 6.6e-81;
32; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P91891; Q9VV85;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2003 (Rel. 42, Last sequence update)
MO25 protein (dMo25).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
                                                                                                                         80.88;
                                                                                                                                                80.78;
                                                                                                                                                                                   Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MO25 OR CG4083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DROME
                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT NO SET NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ОD
                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

```
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H.,
Jalali M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lu X., Mattei B. M., Chitcsh T.C., McLeod M.P., McPherson D.,
RA Luako P., Lei Y., Levitsky A.A., Li J. J.H., Li Z., Liang Y., Lin X.,
RA Lu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Wurphy B., Murphy L., McInton D.L.,
RA Mount S.M., Moy M., Wurphy B., Murphy L., McInton D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G.,
Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G.,
Raichert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shier B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Shier B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Syier B., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
M. Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X., Smith H.O.,
RA Shos R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
R. Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ж
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 E-AVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISAH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHILFMLLKGYE--APQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DYVVAQLSQELYNSNLLLLIQNLHRIDFEGKKHVALIFNNVLRRQIGTRSPTVEYICTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 PEILFTLMAGYEDAHPEIALNSGTMLRECARYBALAKIMLHSDEFFKFFRYVEVSTFDIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 MPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MPLFGKSQKSPVELVKSLKEAINALBAGDRKVEKAQEDVSKNLVSIKNMLYGSSDAEPPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 SDAFSTFKELLTRHKLLCAEFLDANYDKFFSQHYQRLINSENYYTRQSLKTLGELLLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 HNFTVMTRYISEPENLKLMMNMLKEKSRNIQFEAFHVFKVFVANPNKPKPILDILLRNQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDAFATFKDLLTRHKVLVADFLEQNYDTIF-EDYEKLLQSENYVTKRQSLKLLGELILDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.2%; Score 1111; DB 1; Length 339; 65.0%; Pred. No. 5e-64; ive 59; Mismatches 54; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             339 AA; 39385 MW; 5790BD91754C1C74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> H (IN REF. 1)
-> L (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 KLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 KLVDFLINFHTDRSEDEQFNDEKAYLIKQIKELK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB000402; BAA19098.1; -. EMBL; AE003526; AAF49432.1; -. Flybase; PBG0017572; MO25. INTERPO; IPR008938; ARM. INTERPO; IPR004892; MO25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF03204; Mo25; 1
CONFLICT 51
CONFLICT 102 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

KESULT 6 MO2M_CAEEL

```
ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 EPNNEQVTQLAQEVYNANVLPMLIKHIHKFEFECKKDVASVFNNLLRRQIGTRSPTVEYL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 EPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 SAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 ASDAFATFKOLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 HNFSTWNKYITSPENLKTVMELLRDKRRNIQYEAFHVFKIFVANPNKPRPITDILTRNRD 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 PLFSKSHKNPAEIVKILKDNLAILEK-----QDKKTDKASEEVSKSLQAMKEILCGTNEK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 ATDAFSTFKDLMTKHKNMCAEYLDNNYDRFFGQYSALTNSENYVTRRQSLKLLGELLLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.1%; Score 1006.5; DB 1; Length 338;
                    018211;
16-0CT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last amotation update)
16-OCT-2001 (Rel. 40, Last amotation update)
Hypothetical MO25-like protein Y53C12A.4 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78; Indels
                                                                                                                                                                                                                                                                                                                                         Kershaw J., Lennard N.; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEOUENCE 338 AA; 39431 MW; 1D0C34A35D9116F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 KLVEFLTAFHNDRTNDEQFNDEKAYLIKQIQELR 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 KLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2.3e-57
       338 AA
                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the Mo25 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z99277; CAB16486.1; -. PIR; T27129; T27129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormPep, Y53C12A.4; CE14890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
Pfam; PF03204; Mo25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 57.2
Matches 191; Conservative
  STANDARD:
                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       STRAIN=Bristol N2;
                                                                                                                                                                                                                                             NCBI_TaxID=6239;
MO2M CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
YFV6_SCHPO
DDAY BENEVIA B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
RAGALNES-1846401; PubMed=11859360;
RAGALNES-1846401; PubMed=11859360;
RA MEDELINE=21846401; PubMed=11859360;
RA Squros J., Peat N., Rajandream M.A., Lyne M., Lyne R., Stewart A., Ragarores K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Brocks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gantles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Hunckle E.J., Hunt S., Jagels K.,
A Holroyd S., Moules M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger R., Stevens K.,
RA Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitchead S.,
RA Gabel C., Fuchs M., Signares R., Schaefer M., Mulbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert E., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RA Nature 415:911-880 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as a long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 ATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHNFAI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 LFNKRPKSTODVVRCLCDNLPKLEINNDKK--KSFEEVSKCLONLRVSLCGTAEVEPDAD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LFSKSHKNPAEIVKILKDNLAILE-KODKKTDKASEEVSKSLOAMKEILCGTNEKEPPTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 AVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISAHPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 ILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIASDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.0%; Score 834.5; DB 1; Length 51.5%; Pred. No. 2e-46; Live 63; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. SEGUENCE 329 AA; 38521 MW; 073DD0607A64C952 CRC64;
                                        Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the Mo25 family.
Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GeneDB_SPombe; SPAC1834.06c; -. InterPro; IPR008938; ARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL157734; CAB75774.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004892; Mo25.
Pfam; PF03204; Mo25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 169; Conservative
                                                                                                            Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T50117; T50117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                         NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
```

181

16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C1834.06c in chromosome I.
SPAC1834.06C.

STANDARD;

SCHPO

YFV6 SCH Q9P7QB;

GEDTAC

Φ

```
16-OCT-2001
            ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
MOZM_ARATH
MO2N ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
             ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QFEAFHVFKVFVANDNKTKPVADILVANKKLTYLEDFHNDR-DDEQFKEEKAVIIKEI 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRHEPLAKIILFSNOFRDFFKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTI 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSQLDXLLTSDNYVTRRQSLKLLGELLLDRVNVKIMMQYVSDVNNLILMMNLLKDSSRSI 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QFEAFHVFKVFVASPHKTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIXQI 329
             MTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPKLIEF 304
                             242 MTRYISSAENLKLMMILLENDKSKNIQFEAFHVFKLFVANPEKSEEVIEILRRNKSKLISY 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
                                                                                                                                                                                                                                                Chlorella protothecoides.
Eukaryota, Viridiplantae, Chlorophyta, Trebouxiophyceae, Chlorellales,
Chlorellaceae, Auxenochlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETRKDVVQIFCALIRITLEDGGR-PGRDYVLAHPDVLSTLFYGYEDPEIALNCGGMFREC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 DKKTDKASEEVSKSLQAMKEILCGTNEKEPPTEAVAQLAQELYSSGLLVTLIADLQLIDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | |: |::||: ::|| ESKQDRVVEDISKAIMSIKEAIFGEDEQSSSKEHAQGIASEACRVGLVSDLVTYLTVLDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGKKDVTQIFNNILRRQI--GTRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLREC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEDYEKLLQSENYVTKRQSLKLLGEL1LDRHNFA1MTKY1SKPENLKLMMNLLRDKSPN1
                                                                                                                                                                                                                                                                                                                                                         Hortensteiner S., Chinner J., Matile P., Thomas H., Donnison I.S., "Chlorophyll breakdown in Chlorella protothecoides: characterization of degreening and cloning of degreening-related genes."; Plant Mol. Biol. 42:439-450(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37262 MW; 918FD02964B09071 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 776; DB 1;
                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                          321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56; Mismatches
                                                                                       302 LSAFHTDRKNDEQFNDERAFVIKQIERL 329
                                                                                                                                                                                16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Degreening related gene dee76 protein.
                                                                 305 LSSFQKERTDDEQFADEKNYLIKQIRDL
                                                                                                                                                                                                                                                                                                                                              MEDLINE=20256472; PubMed=10798614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ238632; CAB42595.1; -.
InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.5%;
52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 156; Conservative
                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03204; Mo25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 AA;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           NCBI_TaxID=3075;
                                                                                                                                                                                                                                                                                                                                 STRAIN=ACC25;
                                                                                                                                                         CHLPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                     O9XFY6;
                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
             ð
                                     g
                                                                ð
                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
```

RESULT 9

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 AEPVAEACAĢITĢEFFKEDTLRILITCLPKINLĒTRKDATĢVVANLGRĢĢVNSRLIASDY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 ISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 DRSNSAVMTKTVSSRDNLRILMNLLRESSKSIQIEAFHVPKLFAANQNKPADIVNILVAN 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 LEANIDLMDVLIEGFENTDMALHYGAMFRECIRHQIVAKYVLESDHVKKFFDYIQLPNFD 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 IASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDY-EKLLQSENYVTKRQSLKLLGELIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 DRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 LFKSKPRTPADLVRQTRDLLLFSDRSTSLPDLRDSKRDEKMAELSRNIRDMKSILYGNSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LFSKSHKNPAEIVKILKDNLAILEK-----QDKKTDKASBEVSKSLQAMKEILCGTNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 KEPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEY
                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Kaneko I., Katoh I., Asamizu E., Sato S., Nakamura Y., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Mo25 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 AA; 39457 MW; 46950D6A9A82FBB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 QPKLIEFLSSFQKERTDDEQFADEKNYLIKQI----RDL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 RSKLLRLLADLKPDK-EDERFEADKSQVLREIAALEPRDL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.2%; Pred. No. 4.00
tive 79; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.7%; Score 728; DB 1; 43.2%; Pred. No. 1.3e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MO2M_ARATH STANDARD; PRT; 343 AA. 09M0M4; 023570; 16-00T-2001 (Rel. 40, Created) 15-0CT-2001 (Rel. 40, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                            16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical MO25-like protein At5947540.
   343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB025628; BAB09080.1; -.
                                                             40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
Pfam; PF03204; Mo25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 147; Conserv
                                                                (Rel.
                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=3702;
```

RAY MELLEY. COLUMBIA.

RAY STRAIN-cr. COLUMBIA.

RAY STRAIN-cr. COLUMBIA.

RAY MEDITE-20083486; PubMed-10617198;

RAY MEDITE-20083486; PubMed-10617198;

RAY MEDITE-20083486; PubMed-10617198;

RAY HOLDE-20083486; PubMed-10617198;

RAY HOLDER B., Ansorpe W., Brandt P., Grivell L.A., Rieger M., Cannidthani T., Reichert B., Macher R., Mueller M., Reichert B., Macher R., Mueller M., Reichert B., McCulladhani T., Ray Medicher B., Maching M., Bancroft I., Ray Weller H., Ridley P., Brandrad B., Langham S.-A., McCulladhan D., Berze-Alonso M., Schmidthani T., Ray M., McCulladh B., Bliham L., Robben J., Vandenbussche F., Bracken M., Weller H., Ridley P., Wandenbussche F., Bracken M., McLipen I. Voet M., Bastiaens II., Aert R., Defcor E., Weizenegger T., Borde G., Rangperger U., Hilbert H., Braun M., Holzer E., Brandt A., Peters S., Van Stavern M., Ditkse W., Mocilman P., Rein Landhorst R., Nan Stavern M., Ditkse W., Mocilman P., Ray Macher B., Wanderd W., William P., Robert G., Gollen U., Villarroel R., Dogett G., Gollen U., Villarroel R., Dogett G., Gollen U., Villarroel R., Dogett G., Gollen U., Willarroel R., Dogett G., Rangpers G., Gollen U., Willarroel R., Dogett G., Ray M., Lennard N., McLing K., Dogett G., Ray M., Lennard N., McLing R., Ray M., Lennard N., McLing R., Ray M., Lechar S., Gollen G., Ruddey K., Danger G., Gollen D., Hangel S., Farnder R., Massen C., Schaffer M., Willer R., Perlay R., Ray Massen C., Gollen G., Mendler M., Tenlan B., Granderath K., Danger S., Grands R., Ray Massen C., Gollen G., Mendler M., Petron D., Jesser T., Ray Massen C., Gollen D., Lidyori R., Palan R., Ray Massen C., Schmidt W., Lechardie M., Tenlan R., Andrews S., Francs P., Francs B., Ray Armerl D., Schmidt W., Lechardie M., Tenlan R., Schmidt W., Lechardie M., Tenlan R., Schmidt W., Lechardie M., Schmidt M., Schmidt M., Schwig C., Sun H., M., Scott K., Mewes H., W., Stocker S., Paralet D., Courdes W., Mandis E., Dante M., Debin S., Schmidt W., Schwig C., Sun H., Lanz B., Berley D., Preston M., Maris E., Dante M., Debin S., Scho MEDLINE-98121113; PubMed-9461215;
MEDLINE-9812113; PubMed-9461215;
MEDLINE-981213; PubMed-9461213;
MEDLINE-981213; PubMed-981213;
MEDLINE-981213;
MEDLINE-981213; PubMed-981213;
MEDLINE-AT4G17270 OR DL4670W.

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TAXID=3702; Hypothetical MO25-like protein At4g17270. Nature 391:485-488(1998). Arabidopsis thaliana."; SEQUENCE FROM N.A. SEQUENCE FROM N.A.

between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN=cv. Columbia;

MEDIAINE=2554850; PubMed=14593172;

A Yamada K., Lim J., Daled J.M., Chen H., Shinn P., Palm C.J.,

A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Coriumi M.J.,

A Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

A Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

Kamiya A., Meyers C., Nakajima M., Narusaka M., Saki M., Sakurai T.,

Satou M., Tamse R., Vayaberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis This SWISS-PROT entry is copyright. It is produced through a collaboration 59 KEPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEY 118 119 ISAHPHILFMILKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFD 178 179 IASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDY-EKLLQSENYVTKRQSLKLLGELIL 237 DRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKN 297 244 DRSNSAVWIKYVSSMDNLRILMNLLRESSKTIQIEAFHVFKLFVANQNKPSDIANILVAN 303 28 4 LFKSKPRTPADIVRQTRDLLLYADRSNSFPDLRESKREEKMVELSKSIRDLKLIYGNSE 63 6 LFSKSHKNPAEIVKILKDNLAILEK-----QDKKTDKASBEVSKSLQAMKEILCGTNE -!- SIMILARITY: Belongs to the Mo25 family. Gaps Chen E., Marra M.A., Martienssen R., McCombie W.R.; "Seguence and analysis of chromosome 4 of the plant Arabidopsis , 6 Length 343; Indele 343 AA; 39650 MW; D340B49A4924B7D1 CRC64; 42.0%; Score 716.5; DB 1; 42.9%; Pred. No. 6.9e-39; Live 78; Mismatches 105; : ||: |: :: : ||: | 304 RNKLLRILADIKPDAK-EDERFDADKAQVVREIANLK 338 298 QPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLK 333 EMBL; Z97343; CAB10508.1; ALT_SEQ. EMBL; AL161546; CAB78730.1; -. EMBL; AF380659; AAX55740.1; -. Science 302:842-846(2003). gene model prediction. InterPro; IPR008938; ARM. InterPro; IPR004892; Mo25. Nature 402:769-777(1999). Matches 144; Conservative Pfam; PF03204; Mo25; 1. Hypothetical protein. Local Similarity SEQUENCE Query Match RRARE RRARE RRARE RRAPA ò 셤 ò 셤 δ ద ö g à

ä,

```
16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 ELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILR----RQIGTRSPTVEYI-SAHPHIL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 AMLHEDLLYELAVALHNLPPEARKDTQTIFSHILRFKPPHGNSPDPPVISYIVHNRPEII 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 IELCRGYEHSQSAMPCGTILREALKFDVIAAILLYDQSKEGEPAIRLTEVQPNVPQRGTG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIKROSLKLIGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 KNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPTEAVAQLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 RQPSDVVRSIKDLLLRL-REPSTASKVEDELAKOLSOMKLMVQGTQELEASTDQVHALVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -FRDFFKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEK-LLQSENY
                                                                                                                                                                                                                          conserved and highly expressed protein of Aspergillus nidulans."; Mol. Gen. Genet. 260:510-521(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPHKTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
                                                                                                                                                                        SEQUENCE FROM N.A.
MEDITE=99126010; PubMed=9928930;
Karos M., Fischer R.;
"Molecular characterization of HymA, an evolutionarily highly
                                                                                                                        Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Burotiales, Trichocomaceae, Emericella.
NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 FMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                        44392 MW; 2E203D0D110C5FD6 CRC64;
                                                                                                                                                                                                                                                    FUNCTION: Required for conidiophore development. SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.1%; Score 666; DB 1; 39.8%; Pred. No. 1.3e-35;
                                                          (Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                        384 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 40, Created)
(Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the Mo25 family.
                                                                                                             Emericella nidulans (Aspergillus nidulans)
                                                                                    Conidiophore development protein hymA.
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ001157; CAA04556.1; -.
                                             (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140; Conservative
                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PF03204; MO25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001
16-OCT-2001
                                             16-OCT-2001
                                                          16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MO2L ARATH
Q9ZQ77;
                      HYMA EMENI
060032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
MO2L_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the buspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 ISAHPHILFMLLKGYBAP-QIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 LESNLDVIDSLVEGIDHDHELALHYTGMLKECVRHQVVAKYILESKNLEKFFDYVQLPYF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 IDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFBAFHVFKVFVASPHKTQPIVEILLK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 LFSKSHKNPABIVKILKDNLAILEKQDKKTDKASE-----EVSKSLQAMKEILCGTNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LFKNKSRLPGEIVRQTRDLIALAESEEEETDARNSKRLGICAELCRNIRDLKSILYGNGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 KEPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 DIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYE-KLLQSENYVTKRQSLKLLGELI
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=20083487; PubMed=10617197;
MEDLINE=20083487; PubMed=10617197;
MEDLINE=20083487; PubMed=10617197;
Euin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum T.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam I.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                              Eukaryofa, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.1%; Score 632; DB 1; Length 34 38.7%; Pred. No. 1.7e-33; ive 80; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 NQPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLK----KTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 NRTKILRLFADLKPEK-EDVGFETDKALVMNEIATLSLLDIKTA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l protein.
348 AA; 40000 MW; AB1D92EA2E2B900E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the Mo25 family.
Hypothetical MO25-like protein At2g03410.
AT2G03410 OR T4M8.16.
                                                                 Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AC006284; AAD17435.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
Pfam; PF03204; Mo25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B84448; B84448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYM1_YEAST
ID HYM1_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
```

```
63 TEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISAH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical MO25-like protein T27C10.3 in chromosome I.
T27C10.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhu H.J., Gravee T., Hawkins M.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                           293 ILLKNOPKLIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKK 334
                                                                                                                                                                                                                                                            315 ILVKONRDKLLTYFKTFGLD-SQDSTFLDEREFIVQEIDSLPR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 AA; 40232 MW; E7DA45CA33F2947E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.4%; Score 143.5; DB 1; 9.3%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the Mo25 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.3%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF098504; AAC67411.1; -.
BUR; T3347; T3347.
Wormbep; T27210 3; CE19605.
InterPro; IPR008938; ARM.
InterPro; IPR04892; Mo25.
Pfam; PF03204; Mo25.
Hypothetical procein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                CAEEL
                                                                 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                  CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                        셤
                                                                                                                                                    ద
                                                                                                                                                                                                             Db
                                                              ð
                                                                                                                         ð
                                                                                                                                                                                   8
                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 FSKSHKNPAEIVKILKDNLAILEK----QDKKTDKASEEVSKSLQAMKEILCGTNEKEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20157038; PubMed=10655212;
Dorland S., Deegenaars M.L., Stillman D.J.;
"Roles for the Saccharomyces cerevisiae SDS3, CBK1 and HYM1 genes in
                                                                                                                                                                                                                                                                                             MEDLINE=94205264; PubMed=8154185; Wiemann S., Voss H., Schwager C., Rupp T., Stegemann J., Zimmermann J., Grothues D., Sensen C., Erfle H., Hewitt N., Banrevi A., Ansorge W.; Sequencing and analysis of 51.6 kilobases on the left arm of chromosome XI from Saccharomyces cerevisiae reveals 23 open reading frames including the FASI gene.";
                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Maia e Silva A., Bossier P., Vilela C., Fernandes L., Soares H., Guerreiro P., Rodrigues-Pousada C.; Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                        MEDLINE=33348778; PubMed=8394042;
Cheret G., Mattheakis L.C., Sor F.;
"DNA sequence analysis of the YCN2 region of chromosome XI in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO: GO: 0005622; C:intracellular; IDA.
GO: GO: 0016564; F:transcriptional repressor activity; IMP.
GO: GO: 0007109; P:cytokinesis, completion of separation; IMP.
GO; GO: 0008360; P:regulation of cell shape; IGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.5%; Score 485; DB 1; Length 399; 33.0%; Pred. No. 4.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45853 MW; F48860754C892BA9 CRC64;
            01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the Mo25 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcriptional repression by SIN3.";
Genetics 154:573-586(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X69765; CAA49422.1; -.
EMBL; X74151; CAA52249.1; -.
EMBL; Z28189; CAA82032.1; -.
                                                                                                                                                                                                                                      Saccharomyces cerevisiae.";
Yeast 9:661-667(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    (east 9:1343-1348(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S34681; S34681.
GermOnline; 139944; -.
SGD; S0001672; HYM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03204; MO25
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                               SEQUENCE FROM N.A.
                                                        HYM1 protein.
HYM1 OR YKL189W.
                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [4]
GENE NAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                            232
PHILFMLLKGYE-----APQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELS 175
                                                                                                                                                                                                                                                                                                                                                233 GELILDRHNFAIMTKYISKPENLKIMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVE 292
                                                                                                                                                                                                                                                                                                                                                                                                            255 ASLIVIRSNNALMNIYINSPENLKLIMTLMTDKSKNLQLEAFNVFKVMVANPRKSKPVFD 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 SENYVTKROSLKLIGELILDRHNFAIMTKYISKPENLKIMMNLLRDKSPNIQFEAFHVFK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 TFDIASDAFATFKDLLTRHKVLVA-DFL--EQNYDTIFEDYEKLLOSENYVTKROSLKLL
                                                                                                                                                                                                                                                            159 ILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 CSNFFIQAKSFKFLNELFTAQTNYETRSLMMAEPAFIKLVVLAIQSNKHAVRSRAVSILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 VFVASPHKTQPIVEILLKNQPKLIEFL-----SSPQKERTDDEQFAD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

```
Takahashi M., Shibata H., Shimakawa M., Miyamoto M., Mukai H., Ono Y.; "Characterization of a novel giant scaffolding protein, CG-NAP, that anchors multiple signaling enzymes to centrosome and the Golgi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and characterization of a cDNA encoding an A-kinase anchoring protein located in the centrosome, AKAP450.";
                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
4-Kinase anchor protein (Protein kinase A anchoring protein 9)
(PRKA9) (A-Kinase anchor protein 450 kDa) (AKAP 450) (A-Kinase anchor protein 50 kDa) (AKAP 350) (ARAP 450) (A-Kinase anchor (Hyperion protein) (Yotiao protein) (Centrosome- and Golgi-localized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lin J.W., Wyszynski M., Madhavan R., Sealock R., Kim J.U., Sheng M., "Yotiao, a novel protein of neuromuscular junction and brain that interacts with specific splice variants of NMDA receptor subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Lung;
Milgram S.L., Goldenring J.R., Schmidt P.H.;
"AKAP350: A multiply spliced family of proteins with centrosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schmidt P.H., Dransfield D.T., Claudio J.O., Hawley R.G.,
Trotter K.W., Milgram S.L., Goldenring J.R.,
"AKAP350, a multiply spliced protein kinase A-anchoring protein
associated with centrosomes.";
                                                                                                                                                                                                                                              AKA9 HUMAN STANDARD; PRT; 3911 AA.
Q9996; 014869; 043355; 094895; Q9UQH3; Q9UQQ4; Q9X6RB; Q9X6YZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99219864; PubMed=10202149;
Witczak O., Skaalhegg B.S., Keryer G., Bornens M., Tasken K.,
Jahnsen T., Oerstavik S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANT GLN-1347 INS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kemmner W.A., Deiss S., Schwarz U.;
"Cloning of Hyperion.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C., Becker M., Hawkins M.;
8) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 2157-3911 FROM N.A. (ISOFORM 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1802-3876 FROM N.A. (ISOFORM 5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 323-3911 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKN-associated protein) (CG-NAP).
AKAP9 OR AKAP450 OR AKAP350 OR KIAA0803.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 274:17267-17274(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deiss S., Schwarz U.;
perion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 274:3055-3066(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99287934; PubMed=10358086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Gastric parietal cell;
MEDLINE=99115654; PubMed=9915845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98151389; PubMed=9482789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurosci. 18:2017-2027(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1)
---EKNYLIKQIRDLKK 334
                                        :: : |:: | :: | 268 WDMQRPFTQEQLQDFEE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 18:1858-1868(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hinds K., Sutterer C. Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Lymphoblast;
Hinds K., Sutterer (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apparatus.
                                                                                                                                                                                                             AKA9 HUMAN
                                                              ДQ
                                                                                                                                                                                                                                                  HDD THE SET THE SET OF SET OF
```

```
Wu X., Graves T., Bradshaw H.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Binds to type II regulatory subunits of protein kinases
A. Scaffolding protein that assembles several protein kinases and
phosphatases on centrosome and Golgi apparatus where physiological
events can be regulated by phosphorylation state of protein
substrates. Isoform 4/Yotiao is associated with the N-methyl-D-
aspartate receptor and is specifically found in the neuromuscular
junction (NMJ) as well as in neuronal synapses explaining that its
role may be to organize postsynaptic specializations.

-!- SUBMINT: Interacts with the regulatory region of protein kinase N
(FKN), protein phosphatase 2A (FP2A), protein phosphatase I (FPI)
and the immature non-phosphorylated form of PKC epsilon.

-!- SUBGELLUAR (CONTIONAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isold=099996-6; Sequence=VSP 004106, VSP 004107, VSP 004109; -:- TISSUE SPECIFICITY: Widely expressed. Isoform 4/Yotiao is highly expressed in skeletal muscle and in pancreas.
-:- DOMAIN: RIL-binding site, predicted to form an amphipathic helix, could participate in protein-protein interactions with a complementary surface on the R-subunit dimer.
-:- CAUTION: Ref. 6 sequence differs from that shown due to two frameshifts in positions 3782 and 3811.
-:- CAUTION: Ref. 9 sequence differs from that shown due to four frameshifts in positions 29, 1653, 1699 and 1735.
                                                                                                 MEDLINE=99087487; PubMed=9872452; Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Protani H., Nomura S., Tanaka A., Totani H., Tanaka A., Teotani H., Tomura S., The Complete sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=3; Synonyms=CG-NAP;
IsoId=Q99996-3; Sequence=VSP_004102, VSP_004105, VSP_004107;
                    Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=4; Synonyms=Yotiao;
IsoId=Q99996-4; Sequence=VSP_004103, VSP_004104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q99996-2; Sequence=VSP_004102, VSP_004107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=6;
                                                             SEQUENCE OF 2212-3911 FROM N.A. (ISOFORM 2/3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9996-5; Sequence=VSP_004108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q99996-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC004013; AAB96867.1; ALT_FRAME. AF091711; AAD39719.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AC000066; AAC60380.1; ALT FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytoplasmic in parietal cells. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 604001; -.
GO; GO:0005813; C:centrosome; TAS.
                                                                                                                                                                                                             for large proteins in vitro.";
DNA Res. 5:277-286(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ131693; CAB40713.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AB019691, BAA78718.1; -. AJ010770, CAA09361.1; -. AF026245; AAB86384.1; -.
                                                                                                                                                                                                                                                                             SEQUENCE OF 17-1800 FROM N.A. Wu X., Graves T., Bradshaw H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=6; Synonyms=AKAP350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF083037; AAD22767.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB018346; BAA34523.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:379; AKAP9.
association.";
                                                                                     TISSUE=Brain;
                                                                                                                                                                                                                                                                                                        Wu X., Gra
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
```

```
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005856; C:cytoskeleton; TAS.
GO; GO:0005515; F:N-methyl-D-aspartate receptor-associated pr. .; TAS.
GO; GO:0005515; F:protein binding; TAS.
GO; GO:0007165; P:signal transduction; TAS.
GO; GO:0007268; P:synaptic transmission; TAS.
GO; GO:000610; P:transport; TAS.
Coiled coil; Alternative splicing; Polymorphism.
DOMAIN 164 914 COILED COIL (POTENTIAL)
DOMAIN 944 1022 COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STTOFHAGWRR -> ALSLTTSWQHHSARPTAPLFFEILSH
SLG (in isoform 6).
/FTId=VSP_004109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 VKILKDNLAILEKODKKTDKASEEVSKSLQAMKEILCGTNEKEPPTEAVAQLAQELYSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 115; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP_004106.
YPGPYMMCPSTLC -> GSSIPELAHSDAYOTREICSS
in isoform 2, isoform 3 and isoform 6)
FTId=VSP_004107.
                                                                                                                                                                                                                                                                                                                                                                                  (in isoform 2 and isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 128.5; DB 1; Length 3911;
Pred. No. 3.5;
i Mismatches 116; Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (in isoform 4).

Frid=VSP 004104.

Missing (in isoform 3).

Frid=VSP 004105.

SADTFGKWE.

SADTFGKWE.

Frid=VSP 004106.
                                                                                                                                                                                                                                                                                                                                                                                                FTId=VSP_004102.
|LOEEI -> LATRRD (in isoform 4)
|FTId=VSP_004103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
(2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F. 1 AND 2 AND 2 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND 2)
                                                                                                                                                    (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (in isoform 5).
                                                                                                                                                                                                                                                                                          COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> P (IN REF. 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           010926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REF
                                                                                                                                                  COLLED COLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K -> KQ. T
/FTId=VAR_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N -> P (I
N -> D (I
N -> D (I
N -> P (I
N -> D (I
N -> P (I
N -) P (I
N -> P (I
N -) P (I
N -> P (I
N -) P
                                                                                                                                                                                                                                                                                                                                      GLN-RICH.
GLU-RICH.
                                                                                                                                                                                                                                                                                                                                                                    GLU-RICH,
                                                                                                                                                                                                                                                                                                                                                                                  Wissing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Missing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ^ ^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.5%; Scu.
20.1%; Pred
75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                        3470
3489
3730
292
1010
                                                                                                                                    1022
1185
11885
11392
11459
1659
2455
2561
3092
                                                                                                                                                                                                                                                                                                                                                                                                              1642
                                                                                                                                                                                                                                                                                                                                                                                                                                            3911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1001
1020
1028
1626
1703
1707
1803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              663
913
956
982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                1434
1585
1857
2544
                                                                                                                                                                                                                                                                                                                                                                                                                                           1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2175
                                                                                                                                                                  1253
                                                                                                                                                                                                                                                          2603
                                                                                                                                                                                                                                                                                        3124
3587
3726
                                                                                                                                                                                                                                                                                                                                    203
321
1846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2895
                                                                                                                                                     1100
                                                                                                                                                                                                                                                                                                                                                                                                              1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                  DOMAIN
                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
Matches
   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

-----GIRSPIVEYISAHPHI 125

78 LLVTLIADLQ--LIDFEGKKDVTQIFNNILRRQI

ò

::

-::

```
237
                                                                                                                               918 NPTIVKAKSSVFDEDKTFVA---ETLEMGEVVEKDITELMEKLEVTKREKLELSQRLSDL 974
--ISKLKDLQQSLVNSKSEEMTLQI--NELQKEIEILRQEEKEKGTLEQEVQELQLKTEL 766
                                  LFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIASDAFA 185
                                                                                                                                                                                                                    858 QRNTFSFAEKOFEVNYQELQEEYACLLKVKDDLEDSKOKQELEYKSKLKALNEELHLQRI 917
                                                                                                                                                                                                                                                       265 KSPNIQFEA--FHVFKVFVASPHKTQPIVEILLKNQPKLIEFLSSFQKERTD-DEQFAD- 320
                                                                       ----NDLQEKFAQLEAEN-SILKDEKK 797
                                                                                                                                                                                    ---YISKPENLKLMMNLLRD 264
                                                                                                        TFKOLLTRH-----KVLVADFLE-ONYDTIFEDYEKLLOSENYVTKROSLKLLGELIL
                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: April 12, 2004, 10:27:07 Job time : 20 Secs
                                                                                                                                                                                                                                                                                                                                                        975 SEQLKQKHGEISFLNEEVKSLKQ 997
                                                                                                                                                                                                                                                                                                                                 321 -----EKNYLIKQIRDLKK 334
                                                                                                                                                                                  238 DRHNFAIMTK
                                                                     767 LEKOMKEKE-
                                                                                                          186
                                                                                                                                             198
                                    126
                                                               q
                                                                                                      à
                                                                                                                                     a
                                                                                                                                                                            ठ
                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                     \stackrel{\diamond}{\delta}
                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                               à
                                  ઠે
```

```
April 12, 2004, 10:20:07; Search time 45 Seconds (without alignments) 2362.881 Million cell updates/sec
                                                                                                                                                                            1704
1 MKKMPLFSKSHKNPAEIVKI.....RADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                            1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp fundi: *
sp numan: *
sp invertebrate: *
sp mammal: *
sp mc and sp organelle: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp plant:*
sp rodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPTREMBL 25:*
: sp_archea:*
: sp_bacteria:*
                                                                                                                                                               US-10-025-730-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11:
12:
13:
                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                            Searched:
                                                                                              Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Q8vdz8 mus musculu Q74x0 homo sapien Q803v8 brachydanio Q21643 caenorhabdi Q722a5 caenorhabdi Q8x312 mus musculu Q81312 mus musculu Q813k5 neurospora Q81133 oryza sativ Q813k5 neurospora Q8113 oryza sativ Q813k5 neurospora Q81143 oryza sativ Q86038 helicobacte Q25188 helicobacte Q26049 helicobacte Q9wxu3 thermotoga Q96fgl homo sapien Description SUMMARIES Q96FG1 Q8VDZ8 Q7Z4X0 Q803V8 Q21643 Q7Z2AS Q8K31Z Q8K31Z Q8K31Z Q8K31Z Q8K31Z Q7YYL6 O25188 O26049 Q9WXU3 QBLIF3 QBK038 DB Query Match Length 1381 1243 1266.5 1066.5 1063.5 1063.5 671.5 651.5 630.5 130.5 123.5 Score Result Ño.

_	- 1	O97291 plasmodium Q81eh2 plasmodium Q81eh2 plasmodium Q81ak6 plasmodium Q9yge7 oncorhynchu Q9yge7 hono saplen		രഗയ
6 QBREF7 Q9VGE4 QBIN90 Q9VEC7 Q9VFM7	Q9GSH4 Q8T133 Q9NJQ4 6 Q8EUI7 Q8I293 Q9UOK5	097291 1 08R436 Q81EH2 Q81EK6 3 Q9YGE7 09UFS4	QUENTE QU	Q9VFB1 Q26216 1 Q80WJ9 6 O51465 6 Q98QP8
មេខភភភ	808 808 1135 911 10 1389 51111			429 5 771 5 974 1 166 1 819 1
00000		8		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
119.5 118.5 118.5 118.5	117 116.5 116 116 116	115.5 115 114.5 114.1113.5	113.5 113.5 113.5 113.5 113	111.5 111.5 111 111 111
11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	. W W W W W 4.	4 4 4 4 4 1 5 6 4 5

ALIGNMENTS

7

4,

120

9

180

```
60 EPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                          241 HNFTIMTKYISKPENLKLAMMILRDKSRNIQFRAFHVFKVFVANPNKTQPILDILLKNQA 300
                                                                                                                                                                                                                                                                                                                                                           120 SAHPHILFMILKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDI 179
                                                                                                                                                                                                                                                                                                                                                                                                                        180 ASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKKLGELILDR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 HNFAIMTKYISKPENLKIMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 KEPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 MPL-FSKSHKNPAEIVKILKDNLAILEK----QDKKTDKASEEVSKSLQAMKEILCGTNE 58
                                                                                                                                                                                                                                             4 MPL-FSKSHKNPAEIVKILKDNLAILEKQ---DKKTDKASEEVSKSLQAMKEILCGTNEK
                                                                                                                                                                                                                                                                                                               61 EPQTEAVAQLAQELYNSGLLSTLVADLQLIDFEGKKDVAOIFNNILRROIGTRTPTVEY1
                                                                                                                                                                                                                                                                                                                                                                               61 KEPQTEAVAQLAQELYNTNLLISLIANLQRIDFEGKKOVVHLFSNIVRRQIGARTFTVEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterggii, Neopterggii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae; Danio.
NCBI_TaxID=7955,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 343;
                                                                                                                                                             Length 341;
                                                                                                                                                          Query Match
78.8%; Score 1343; DB 4; Length 3
Best Local Similarity 79.5%; Pred. No. 5.9e-88;
Matches 268; Conservative 31; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.6%; Score 1288.5; DB 13; Lengt 72.3%; Pred. No. 4.6e-84; Live 49; Mismatches 40; Indels
                                          SEQUENCE FROM N.A.
Zhou Y., Yu L., Zhao S.Y.;
Zhou Y., Yu L., Zhao S.Y.;
"cloning of a new human cDNA homologous to MO25 gene.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF134480; AAP97257.1; -.
SEQUENCE 341 AA; 39774 MW; D3A60160E78C7A6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R., Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC044172; AAN44172.1; -.
InterPro; IPR00893; ARM.
InterPro; IPR004892; Mo25.
Fram; PF03204; Mo25; 1.
SEQUENCE 343 AA; 39820 MW; F10450DA0446268A CRC64;
Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 KLIBFLSSFQKERTDDEQFADEKNYLIKQIRDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similar to MO25 protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 72.3
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                  NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003
Mammalia;
                                                                                                                                                          Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q803V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
Q803V8
SORRERES
                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                    엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                     임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                              LKLLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQ 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 EPPTEAVAQLAQELYSSGLLVTLIADLQLIDFECKKDVTQIFNNILRRQIGTRSPTVEYI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 SAHPHILFMLLKGYBAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CTQQNILFMLLKGYESPEIALNCGIMLRECIRHEPLAKIILWSEQFYDFFRYVEMSTFDI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 ASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 HNFTIMTKYISKPENLKLMMNLLRDKSRNIQFEAFHVFKVFVANPNKTQPILDILLKNQT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 MPL-FSKSHKNPAEIVKILKDNLAILEKQ---DKKTDKASEEVSKSLQAMKEILCGTNEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MO25-like protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                              Score 1381; DB 11; Length 341; Pred. No. 1.2e-90;
                                                                        289 PIVEILLKNOPKLIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC020041; AAH20041.1; -.
MGD; MGJ: INCA438; Cab39.
InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39843 MW; E7FECA529D6FE811 CRC64;
                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 KLIEFLSKFONDRIEDEGFNDEKTYLVKQIRDLKRAA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 KLIEFLSSFOKERTDDEOFADEKNYLIKQIRDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.0%;
81.0%;
                                                                                                                                                                                                                       20,
20,
25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 81.0 Matches 273; Conservative
                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                 MO25 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q7Z4X0;
                                                                                                                                                                                      Q8VDZ8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q7Z4X0
                                                                                                                                                                                                                                                                                    CAB39
                                                                                                                                                     RESULT 2
Q8VDZ8
ID Q8V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7Z4X0
                                      g
                                                                                                                                                                                                      AC AC DIT DIT DIT DIT DIT OC OC
                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db
```

'n

Gaps

. .

9

224

```
225 KROSLKLLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASP 284
  LRRQIGTRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQ 164
                                                                               165 FRDFFKYVELSTFDIASDAFATFKDLITRHKVLVADFLEQNYDTIFEDYEKLLQSENYVT
                                                                                                                                                                                                                                               285 HKTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKKT 335
                                                                                                                                                                                                                                                                       "The sequence of C. elegans cosmid R02E12.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43470 MW; 8F9B8AA070216176 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein R02E12.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.4%; Score 1063.5; DB 60.5%; Pred. No. 5.9e-68; ive 53; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                377 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 MP-LFSKSHKNPAEIVKILKDNLAILEK-----
                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     investigating biology. The C.
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; US3337; AAP40522.1; -. Hypothetical protein. SEQUENCE 377 AA; 43470 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 60.5 Matches 211; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=Bristol NZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leimbach D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R.;
105
                                         378
                                                                                                                                                                                                                                                                                                                                                                                         Q722A5
Q722A5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R02E12.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                              g
                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                   ACCOCCOORDITATION OF THE SECTION OF 
                            g
                                                                         ⋩
                                                                                                                                                               à
                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                  RHNFAIMTKYISKPENLKIMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQ 298
                                                                                                                                                                                                      241 RHNFTVATKYISRAENLKLAMAMALRDNSRNIQFEAFHVFKVFVANPNKTQPVLDILLKKNG 300
          ISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 AMKEILCGTNEKEPPTE---AVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------QDKKTDKASEEVSKSLQ 47
                                                                                        179 IASDAFATFKDLITRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The sequence of C. elegans cosmid R02E12.";
Submitted (##R~1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72282 MW; 85D5853E9F0E3193 CRC64;
                                                                                                                                                                                                                                                          PKLIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                               301 SKLVEFLSHFQTDRSEDEQFCDEKNYLIKQIRDLKRPAP 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
62.6%; Score 1066.5; DB
Best Local Similarity 60.4%; Pred. No. 6.8e-68;
Matches 212; Conservative 53; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKMP-LFSKSHKNPAEIVKILKDNLAILEK----
                                                                                                                                                                                                                                                                                                                                                                                                             636
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2001) to the EM EMBL; U53337; AAA96186.2; PIR; T16650; T16651. PIR; T16651; T16651. WormPep; R02812.2a; CB28410. InterPro; IPR008938; ARM. InterPro; IPR004892; Mo25.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 01, (TrEMBLrel. 18, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF03204; Mo25; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. R02E12.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l protein.
636 AA; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leimbach D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston
                                                                                                                                                                          239
                                                                                                                                                                                                                                                            299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            021643;
                                                                                                                                                                                                                                                                                                                                                                                                        021643
                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                              Op
                                                                                      ð
                                                                                                                      qq
                                                                                                                                                                    ò
                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                            g
        8
                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ωþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

```
Э,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KSFIYGNDSAEPSSEHVVQVAQLAQEVYNANILPMLIKMLPKFEFECKKDVGQIFNNLLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 RQIGTRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ODKKTDKASEEVSKSLQAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 KEILCGINEKEPPTE---AVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILR
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68; Indels 17; Gaps
                                                                                                                                                                                        "Genome Sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5; Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
```

```
Q7XIQ4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                       임
                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                   181 TFFLYVQSEVFDISSDAFSTFKELTTRHKAIJABFLDSNYDTFFAQYQNLLNSKNYVTRR 240
                                                                  61 LLSARFLEQHYDRFFSEXEKLIASENYVTKRQSLKLIGELLIDRHNFTIMTKYISKPENI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 KLAMALLEDKSRNIQFEAFHVFKVFVANPNKTQPILDILLKNQTKLIEFLSKFQNDRTED 180
                                                     QSLKLLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 PQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 VLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHNFAIMTKYISKPENL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLMMNILRDKSPNIQFBAFHVFKVFVASPHKTQPIVEILLKNQPKLIEFLSSFQKERTDD 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFFKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypotherical profess.

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                301 PKPISDILNRNREKLVEFLSEFHNDRTDDEQFNDEKAYLIKQIQEMKSS 349
                                                                                                   287 TQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKKT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC029053; AAH29053.1; -.
InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
Pfam; PF03204; Mo25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   205 AA; 24582 MW; 015261A02F808169 CRC64;
                                                                                                                                                                                                      01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to calcium binding protein, 39 kDa (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.3%; Score 875; DB 11;
83.6%; Pred. No. 7.9e-55;
                                                                                                                                                                                    205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 AA
                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQFADEKNYLIKQIRDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity 83.6
168; Conservative
                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                      227
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8L9L9;
                                                                                                                                                                                              Q8K312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  616180
                                                                                                                                                                                  Q8K312
                                                                                                                                                                                                                                                       CAB39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     081919
1D 08
AC 08
AC 08
DT 01
DT 01
DE HY
OC BU
OC SE
OC SE
OC OC OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best
                                                                                                                                                                       Q8K312
                                                                           g
                                                                                                                      a
                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                           QQ
                                                   ð
                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \overset{\circ}{\alpha}
```

```
247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 QLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISAHPHILF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 MLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIASDAFATF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 YISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPKLIEFLSS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 KNPAEIVKILKDNLAILEKQD----KKTDKASEEVSKSLQAMKEILCGTNEKEPPTEAVA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 KTPQEVVKAIRDSLMALDTKTVVEVKALEKALBEVEKNFSSLRGILSGDGETBPNADQAV 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 KDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHNFAIMTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza Sativa (japonica cultivar-group).
Bukaryota, Viridplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                            z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٠.
د
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 345;
                                                    Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; "Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, 10-10-201316, A04.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003822; BAC79608.1;
Hypothetical protein.
SEQUENCE 337 AA; 38866 MW; B43138F9464720C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.4%; Score 671.5; DB 10; Length 42.9%; Pred. No. 5e-40; ive 68; Mismatches 113; Indels
                                                                                                                                                                                                                                               Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell Feldmann K.,
                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AX088359, AAM65898.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 345 AA; 39841 MW; 2C46A3D3DEBB47AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                      "Full-Length cDNA from Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 LSPGKGSEDDQFEEEKELIIBEIQKL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 FOKER-TDDEOFADEKNYLIKOIRDL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2003 (TrEMBLrel, 25, Last and
Hypothetical protein OJ1316_A04.107.
OJ1316_A04.107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
Pfam; PF03204; Mo25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 140; Conservative
                                                                                                                                                                 Genome Biol. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=39947;
                                                                                                                                          annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
```

2,

```
clone:0J1316
                                                                                                                                                      216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSLIF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                  셤
                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                               ò
                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCOCCOS DETAILS OF THE SERVICE OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                    'n
                                                                                                                                                                                                                                                                   EKEPPTBAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVE 117
                                                                                                                                                                                                                                                                                                             DIASDAFATFKDLLITRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 DRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVELLLKN 297
                                                                                                                                                                                                                                                                                                                                                                                                         YISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 MPLFSKSHKNPA----EIVKILKDNLAILEKQDKKTD-KASEEVSKSLQAMKEILCGTN 57
                                                                                                                                                                        68 QLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVE-----YISA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 ÓLVTGMIBEDLLYLLAINLYRLPFDSRKDTQVIFSYVFRFRPPNAPARAEPLALAYVVER 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 RPOVLIELCKGYDHKESAQHAGTVLKELİKSSEAATAVILHDDGDEPGSSARGVGAIDRN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 DIASDAINTEKDLLIKHEAAVSEFLCSHYEQFFELYTRLLISINYVIRRQSVKFLSEFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 SKSHKNPAEIVKILKDNLAILEKODKKTDKASEEVSKSLQAMKEILCGINEKEPPTEAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S ARTRINVSDLPRQAREHVV----KLDQGPQGKVEBLAKVLSQMKQLLQGTHEQEASLEHQY
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Holland R.,
                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35;
              Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.5%; Score 639.5; DB 3; Length 370; 37.2%; Pred. No. 1e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 HPHILFMLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
38.2%; Score 651.5; DB 10; Length 40.9%; Pred. No. 1.3e-38; Live 76; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         German Neurospora genome project;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX284746; CAD70300.1;
InterPro; IPR00838; ARM.
InterPro; IPR004892; Mo25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probable protein required for conidiophore development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42812 MW; 2E82C63BD06D8B9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 HRELLKLIGNLPTSKGEDEQLESERDLIIKEIEKL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 OPKLIEFLSSFOKERTDDEOFADEKNYLIKOIRDL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF03204; Mo25;
                               Local Similarity
les 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                                                       28
                                                                                                                                                                                                                                                                                                                                                                                                            118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178
       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q873K5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
2873KS
AC 2873K
AC 2873K
DT 01-JC
DT 0
                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                           Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
4;
                             185 RKQTGNGIFWSFFDWIDRGSFEVAADAFTTFRELLTRHKDLVPHYLQTNFDLFFSKYNSI 244
                                                                                                                                         245 LIQSTSYVTKRQSIKLIGEILLDRSNYNVMTAYVDRGEHLKICMNLLRDDRKONVQYEGFH 304
                                                                                                                                                                                                                         276 VFKVFVASPHKTOPIVEILLKNOPKLIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKT 335
                                                                                                                                                                                                                                                      -----FRDFFKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEK- 215
                                                                                                         LLOSENYVTKROSLKLLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFH 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 EKEPPTEAVAQLAQELYSSGLLVTLIADLQLIDPEGKKDVTQIFNNILRRQIGTRSPTVE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 EVEPNOGOVLÓIALEICKEDVLSLFVONMPSLGWEGRKDLAHCWSILLROKVDEAYCCVO 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 DRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 YISAHPHILFMLLKGYBAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 MPLFSKSHKNPA----EIVKILKDNLAILEKQDKKTD-KASEEVSKSLQAMKEILCGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ol-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
Hypothetical protein (19603109.26 protein).
Olyas Sativa (japonica cultivar-group).
Oryas Sativa (japonica cultivar-group).
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
34.6%; Score 590; DB 10; Length 322;
Best Local Similarity 38.5%; Pred. No. 3e-34;
Matches 129; Conservative 73; Mismatches 109; Indels 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki T., Marsumoto T., Yamamoto K.; "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322 AA; 37091 MW; 99434DFA7C2DCD21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Æ
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP003822; BAC06992.1; -. EMBL; AP005455; BAC16736.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
Pfam; PF03204; Mo25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::
::
::
                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone: P0503D09."
```

```
SMART; SM00437; TOPLAC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H64574; H64574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter J.C
                                                           113
                                                                                                                                                                                                                                                                  487
                                                                                                                                                                                                                                                                                                                           025188
                                                                                                                                                                                                                                                                                                    RESULT 14
025188
                                                                             g
                                                                                                                          g
                                                                                                                                                                                                                   엄
                                                                                                                                                                                                                                                                g
                              셤
                                                        ð
                                                                                                     ò
                                                                                                                                                 ð
                                                                                                                                                                        g
                                                                                                                                                                                               à
                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                       ö
  ------KVFVANPNKPRDIIQVLVDN 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : | : : | : : | : : | | : : | | 135 SLRGPLDEIXFI--FLDLVDKQEKELMLMLNDRNQQKMEWNERVERIYKQIFTLSEIFCD 192
                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                              1 MPLFSKSHKNPABITVKILKDNLAILBKQDKKTDKASBEVSKSLQAMKEILCGTNDKBPPT
                                                                                                                                                                                                                                                                                                                                                                              4 MPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 SHKNPAEIVKILKDNLAILEKQDKKT-------DKASEEVSKSLQAMKEILCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bankier A.T., Spriggs H.F., Fartmann B., Konfortov B.A., Madera M., Vogel C., Teichmann S.A., Ivens A., Dear P.H.;
"Integrated mapping, chromosomal sequencing and sequence analysis of
                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5; Length 509;
                                                                                                                                                                                                                                                                                                                                  Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2.4e-13;
76; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                   Strausberg R.; Strausberg R.; Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BCO34159; AA43159.1; -. InterPro; IPR004892; Mo25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida,
Cryptosporidiidae, Cryptosporidium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 0:0-0(2003).
EMBL; BX538352; CAD98465.1; -.
SEQUENCE 509 AA; 59610 MW; CD0E7B88ECED9417 CRC64;
                                                                                                                                                                                                                                                                                             Pfam; PF03204; Mo25; 1.
SEQUENCE 103 AA; 11291 MW; BA86A9F6E9E426E0 CRC64;
                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                     298 QPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDL 332
                                                                                                                                                                                                                                                                                                                                  , DB 11;
8.5e-24;
                                        283 HRELLKLLGNLPTSKGEDEQLEEERDLIIKEIEKL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           509 AA.
                                                                                                     103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                           EAVAQLAQELYSSGLLVTLIADLQLIDFEGK 94
                                                                                                                                                                                                                                                                                                                                              Pred. No. 8.5e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAVAQLAQELYSSGLLVTLIADLQLIDFEVK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 300.5;
                                                                                                                                                                                                                                                                                                                                 Score 435;
                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Last annot:
Similar to RIKEN cDNA 1500031K13 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 25, Created)
238 EAPNAQIMKRYIVEVSYLNIMIGLL--
                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MO25-family protein, possible.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.6%;
26.6%;
                                                                                                                                                                                                                                                                                                                                   25.5%;
                                                                                                                                                                                                                                                                                                                                              97.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 25, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cryptosporidium parvum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                           Local Similarity 97.8
les 89; Conservative
                                                                                                   PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cryptosporidium parvum.
                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5807;
                                                                                                                                                                                                                                       TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Iowa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2003
01-0CT-2003
                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1MB.602
                                                                                                   Q8K038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7YYL6
                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                       Q8K038
                                        a
                    ò
                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                               d
```

```
247 NFVILEWINKNCDEFFSLLLKQYSIIPITYKIGEVLRDISTILNLAQGPGIVDKQNNKTF 306
                                                                                                                                                                                                                                                                      201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T---NEKEPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 LIRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKONQPKLIEFLSSFQKERTDDEQFAD 320
                                                                                                                                                                                                                                                               160 LFSNQFRD------FFKYVELS---TFDIASDAFATFKDLLTRHKVLVADF
                                                                                                                                                                                                                                                                                                                                                                                                        202 LEONYDTIFED-YEKLLOSENYVTKROSLKLIGELILDRHNFAIMTKYISKPENLKLMMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97394467; PubMed-9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchnum K.A., Kienk H.-P., Gill S., Dougherry B.A.
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Inftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., Flizderald L.M., Lee N., Adams M.D., Hickey B.K.,
Berg D.E., Gocayne J.D., Utterback T., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Pujji C., Bowman C., Watthey L., Wallin i
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA topoisomerase type I activity; IEA.
GO; GO:0016853; F:isomerase activity; IEA.
GO; GO:006286; P:DNA modification; IEA.
GO; GO:006286; P:DNA topological change; IEA.
GO; GO:006286; P:DNA unwinding; IEA.
InterPro; IRR003601; DNAtopI ATP bind.
InterPro; IRR003602; DNAtopI_DNA_bind.
                                                                                                                          SPTV-EYISAHPHILF-MILKGYEAPQIALRCGIMLRECIRHEPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN'-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
DNA toposisomerase I (TOPA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000380; DNA_tpieomraee.
InterPro; IPR00617; Toprim dom.
InterPro; IPR006154; Toprim gub.
Pfam; PF01131; Topoisom_bac; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000559; AAD07502.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01131; Topoisom bac; I
Pfam; PF01751; Toprim; I.
PRINTS; PR00417; PRTPISMRASEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321 EKNYLIKQIRDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------KQVSHLLHTS 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=26695 / ATCC 700392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 388:539-547(1997)
```

us-10-025-730-1.rspt

Page

```
222 FKFKDKNEASQFLKDLKDGLGSMSVLVSLKESLSNKEPKKPFTTSKLLSQASKSLKI--- 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 ILCGTNEKEPPTEAVAQLAQELYSSGLLVTLIADLQLIDFECKKDVTQIFNNILRRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- PIKEIAQLAQKLFEAGLITYHRTDSEFLSPEYLKEHEVFFEPIY----- 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 RSPTV----EYIS------AHPHILFMLLKGYEAPQIALRCGIMLRECIRHE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --PSVYQYREYKAGKNSQAEAHEAIRITHPHALKDLEKVCSDAKISEELALKLYQLIYTN 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 PL---AKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIF 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 EDYEKLLOSENYVTKROSLKLLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQ 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --PKLIEFLSSFOKERTDD- 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                381 TICSQSRNALY-NQYDCIFK-----IKSESFKLISFKLLKEKGFLEIEELIQGKEEIN 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | :::|| : | :::|| : | :::|| : | :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| :::|| ::
                                                                                                                                                                                                                                                             7.9%; Score 134.5; DB 16; Length 677;
21.6%; Pred. No. 0.24;
tive 58; Mismatches 134; Indels 127; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSKSHKNPA-EIVKILKDNL------AILEKQDKK---IDKASEEVSKSLQAMKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97394467; PubMed=9252185;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Teleischman R.D., Ketchum K.A., Klenk H.-F., Gill S., Dougherty B.A.
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FlizGerald L.M., Lee N., Adams M.D., Hickey E.R.,
Berg D.B., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujil C., Bowman C., Watthey L., Wallin E.
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------BQF-----BQF-----336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           532 IALTSKDKSKLGNTTKQFEECLDLIMRGEASYEKFMLEVISKLKSTA 578
                                                                                                    Hypothetical protein; Isomerase; Complete proteome. SEQUENCE 677 AA; 77677 MW; 4B285B81F1092BB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein, Complete proteome.
SEQUENCE 430 AA; 50573 MW; 23DCGFE5E956B629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             430 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 FEAFHVFKVFVASPHKTQPIVEILLKNQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bactería; Proteobactería; Epsilo
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein HP1520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000650; AAD08565.1;
SMART; SM00436; TOPIBC; 1. SMART; SM00493; TOPRIM; 1.
                                                                                                                                                                                                   Query Match
Best Local Similarity z...
Best Local Similarity z...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pylori.";
Nature 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR, H64709, H64709.
TIGR, HP1520, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        026049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   026049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226049

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020

2020
          S KW DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
```

```
20;
                                                                                                                           60 FYPNRKSKIEIEFNGEKILKENVAVFHSYDE--EFSSEDSVTTFMAKSDL-----KQQY 111
                                                                                                                                                                                                                                                                                     107 -----RQIGTRSPTV-EYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKII 159
                                                                                                                                                                                                                                                                                                                                                                                                                 63 TEAVAQLAQELYSSGLLVTL--IA-----DLQLIDFEGXXDVTQIFNNILR----- 106
                                                                                                                                                                                                                                        112 DNILLELEKE--KKALLKSLRDIASGFDYEEEIKTIKNEKNKSFYEILDNHLTEIESSEK 169
                                                                                                                                                                                                                                                                                                                                     170 HYSFKYRDIFDGSKKVKDFVNKHHDLIEQYFNKYO-------BLLSQSK 211
                                                                                                                                                                                                                                                                                                                                                                                      160 LF-----SNOFRDFFKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQ----- 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 NYDTIFEDYEKLLQSENYVTKRQSLKLLGELI------LDRHNF--AIMTKYISKP 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : : | :: | : | : | : | : | 271 NNBELKESFDKI---EKVINANKELKAFKDAISKDNTLLTEFLDYDSFRKKVLFSYLKQV 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 -ENLKLAMMILLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPKLIEFLSSFQKE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 IQNVKSLVNLYREKKPEIE----EIIKQASKDQKEWESVIEIF--NQRFLVPFKVELQNQ 381
                                                                                             7 FSKSHKNPAEI-----VKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPP 62
                                                Indels 102; Gaps
  DB 16; Length 430;
7.5%; Score 128; DB 16; 1
20.9%; Pred. No. 0.39;
:ive 73; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 R----TDDEQ----FADEKNYLIKQIRDLKK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | ||:|
382 KDILLNKDAAQFRFIFSDDNQDMNVQKEDLQK 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: April 12, 2004, 10:28:39
Query Match 7.5%
Best Local Similarity 20.9%,
Matches 82, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Job time : 47 secs
                                                                                                ઠ
                                                                                                                                        a
                                                                                                                                                                                        ò
                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

April 12, 2004, 09:47:16; Search time 59 Seconds (without alignments) 1613.873 Million cell updates/sec

US-10-025-730-1

Perfect score:

1 MKKMPLFSKSHKNPAEIVKI......FADEKNYLIKQIRDLKKTAP 337 Sequence:

Gapop 10.0 , Gapext 0.5

BLOSUM62

Scoring table:

1586107 seqs, 282547505 residues

1586107

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 08 Maximum Match 1008

A Geneseq 29Jan04:* geneseqp1990s:* geneseqp2000s:* geneseqp1980s:* Database :

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Human ANI Gal4-huma LexA-huma Mouse cal Novel hum Human pol Drosophil Drosophil C. elegan Arabidops Arabidops Arabidops Aag05089 Arabidops Aag05090 Arabidops Aay94247 Human cal Human Human Human Arabi Aab48970 Aae10858 Aay94248 Abg23844 Aab20387 Aam40864 Abb60392 Aay94249 Aay94250 Aag45273 Aag45274 Aag30714 Aam39078 Aae10859 Aag51052 Aag51051 SUMMARIES AAG23887 AAG05089 AAG05090 AAY94248 ABG23844 AAG51052 AAG51051 AAG30713 AAG51053 AAY94247 AAM39078 AAB94139 AAE10858 AAG23886 AAE10859 AAB20387 AAM40864 AAY94249 AAY94250 AAG45274 AAG30714 Query Match Length DB 100.0 1111 100 1003.5 716.3.5 689.5 685.5 685.5 685.6 685.6 685.6 685.5 Score 1381 1376 1354 1297.5 1162 1466 1381 1381 Result No.

acu

	Aag05991 Arabiadops Aag41151 Zea mays Aag41152 Zea mays Aag41152 Zea mays Abn0991 Himan OPP	Abg25372 Novel hum Abg34081 Human ORF Abg2843 Novel hum	Abr22047 Human Cer Abr22047 Human cer Adb67140 Human A-k Abr292050 Human cer Abr29749 Human cer	
AAG23888 AAG30715 AAG45275	AAG41151 AAG41152 AAG41153 AAG41153 AAG02921	ABG25372 ABP34081 ABG23843	ABK92048 ABK92047 ADB67140 ABK92050 ABK92049	ABB30817 ABG38772 ABU25521 ABG70293
пппп	ոտատո	454	0 9 7 9 9	4000
213 213 213	154 154 139 236	133 133 383	3917 3917 3917	660 660 1182 709
31.7 31.3 31.3	26.6 25.7 25.7	14.61 14.61 14.61	. r. r. r. i r. r. r. r.	7.3
539.5 533 533	4467 467 467 438 438 438 438 438 438 438 438 438 438	227.5 226.5	128.5 128.5 128.5	125 125 120.5 117.5
227	30H04	333	0 8 8 4 4 8 6 0 1	4 4 4 4 4 4 5 5 4 4 5 5 5 5 5 5 5 5 5 5

ALIGNMENTS

Human; calcium binding protein; cancer; inflammation; CBP; reproductive disorder; autoimmune disorder; developmental disorder; seizure disorder; immune disorder; infection. AAY94247 standard; protein; 337 AA. Human calcium binding protein hCBP. (first entry) 10-AUG-2000 AAY94247; AAY94247 ID AAY9 RESULT 1

99WO-US027027. WO200029580-A1. 12-NOV-1999; 25-MAY-2000

(INCY-) INCYTE PHARM INC.

98US-00190965.

13-NOV-1998;

Corley NC, Gorgone GA; Guegler KJ, Tang YT,

WPI; 2000-387793/33. N-PSDB; AAA27332 Human hCBP protein, and the nucleic acid encoding it, useful for e.g. diagnosis, prevention and treatment of cancers, immune, developmental or reproductive disorders.

Claim 1; Fig 1; 72pp; English.

The present sequence is the human calcium binding protein hCBP. It was obtained by screening a coronary artery smooth muscle cDNA library, from which five overlapping nucleic acids were isolated, sequenced and expressed to give the protein. The protein and the gene encoding it are useful for the diagnosis and treatment of the following types of disorder: cancers (such as adenocarcinomas), reproductive disorders (such as infertility, ovulatory defects, endometriosis, disruptions of the oestrus and menstrual cycles, polycystic overy syndrome and overian hyperstimulation), autoimmune disorders (such as benign prostatic hyperplasia and prostatitis), developmental disorders (such as Cushing's syndrome, muscular dystrophy and gonadal dysgenesis), hereditary

```
ö
                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                        PPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKUVTQIFNNILRRQIGTRSPTVEYIS 120
                                                                                                                                                                                                                                                                                                                               AHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDIA 180
                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPK 300
                                                                                                                                                                                                        09
                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human acute neuronal induced calcium binding polypeptide, and polynucleotides encoding them useful for diagnosing or treating stroke, acute head trauma, multiple sclerosis and spinal cord injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cerebroprotective; neuroprotective; vulnerary; vaccine; gene therapy; Acute Neuronal Induced Calcium Binding Protein; ANIC-BP; stroke; acute head trauma; multiple sclerosis; spinal cord injury.
                                                                                                                                                                                                                            MKKWPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKE
                                                                                                                                                                                                                                                                                                                                                     SDAFATFKOLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRH
                                                                                                                                                                                                                                                                  PPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYIS
                                                                                                                                                                                                                                                                                                                                                                                                                           SDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRH
                                                                                                                                                                                                     1 MKKMPLFSKSHKNPAEIVKILKDNLAILEKODKKTDKASEEVSKSLQAMKEILCGTNEKE
                                                                                                                                                                           Gарв
              allergies, anaemia, asthma, atherosclerosis, cholecystitis, Crohn's disease, diabetes, Graves' disease, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, Sjogren's syndrome and ulcerative colitis), and viral, bacterial, fungal, parasitic, protozoal and
                                                                                                                                                                        .,
0
                                                                                                                                        100.0%; Score 1704; DB 3; Length 337; 100.0%; Pred. No. 3.1e-146; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Acute Neuronal Induced Calcium Binding Protein, ANIC-BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIEFLSSFOKERTÖDEOFADEKNYLIKQIRDLKKTAP 337
 seizure disorders, immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB82090 standard; protein; 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-2000; 2000WO-EP009132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-00118848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MERE ) MERCK PATENT GMBH
                                                                                                                                                    Best Local Similarity 100.
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Den Daas I, Duecker K;
                                                                           helminthic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-308142/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAF86462.
                                                                                                           Sequence 337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200123552-A1
neuropathies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2001
                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB82090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
AAB82090
8X88888888888
                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                           Db
                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
ö
                          The present sequence is the protein sequence for human Acute Neuronal Induced Calcium Binding Protein (ANIC-BP). ANIC-BP coding sequence and protein are useful for treating stroke, acute head trauma, multiple sclerosis and spinal cord injury. ANIC-BP coding sequence and protein are also useful as vaccines for inducing an immunological response in a
                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                          120
                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                               9
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                   PPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKOVTQIFNNILRRQIGTRSPTVEYIS
                                                                                                                                                                                                                                                                                                                                                                                                                SDAFATEKDLLTRHKVLVADFLEQNYDTIFEDYEKLLOSENYVTKROSLKLLGELILDRH
                                                                                                                                                                                                                   1 MKKMPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKE
                                                                                                                                                                                                                                       MKKMPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKE
                                                                                                                                                                                                                                                                             PPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYIS
                                                                                                                                                                                                                                                                                                                                      AHPHILFMLLKGYBAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIA
                                                                                                                                                                                                                                                                                                                                                                  121 AHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFAIMTKY I SKPENLKLMMNLLRDKSPNI OFEAFHVFKVFVASPHKTOPI VEILLKNOPK
                                                                                                                                                                                                                                                                                                                                                                                               SDAFATFKDLLTRHKVLVADFLEQNYDT1FEDYEKLLQSENYVTKRQSLKLLGEL1LDRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; CNS; peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral scletches; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                       0
                                                                                                                                                          100.0%; Score 1704; DB 4; Length 337; 100.0%; Pred. No. 3.1e-146;
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIEFLSSFOKERTDDEOFADEKNYLIKOIRDLKKTAP 337
                                                                                                                                                                                         ö
                                                                                                                                                                                       0; Mismatches
Page 41-42; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human polypeptide SEQ ID NO 2223.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM39078 standard; protein; 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-00488725.
2000US-00552317.
2000US-00598042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-DEC-2000; 2000WO-US034263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-00653450.
2000US-00662191.
2000US-00693036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-00620312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                          Best Local Similarity 100.
Matches 337; Conservative
                                                                                                                               Sequence 337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUN-2000; 2
19-JUL-2000; 2
03-AUG-2000; 2
14-SEP-2000; 2
19-OCT-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-2001
                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301
Claim 1;
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
$$000000x8
                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

Zhao OA;

Wang D;

```
The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral neuropaths of the invention may be used to treat diseases of the peripheral neuropaths of the invention may be used to treat diseases of the peripheral neuropaths of contains and central nervous singuries, speem disease, such as alzaeinsed neuropathies and central nervous system disease, such as alzaeins as peripheral neuropaths and central nervous system disease, such as takeral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, cancer is immune system suppression, activity cancer diseases and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C. N. S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                              Novel nucleic acids and polypeptides, useful for treating disorders such
                                                                                  Ren F, Wa
Zhang J,
                                                                                  Qian XB,
Yang Y,
                                                                                  Ma Y, (
Xue AJ,
                                                                                                                                                                                                                                                                                             Example 4; SEQ ID NO 2223; 10078pp; English.
                                                                                  Chen R,
                                                                                                        Xu C,
                                                                                                                                                                                                                                                      as central nervous system injuries.
                                                                                Liu C, Asundi V, Chen
Wang Z, Wehrman T, Xu C
Goodrich R, Drmanac RT;
  29-NOV-2000; 2000US-00727344
                                                                                                                                                               2001-442253/47
                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                       N-PSDB; AAI58234
                                                                                rang YT,
                                                                                                      Wang J,
Zhou P,
                                                                                                      Wang
```

Sequence 337 AA;

```
61 PPTEAVAQLAQELYSSGLLVTLIADLQLIDFBGKKDVTQIFNNILRRQIGTRSPTVEYIS 120
                                                                                                                                                                                                                                                                                                                                                                        181 SDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRH 240
                                                                                                                                                                    61 PPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYIS 120
                                                                                                                                                                                                                                                 121 AHPHILFMLLKGYBAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIA 180
                                                                                                                                                                                                                                                                             SDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRH 240
                                                                                                                                                                                                                                                                                                                                                                                                                   241 NFAIMTKYISKPENLKLAMMULLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 NFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPK 300
                                                                                                                1 MKKMPLFSKSHKNPAEIVKILKDNLAILERQDKKTDKASEEVSKSLQAMKEILCGTNEKE 60
                                                                                    1 MKKMPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKE
                                                 Gaps
                                               .
0
        Length 337;
                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 LIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTAP 337
100.0%; Score 1704; DB 4;
100.0%; Pred. No. 3.1e-146;
iive 0; Mismatches 0;
                                         Matches 337; Conservative
                     Local Similarity
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                      DD
                                                                                                                                                               à
                                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

0

Human protein sequence SEQ ID NO:14408.

(first entry)

26-JUN-2001

AAB94139;

RESULT 4
AAB94139
ID AAB9
XX
AC AAB9
XX
DT 26-J
XX
DE HUMA
XX

AAB94139 standard; protein; 289

```
the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in particularly. The primers are useful for synthesising polynucleotides, particularly full-length DNMs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNMs. The primers allow obtaining of the full-length cDNMs easily without any specialised methods. AMH03166 to AMH13628 and AMH13631 to AMH13621 represent human amino acid sequences; and AMH13629 to AMH13632 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-length CDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide complementary to the nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence of on oligonucleotide comprises a 3'-end sequence of only properties and an oligonucleotide sequence and an oligonucleotide sequence of on oligonucleotide objectides also sequence of on oligonucleotide objectides at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 MKEILCGTNEKEPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 FKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 IGTRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLVKIILFSNQFRDF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKEILCGTNEKEPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 FKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 IGTRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 LKLIGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQ
Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID NO 14408; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1466; DB 4; Length 289;
Pred. No. 1e-124;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Saito K,
Otsuki
                                                                                                                                                                                                                                                                                                                                                                                  hikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
                                                                                                                                                                         Nishikawa T,
                                                                                                                                                                                                                                 27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.0%;
                                                                                                                                                                  28-JUL-2000; 2000EP-00116126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288; Conservative
                                                                                                                                                                                                                                                                                                                                        (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                        Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 289 AA;
                                          Homo sapiens.
                                                                                  EP1074617-A2
                                                                                                                                                                                                           29-JUL-1999;
                                                                                                                          07-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                        shii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
```

```
The invention relates to human acute neuronal induced calcium-binding protein (ANIC-BP) and to nucleic acid encoding it. The invention also relates to expression systems and recombinant host cells comprising ANIC-BP DNA, the recombinant production of ANIC-BP, antibodies specific for ANIC-BP, fusion proteins comprising ANIC-BP and immunoglobulin FC region, and methods of screening for modulators of ANIC-BP function. ANIC-BP has homology and structural similarity to HymA and MoS2 proteins. ANIC-BP proteins and nucleotides are useful for treating stroke and acute head trauma, multiple sclerosis and spinal cord injury. ANIC-BP proteins are useful in screening assays, for identifying membrane bound or soluble receptors, and also in vaccines. MIC-BP nucleotides are useful as diagnostic reagents, as tools for tissue expression studies, for chromosome localisation studies, and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel acute neuronal induced calcium binding protein, useful for treating acute head trauma, stroke, multiple sclerosis and spinal cord injury.
 181 LKLLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome localisation studies, as genetic vaccines, and in the generation of transgenic animals. The present sequence represents human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                     MO25 homologue, HymA homologue; drug screening; stroke; acute head trauma; multiple sclerosis; spinal cord injury; vaccine; cerebroprotective; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4,
                                                                                                                                                                                                                                                                                                                   Human; acute neuronal induced calcium-binding protein; ANIC-BP;
                                     289 PIVEILLKNOPKLIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                           241 PIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKKTAP 289
                                                                                                                                                                                                                                                                                  Human ANIC-BP (acute neuronal induced calcium-binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Von Melchner L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.0%; Score 1381; DB 4;
81.0%; Pred. No. 6.9e-117;
ive 31; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seyfried C,
                                                                                                                                                                   AAB48970 standard; protein; 341 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Page 37; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUN-2000; 2000WO-EP005457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99EP-00112024.
                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Den Daas I, Fischer V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-102721/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAC91772
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200078947-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-1999;
                                                                                                                                                                                                                                              27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-DEC-2000.
                                                                                                                                                                                                         AAB48970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                            吕
                                     ò
                                                                       g
```

```
protein type 1 (ANIC-BP-1) ligand polypeptides and polynucleotides. Sequences of the invention are useful for treating human diseases including stroke, head trauma, multiple sclerosis, Parkinson's disease, Alzheimer's disease and spinal cord injury. They are also useful as vaccines. ANIC-BP-1 ligands are useful for identifying membrane bound soluble receptors. Polynucleotides of the invention are useful as diagnostic reagents, for chromosome localization studies, and as valuable tools for tissue expression studies. They are also useful in gene therapy. The present sequence is Gal4-human ANIC-BP-1 fusion protein comprising the Gal4 protein and a C-terminally linked human ANIC-BP-1
                                                                                              181 ASDAFATFKDLITRHKLLSAEFLEQHYDRFPSEYEKLLHSENYVTKRQSLKLLGELLLDR 240
                                                                                                                                                                    241 HNFTIMTKYISKPENLKLMMNLLRDKSRNIOPEAFHVFKVFVANPNKTOPILDILLKNOA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides, useful in the treatment of stroke, head trauma, multiple sclerosis, Parkinson's disease, Alzheimer's disease and spinal cord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; acute neuronal induced calcium binding protein type 1 ligand; ANIC-BP-1; human disease; stroke; head trauma; multiple sclerosis; Parkinson's disease; Alzheimer's disease; spinal cord injury; vaccine; gene therapy; fusion protein; Gal4 protein.
120 SAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDI
                                121 CTQQNILFMLLKGYESPEIALNCGIMLRECIRHEPLAKIILWSEQFYDFFRYVEMSTFDI
                                                                                                                                                HNFAIMTKY1SKPENLKLMMNLLRDKSPN1QFEAFHVFKVFVASPHKTQP1VEILLKNQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human acute neuronal induced calcium binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel acute neuronal induced calcium binding protein type I ligand
                                                                                                                                                                                                                                           KLIBFLSKFONDRTEDEOFNDEKTYLVKOIRDLKRPA 337
                                                                                                                                                                                                                        300 KLIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 42-44; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gal4-human ANIC-BP-1 fusion protein.
                                                                                                                                                                                                                                                                                                                                                    AAE10858 standard; protein; 496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAR-2001; 2001WO-EP003149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAR-2000; 2000EP-00106110
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duecker K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-607519/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200170771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Den Daas I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                        AAE10858;
                                                                         180
                                                                                                                                                240
                                                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        injury
                                                                                                                                                                                                                                                                                                                                    AAE10858
                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                       à
                                                                                                        g
                                                                                                                                                à
                                                                                                                                                                               g
                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                         심
```

Sequence 496 AA;

59

61 EPQTEAVAQLAQELYNSGLLSTLVADLQLIDFEGKKDVAQIFNNILRRQIGTRTPTVEYI 120 EPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI 119

09

g 8 g

à

4 MPL-FSKSHKNPAEIVKILKDNLAILEKQ---DKKTDKASEEVSKSLQAMKEILCGTNEK

```
4
                                                              179
                                                                                                                BPQTEAVAQLAQELYNSGLLSTLVADLQLIDFEGKKDVAQIFNNILRRQIGTRTPTVEYI 275
                                                                                                                                                               276 CTQQNILFMLLKGYESPEIALNCGIMLRECIRHEPLAKIILWSEQFYDFRRYUEMSTFDI 335
                                                                                                                                                                                                 ASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDR 239
                                                                                                                                                                                                                 HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel acute neuronal induced calcium binding protein type 1 ligand polypeptides, useful in the treatment of stroke, head trauma, multiple sclerosis, Parkinson's disease, Alzheimer's disease and spinal cord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; acute neuronal induced calcium binding protein type 1 ligand; ANIC-BP-1; human disease; stroke; head trauma; multiple sclerosis; Parkinson's disease; Alzheimer's disease; spinal cord injury; vaccine; gene therapy; fusion protein; LexA protein.
                                                4 MPL-FSKSHKNPAEIVKILKDNLAILEKQ---DKKTDKASEEVSKSLQAMKEILCGTNEK
                                                                                                                                                 SAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDI
                                                                                                EPPTEAVAQLAQELYSSGLLVTL1ADLQLIDFEGKKDVTQIFNN1LRRQIGTRSPTVEY1
                           Gaps
                           4
   Length 496;
                          29; Indels
                                                                                                                                                                                                                                                                                                  KLIEFLSSFÇKERTDDEQFADEKNYLIKQIRDLKKTA 336
                                                                                                                                                                                                                                                                                                                 81.0%; Score 1381; DB 4;
81.0%; Pred. No. 1.1e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "LexA protein"
203. .552
/note= "Human ANIC-BP-1 protein"
             ; Pred. No. 1.1e-31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LexA-human ANIC-BP-1 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       AAE10859 standard; protein; 552 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hock B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAR-2001; 2001WO-EP003149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2000; 2000EP-00106110.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MERE ) MERCK PATENT GMBH.
                        273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Χ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-607519/69,
             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200170771-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Den Daas I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2001
Query Match
Best Local S.
Matches 273
                                                                                                                                                 120
                                                                                                9
                                                                                                                                                                                                 180
                                                                                                                                                                                                                          336
                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                          396
                                                                                                                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                                                                         456
                                                                                                                                                                                                                                                                                                                                                                                                               AAE10859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                              RESULT 7
                                                                      g
                                                                                               ò
                                                                                                                     g
                                                                                                                                               à
                                                                                                                                                                   임
                                                                                                                                                                                                \overset{\circ}{2}
                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                       \delta
                                                                                                                                                                                                                                                 \delta
```

```
The invention relates to human acute neuronal induced calcium binding protein type 1 (ANIC-BP-1) ligand polypeptides and polynucleotides. Sequences of the invention are useful for treating human diseases including stroke, head trauma, multiple sclerosis, Parkinson's disease, Alzheimer's disease and spinal cord injury. They are also useful as vaccines. ANIC-BP-1 ligands are useful for identifying membrane bound soluble receptors. Polynucleotides of the invention are useful as diagnostic reagents, for chromosome localization studies, and as valuable tools for tissue expression studies. They are also useful in gene therapy. The present sequence is LexA-human ANIC-BP-1 fusion protein comprising the LexA protein and a C-terminally linked human ANIC-BP-1
                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                                                        119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452 HNFTIMTKYISKPENLKLMMNLLRDKSRNIQFEAFHVFKVFVANPNKTQPILDILLKNQA 511
                                                                                                                                                                                                                                                                                                                                                                         271
                                                                                                                                                                                                                                                                                                                                                                                                                                      331
                                                                                                                                                                                                                                                                                                                                           23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 CTQQNILFMLLKGYESPBIALNCGIMLRECIRHEPLAKIILWSEQFYDFFRYVEMSTFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392 ASDAFATFKDLLTRHKLLSABFLEQHYDRFFSEYEKLLHSENYVTKRQSLKLLGELLLDR
                                                                                                                                                                                                                                                                                                                                        4 MPL-FSKSHKNPAEIVKILKDNLAILEKQ---DKKTDKASEEVSKSLQAMKEILCGTNEK
                                                                                                                                                                                                                                                                                                                                                          EPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI
                                                                                                                                                                                                                                                                                                                                                                                                                         272 EPQTEAVAQLAQELYNSGLLSTLVADLQLIDFEGKKDVAQIFNNILRRQIGTRTPTVEYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 SAHPHILFMLLKGYBAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 ASDAFATFKOLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reproductive disorder; autoimmune disorder; developmental disorder; seizure disorder; immune disorder; infection.
                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                         81.0%; Score 1381; DB 4; Length 552; 81.0%; Pred. No. 1.3e-116; ive 31; Mismatches 29; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLIEFLSSFOKERTDDEOFADEKNYLIKQIRDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gorgone GA;
Disclosure; Page 44-46; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse calcium binding protein MO25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY94248 standard; protein; 341 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guegler KJ, Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INCX-) INCYTH PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US027027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-00190965.
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                        Local Similarity
es 273; Conserv
                                                                                                                                                                                                                                         Sequence 552 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200029580-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY94248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT,
                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp
                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY94248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
à
                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
```

us-10-025-730-1.rag

```
used in a sequence alignment to identify human calcium binding procein diagnosis and treatment of the following types of disorder: cancers (such as adenocarcinomas), reproductive disorders (such as infertility, ovulatory defects, endometriosis, disruptions of the oestrus and menstrual cycles, polycystic ovary syndrome and ovarian myperstimulation), autoimmune disorders (such as benign prostatic hyperplasia and prostatitis), developmental disorders (such as AIDS, neuropathies, seizure disorders, immune disorders (such as AIDS, allergies, anaemia, asthma, atherosclerosis, cholecystitis, Crohn's disease, diabetes, Graves' disease, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, Sigoren's syndrome and ulcerative collisis), and virial, bacterial, fungal, parasitic, protozoal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 SAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CTQQNILFMLLKGYESPEIALNCGIMLRECIRHEPLAKIILWSEQFYDFFRYVEMSTFDI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 ASDAFATFKOLLTRHKVLVADFLEGNYDTIFEDYEKLLQSENYYTKRQSLKLLGELILDR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 HNFAIMTKYISKPENLKLAMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 HNFTIMTKYISKPENLKLMMNLLRDKSRNIQFEAFHVFKVFVANPNKTQPILDILLKNOT 300
                                                Human hCBP protein, and the nucleic acid encoding it, useful for e.g. diagnosis, prevention and treatment of cancers, immune, developmental or reproductive disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                           present sequence is the mouse calcium binding protein MO25. It was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 MPL-FSKSHKNPAEIVKILKDNLAILEKQ---DKKTDKASEEVSKSLQAMKEILCGTNEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n; chromosome mapping; gene mapping; gene therapy; forensic; supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.8%; Score 1376; DB 3; Length 341;
80.7%; Pred. No. 2e-116;
ive 32; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTA 336
                                                                                                                         Disclosure; Page 66-67; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #23835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG23844 standard; protein; 354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               helminthic infections
              2000-387793/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG23844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

```
The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating of supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WHOO at the printed specification, but was obtained in electronic format directly from WHOO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 SAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 DPQTEAGAQLAQELYNSGLLITLVADLQLIDFEGKKDVAQIFNNILRRQIGTRTPTVEYI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 MPPPFGKSHKSPADIVKNLKESMAVLEKQDISDKKAEKATEEVSKNLVAMKEILYGTNEK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASDAFATFKGLLTRHKLLSAEFLEQHYDRFFSEYEKLLHSENYVTKRQSLKLLGELLLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 MPL-FSKSHKNPAEIVKILKDNLAILEKQ---DKKTDKASEEVSKSLQAMKEILCGTNEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 EPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 ASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLOSENYVTXROSLKLLGELILDR
                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLIEFLSKFONDRIEDEOFNDEKTYLVKOIRDLKRPA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.5%; Score 1354; DB 4;
79.2%; Pred. No. 2.1e-114;
tive 33; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 54203; 103pp; English.
                                                                                                                                                                                                                      Tang YT;
                                                          30-MAR-2001; 2001WO-US008631
                                                                                                      31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 354 AA;
                                                                                                                                                                                                                                                                                   N-PSDB; AASB8031
                                                                                                                                                                                                                                                                                                                                                                                                 biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Simi
Matches 267;
                  11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

119

193 239 253 299

WO200175067-A2

```
The present sequence is that of a novel human acute neuronal induced calcium binding protein-like protein splice variant, ANIC-NP-1B. The protein shows homology to other members of the calcium binding protein family, including ANIC-BP, a protein discovered by mRNA differential display that is upregulated in a rat model of head trauma. ANIC-BP and ANIC-BP-1B differ in their C-terminal pottions. The variant protein could serve as a novel drug target. The invention provides ANIC-BP-1B polynucleotides (see AAF19688) and polypeptides, expression vectors, host cells and antibodies, as well as methods for producing the protein and cortism or preventing disorders associated with expression of the protein by inhibiting or activating the action of ANIC-BP-1B. Diseases that may be treated include stroke and acute head trauma, Parkinson's disease, Alzheimer's disease, multiple sclerosis and spinal cord injury. The polynucleotides and polypeptides can also be used in disgnostic assays and in vaccines, and to identify agonists and antagonists useful for treating conditions associated with ANIC-BP-1B imbalance
                                                                                                                                                                                            Acute neuronal induced calcium binding protein; ANIC-BP-1B; spice variant; human; stroke; head trauma; Parkinson's disease; Alzheimer's disease; multiple sclerosis; spinal cord injury; cerebroprotective; antiparkinsonian; nootropic; neuroprotective; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human acute neuronal induced calcium-binding protein like protein splice variant, useful for treating stroke, acute head trauma, Parkinson's disease, Alzheimer's disease multiple sclerosis, spinal cord
                                                                                                                                                       Human acute neuronal induced calcium binding protein ANIC-BP-1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 44-45; 49pp; English.
                                   AAB20387 standard; protein; 350 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   28-SEP-2000; 2000WO-EP009475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99EP-00119113
                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Den Daas I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-266306/27.
N-PSDB; AAF30688.
                                                                                                                                                                                                                                                                          diagnosis; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 350 AA;
                                                                                                                                                                                                                                                                                                                                                         WO200125423-A1.
                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-1999;
                                                                                                                 11-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                12-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duecker K,
                                                                            AAB20387;
RESULT 10
```

```
EPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI 119
                                                                                                                                                        61 EPQTEAVAQLAQELYNSGLLSTLVADLQLIDFEGKKDVAQIFNNILRRQIGTRTPTVEYI 120
                                                                          29
                                                                                                          9
                                                                       4 MPL-FSKSHKNPAEIVKILKDNLAILEKQ---DKKTDKASEEVSKSLQAMKEILCGTNEK
                                                                                         Gaps
                                        13;
          DB 4; Length 350;
                                          38; Indels
        76.1%; Score 1297.5; DB 4
76.0%; Pred. No. 2.8e-109;
ive 32; Mismatches 38;
Query Match
Best Local Similarity 76.09
Matches 263; Conservative
                                                                                                                                         9
                                                                                                  g
                                                                                                                                                             g
```

à

```
240
                121 CTQQNILFWLLKGYESPEIALNCGIMLRECIRHEPLAKIILWSEQFYDFFRYVEMSTFDI 180
                                                          239
                                                                                                               240 HNFAIMTKYISKPENLKIMMNLLRDKSPNIQFBAFHVFKVFVASPHKTQPIVEILLKNQP 299
                                                                                                                                The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymuclectides are useful in gene therapy. A composition containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang D;
, Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating disorders such
                                                       180 ASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDR
                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
120 SAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDI
                                                                                                                                                                                                                                                                                                                                                                                                            peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntingron's disease; Huntingron's disease; hemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ren F, Wa
Zhang J,
                                                                                                                                                                                                  301 KLIEFLSKFONDRIDCMSSSVPTINSRVDLRVKPRIRGIRDLKRPA 346
                                                                                                                                                                           -----DEQPADEKNYLIKQIRDLKKTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ma Y,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 5795; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as central nervous system injuries.
                                                                                                                                                                                                                                                                            AAM40864 standard; protein; 237 AA
                                                                                                                                                                                                                                                                                                                                                                   Human polypeptide SEQ ID NO 5795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C, Asundi V,
Vang Z, Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-0059312.
03-AUG-2000; 2000US-00655450.
14-SEP-2000; 2000US-00665191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-DEC-2000; 2000WO-US034263,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00471275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-OCT-2000; 2000US-00693036
29-NOV-2000; 2000US-00727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-00488725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-2000; 2000US-00552317
                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAI60020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                    22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leukaemia.
                                                                                                                                                                          300
                                                                                                                                                                                                                                                                                                          AAM40864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang J,
Zhou P,
                                                                                                                                                                                                                                                                 AAM40864
                                                                                                                                                                                                                                                                                           a
                                                                                                                                        g
                                                     à
                                                                                                                                                                        à
```

```
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                         171 YVELSTFDIASDAFATFKDLITRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLK 230
                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                           231 LLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPI 290
                                                                                                                                                                                                                                                                                                                                                                                                                       122 LIGELILDRANFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPI 181
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic thateral scalerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhishin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                           2 TRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more
                                                                                                                                                                                                                                                                                                                                                62 YVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                      111 TRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFK
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 7968; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEILLKNOPKLIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 7968
                                                                                                                                                                                      Score 1162; DB 4;
Pred. No. 3.4e-97;
                                                                                                                                                                                                                         .
0
                                                                                                                                                                        68.2%; Scor.
100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB60392 standard; protein; 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002 (first entry)
                                                                                                                                                                                                                      Matches 227; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-656860/75
                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; ABL04495
                                                                                                                                                    Sequence 237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB60392;
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                         Ωp
                                                                                                                                                                                                                                                                                    덤
                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                     Пp
                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

```
ب
.
                                                                                                                                                                                                                                                                                    64 E-AVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISAH 122
                                                                                                                                                                                                                                                                                                       61 DYVVAQLSQELYNSNILLILIIQNLHRIDFEGKKHVALIFNNVLRRQIGTRSPTVEYICTK 120
                                                                                                                                                                                                                                                                                                                                                   PHILFMILKGYE--APQIALRCGIMIRECIRHEPLAKIILFSNQFRDFRYVELSTFDIA 180
                                                                                                                                                                                                                                                                                                                                                                         241 HNFTVMTRYISEPENLKLMMMMLKEKSRNIQFEAFHVFKVFVANPNKPKPILDILLRNQT 300
                                                                                                                                                                                                                    4 MPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPT 63
                                                                                                                                                                                                                                       or
insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins (ABB57737-ABR72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                      181 SDAFSTPKELLTRHKILCAEFLDANYDKFFSQHYQRLINSENYYTRQSLKLLGELLLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human hCBP protein, and the nucleic acid encoding it, useful for e.g. diagnosis, prevention and treatment of cancers, immune, developmental
                                                                                                                                                                                                                                                                                                                                                                                                                     SDAFATFKDLLTRHKVLVADFLEQNYDTIF-EDYEKLLQSENYVTKRQSLKLLGELILDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HNFAIMTKYISKPENLKLAMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila, calcium binding protein, cancer, inflammation, DMO25, CE reproductive disorder, autoimmune disorder; developmental disorder; seizure disorder; immune disorder; infection.
                                                                                                                                                                                    4
                                                                                                                                                65.2%; Score 1111; DB 4; Length 339; 65.0%; Pred. No. 2.3e-92;
                                                                                                                                                                                 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 KLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 XLVDFLINFHIDRSEDEQFNDEKAYLIKQIKELK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gorgone GA
                                                                                                                                                                                 59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila calcium binding protein DMO25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 67-68; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY94249 standard; protein; 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US027027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00190965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                 Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reproductive disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT, Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-387793/33
                                                                                                                                                                 Best Local Similarity
                                                                                                                  Sequence 339 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200029580-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY94249;
                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY94249
   8888888
                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
```

```
The present sequence is the Drosophila calcium binding protein DW025. It was used in a sequence alignment to identify human calcium binding protein hCDP. The hCDP protein and the gene encoding it are useful for the diagnosis and treatment of the following types of disorder: cancers (such as adenocarcinomas), reproductive disorders (such as infertility, ovulatory defects, endometriosis, disruptions of the oestrus and menstrual cycles, polycystic ovary syndrome and ovarian hyperstimulation), autoimmune disorders (such as benign prostatic hyperstimulation), autoimmune disorders (such as benign prostatic or hyperplasia and prostatitis), developmental disorders (such as Cushing's syndrome, muscular dystrophy and gonadal dysgenesis), hereditary neuropathies, estaure disorders, immune disorders (such as AIDS, allergies, anaemia, asthma atheroscalerosis, cholecystitis, Crohn's disease, diabetes, Graves' disease, multiple sclerosis, psoriasis, chleuris), and viral, bacterial, fungal, parasitic, protozoal and helminthic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                  E-AVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSFTVEYISAH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEILFTLMAGYEDAHPEIALNSGTWIRECARYEALAKIMIHSDEFFKFFRYVEVSTFDIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                          PHILFMLLKGYE - - APQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 MPLFSKSHKNPAEIVKILKDNLAILEKODKKTDKASEEVSKSLQAMKEILCGTNEKEPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDAFATFKDLLTRHKVLVADFLEQNYDTIF-EDYEKLLQSENYVTKRQSLKLLGELILDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calcium binding protein; cancer; inflammation; yeast-like CBP; CBP; reproductive disorder; autoimmune disorder; developmental disorder;
                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                        Length 339;
                                                                                                                                                                                                                                                                                                                                                     IndelB
                                                                                                                                                                                                                                                                                                                                                      54;
                                                                                                                                                                                                                                                                                                                     Score 1109; DB 3;
Pred. No. 3.6e-92;
59; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLK 333

    C. elegans yeast-like calcium binding protein.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seizure disorder; immune disorder; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY94250 standard; protein; 377 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US027027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00190965
                                                                                                                                                                                                                                                                                                                       65.18;
                                                                                                                                                                                                                                                                                                                                  65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                 Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                     Sequence 339 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200029580-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY94250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ⋩
```

```
241 QSLKLIGELLILDRHNFNIMIKYYISNPDNIRLMMELLRDKSRNIQYBARHVFKVFVANPNK 300
                                                                                                                       Human hCBP protein, and the nucleic acid encoding it, useful for e.g. diagnosis, prevention and treatment of cancers, immune, developmental or
                                                                                                                                                                                                                                           The present sequence is the C. elegans yeast-like CBP. It was used in a sequence alignment to identify human calcium binding protein hCBP. The hCBP protein and the gene encoding it are useful for the diagnosis and treatment of the following types of disorder: cancers (such as adenocarcinomas), reproductive disorders (such as infertility, ovulatory defects, endometriosis, disruptions of the osetrus and menstrual cycles, polycystic ovary syndrome and ovarian hyperstimulation), autoimmune disorders (such as benign prostatic hyperplasis and prostatitis), developmental disorders (such as Cushing's syndrome, muscular dystrophy and gondal dysgensis), hereditary neuropathies, seizure disorders, immune disorders (such as ALDS, allergies, anaemia, asthma, attherosclerosis, cholecystitis, Crohn's disease, diabetes, Graves' disease, multiple sclerosis, psoriasis, returnitis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TFFLYVQSEVFDISSDAFSTFKELTTRHKAIIAEFLDSNYDTFFAQYQNLLNSKNYVTRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----QDKKTDKASEEVSKSLQAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 KEILCGTNEKEPPTE---AVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 RQIGTRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNOFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 DFFKYVELSTFDIASDAFATFKOLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSLKLLGEL1LDRHNFA1MTKY1SKPENLKLMMNLLRDKSPN1QFEAFHVFKVFVASPHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          scleroderma, Sjogren's syndrome and ulcerative colitis), and viral,
bacterial, fungal, parasitic, protozoal and helminthic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 TQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKKT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 PKPISDILNRNREKLVEFLSEFHNDRTDBEGFNDEKAYLIKQIQEMKSS 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.4%; Score 1063.5; DB 3; Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.5%; Pred. No. 5.6e~88; ive 53; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 56816.
                                         Gorgone GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 MP-LFSKSHKNPAEIVKILKDNLAILEK----
                                                                                                                                                                                                        Disclosure; Page 68-69; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG45273 standard; protein; 343 AA
                                         Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 211; Conservative
(INCY-) INCYTE PHARM INC.
                                                                                                                                                               reproductive disorders.
                                       Guegler KJ,
                                                                                WPI; 2000-387793/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 377 AA;
                                     Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG45273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG45273
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ठे
```

ä

49 9 106

240 226

termination sequence.

			.439.	825P.	18P	387	7 L	52P	34P	147	77P	49P	10P	91.6	4 4 7 4 7 5	07P	84P	95P	36P	7 7 7	56P	18P	19P	21P	707	41P	24P	53P	21P	92P	82P	22P	02P	24P	94P	4 7 7	19P	52P	53.4 F C	7 4 7 7 4 7	55P	56P	υς 1000 1100	59P	60P	61P	63P	50P	632	17P	א עע טע	54P	955	23	919
thallana.			2000EP-00301	99US-01218	OUS-0123	3US-0125	9US-0126	OUS-0127	9US-0128	9US-0128	OUS-0130	9US-0130	9US-0130	105-0130	113-0137 9118-0132	9US-0132	9US-0132	9US-0132	9US-0132	2010-506 2013-5118	3US-0134	9US-0134	9US-0134	99US-0134	99US-0134	99US-0134	99US-0135	99US-0135	99US-0136	9510-SD66	99US-0136	99US-0137	99US-0137	99US-0137	99US-0138	99115-0138	99US-0139	99US-0139	99US-0139	99US-0139	99US-0139	99US-0139	99US-0139	99US-0139	99US-0139	99US-0139	99US-0139	99US-0139	99US-0139	99US-0139	9905-0139	99US-0140	99US-0140	99US-0140	99US-014C
rabidopsi	EP1033405-A2	06-SEP-2000.	25-FEB-2000;	25-FEB-1999; 05-MAR-1999;	-MAR-199	-MAR-199	- MAR-199	L-APR-199	5-APR-199	3-APR-199 5-APR-199	9-APR-199	1-APR-1999	3-APR-199	3-APR-1999	3-AFR-1999 3-APR-1999	0-APR-1999	4-MAY-1999	5-MAY-1999	5-MAY-1999 5-MAY-1999	7-MAY-1999	1-MAY-1999	1-MAY-1999	4-MAY-1999	1-MAY-1999	4-MAY-1999 3-MAY-1999	9-MAY-1999	0-MAY-1999	1-MAY-1999 1-MAY-1999	5-MAY-1999	7-MAY-1999	3-MAY-1999	0.001-NTH-2	4-JUN-1999	7-JUN-1999	3-JUN-1999	666T-NIII-0	4-JUN-1999	5-JUN-1999	6-JUN-1999	8-JUN-1999	8-JUN-1999	8-JUN-1999	8-JUN-1999	8-JUN-1999	8-JUN-1999	8-JUN-1999	8-JUN-1999	8-JUN-1999	8-JUN-1999	1-UUN-1999 2-:TIN-1999	3-17TV-1999	3-JUN-1999	4-JUN-1999	8-JUN-199	
3 🕱	NA XX	8	Y P Y	8 K K	PR	R E	PR	PR	PR I	7, U	E	PR	PR	7 E	P P	R	₽ਲ	PR E	7 D	, n	PR	PR	PR	Ж. Е	7, U	PR	PR F	n T	E E	PR.	PR F	P.R.	PR	PR	F. E.	7 C	PR	PR	F. E.	E E	PR	P. F.	PR	PR	PR I	д Д	7. T.	PR	PR I	7, 5 7, 5	7 Z	PR	PR	PR.	

99US-0141287P. 99US-0141842P. 99US-0142154P. 99US-0142390P. 99US-0142390P.	99US-0142920P.	99US-0143542P.	99US-U143624F. 99US-0144005F.	99US-0144085P.	99US-0144086F.	99US-0144331P.	99US-0144332P.	99US-0144333F:	99US-0144335P.	99US-0144352P.	99US-0144632P.	99US-0144814P.	99US-0145086P.	99US-0145088F.	9911S-0145087F	99US-0145089P.	99US-0145192P.	99US-0145145P.	99US-0145218P.	99US-0145224F.	9903-01432/8F.	99US-0145918P.	99US-0145919P.	99US-0145951P.	99US-0146388P.	99US-0146389P.	99US-0147038P.	99US-0147302P.	99US-0147192P.	99US-0147260P.	99US-0147416P.	99US-0147493F.	99US-014/333F;	99US-0148319P.	99US-0148341F.	99US-0148684P.	99US-0149368P.	99US-01491/3F:	99US-0149722P.	99US-0149723P.	9903-0149929F.	99US-0149930P.	99US-0150566P.	99US-0150884P.	99US-0151066P.	99US-0151080P.	99US-0151303P.	99US-0151930P.	99US-0152363P.	99US-0153758P.
30 JUN-1999; 01-JUL-1999; 01-JUL-1999; 02-JUL-1999; 06-JUL-1999; 08-JUL-1999;	09-JUL-1999; 12-JUL-1999;	13-JUL-1999;	14-00L-1999; 15-00L-1999;	16-JUL-1999;	19-JUL-1999;	19-JUL-1999;	19-JUL-1999;	19-000-1393;	19-JUL-1999;	20-JUL-1999;	20-JUL-1999;	21-JUL-1999;	21-JUL-1999;	21-JUL-1999;	22-00E-1999;	22-JUL-1999;	22-JUL-1999;	23-JUL-1999;	23-JUL-1999;	23-JUL-1999;	27-JIII-1999;	27-JUL-1999;	27-JUL-1999;	28-JUL-1999; 02-ATG-1999;	02-AUG-1999;	02-AUG-1999;	03-AUG-1999;	04-AUG-1999;	05-AUG-1999;	05-AUG-1999;	06-AUG-1999;	09-AUG-1999;	10-AUG-1999;	11-AUG-1999;	12-AUG-1999;	13-AUG-1999;	16-AUG-1999;	18-AUG-1999;	20-AUG-1999;	20-AUG-1999;	23-AUG-1999;	23-AUG-1999;	25-AUG-1999;	26-AUG-1999;	27-AUG-1999;	27-AUG-1999;	30-AUG-1999;	01-SEP-1999;	07-SEP-1999;	13-SEP-1999;
	7. A.G.	E E	¥	84 E	¥ £	묎	PR	H H	PR	PR	£ 8	E E	P	7. C	r d	H H	PR	PR	PR	Ed. C	7. U	PR	PR	PR gg	PR	PR	9. PR	PR PR	H.	E G	PR	몺	7. E.	PR	X, 0	. H	R	r r	PR	PR E	A C	H.	PR.	r c	K K	PR	P. 59	PR	PR G	PR
																											-						•	-	•															_
	-																																																	
٤	.00301439.	-0121825P.	.0123548P.	.0125788P.	0126785P.	.0127462P.	0128234P.	0129845P.	.0130077P.	.0130449P.	-0130510P.	0131449P.	.0132048P.	.013240/P.	0132485P.	.0132486P.	.0132487P.	.0132863P.	-0134256P.	.0134218P.	.0134221P.	-0134370P.	-0134768P.	.0134941P.	.0135353P.	-0135629P.	-0136021P.	-0136782P.	-0137222P.	-0137502P.	-0137724P.	-0138094P.	-0138847P.	-0139119P.	-0139452 <i>P</i> .	-0139492P.	-0139454P.	-0139456P.	-0139457P.	-0139458P.	-0139460P.	-0139461P.	-0139462P.	-0139463F. -0139750D	-0139763P.	-0139817P.	-0139899P. -0140353P	-0140354P.	-0140695P.	-0140991P.

Job time : 63 secs

```
59 KEPPTEAVAQLAQELYSSGLLVTLIADLQLIDFBGKKDVTQIFNNILRRQIGTRSPTVEY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 IASDAFATFKDLLTRHKVLVADPLEQNYDTIFEDY-EKLLGSENYVTKRQSLKLIGELIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 DRSNSAVMTKYVSSMDNLRILMNLLRESSKTIQIEAFHVFKLFVANQNKPSDIANILVAN 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 DRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LFSKSHKNPAEIVKILKDNLAILEK-----QDKKTDKASEEVSKSLQAMKEILCGTNE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 42.0%; Score 716.5; DB 3; Length 343; Best Local Similarity 42.9%; Pred. No. 1.7e-56; Matches 144; Conservative 78; Mismatches 105; Indels 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 QPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9905-0154039

9905-0154039

9905-0155439

9905-0155486

9905-0156486

9905-0157639

9905-0157639

9905-0157639

9905-015929

9905-015929

9905-0159299

9905-0159299

9905-0159299

9905-0159339

9905-0159339

9905-0159339

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607418

9905-01607708

9905-01607708

9905-01607708

9905-01607708

9905-01607708

9905-01607708

9905-01607708

9905-01607708

9905-01607708

9905-01607708

9905-01607708

9905-01607708
                                                                                                                                                                                                                                                                    21-OCT-1999)
21-OCT-1999)
21-OCT-1999)
22-OCT-1999)
22-OCT-1999)
25-OCT-1999)
25-OCT-1999)
25-OCT-1999)
26-OCT-1999)
26-OCT-1999)
26-OCT-1999)
28-OCT-1999)
28-OCT-1999)
28-OCT-1999)
                                                                                                                                   13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
18-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
                                       23-SEP-1999
24-SEP-1999
                                                             28-SEP-1999
29-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \delta
```

3;

Search completed: April 12, 2004, 10:26:39

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

US-10-025-730-1 Title: Perfect score:

April 12, 2004, 10:27:48 ; Search time 46 Seconds (without alignments) 1926.306 Million cell updates/sec

1 MKKMPLFSKSHKNPAEIVKI......FADEKNYLIKQIRDLKKTAP 337 1704 Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

1073127 seqs, 262937947 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Sequence 1, Appli	٦.	,	m	Sequence 4. Appli	'n	546								
	ID		US-10-025-730-1	US-10-239-079-5	US-10-239-079-6	US-10-025-730-3	US-10-025-730-4	US-10-025-730-5	US-10-425-114-54669	US-10-425-114-52177	US-10-424-599-224185	US-10-425-114-46025	US-10-425-114-48872	US-10-424-599-209662	US-10-424-599-158029	US-10-424-599-149595	US-10-425-114-70029
	DB		14	14	14	14	14	14	12	12	12	12	12	12	12	12	12
	Query Match Length DB	1 1 1 1	337	496	552	341	339	377	412	446	339	351	342	337	173	184	161
œ	Query Match		100.0	81.0	81.0	80.8	65.1	62.4	44.4	44.1	42.0	38.1	37.0	30.2	23.2	18.9	16.2
	Score		1704	1381	1381	1376	1109	1063.5	756	752	715.5	649	630.5	514	395.5	322.5	275.5
	Result No.	1 1 1 1 4	Н	7	ю	4	S	9	7	89	σ	10	11	12	13	14	15

_	44	56	e 23(32	11	4	equence 2,	10		9	21	4	a)				Sequence 224186,		-	Sequence 4, Appli	-			Sequence 15, Appl	14,	47,	1, 7	14,	Sequence 78, Appl
US-09-864-408A-6108	-10-425-114-4445	10-425-114-5674	4-599-23	9-386-3232	0-608A-1	1-311	1-311	US-10-370-685-100	-10-171-311	-31	0-424-5	-761-479	0-282-122A-53	3-634	3-634-7	m	US-10-424-599-224186	-095	0-023-6	-10-205-6	-10-032-585-71	11-4	2-122A-6	10-256-2	-10-023-6	-09-978-3	-10-2	US-10-256-250-14	US-10-023-634-78
11	13	12	12	14	14	14	14	15	14	14	12	9	12	15	15	15	17	14	15	15	14	12	12	14	15	10	12	14	12
135	83	74	63	820	3878	3899	3907	3911	3917	3925	116	099	1182	709	709	724	57	2184	725	725	769	980	1128	709	709	725	725	725	725
13.4	10.9	0.6	7.7	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.4	7.3	7.1	6.8	6.8	6.8	6.7	9.9							•	•	•	6.2	
227.5	186.5	153	131.5	128.5	128.5	128.5	128.5	128.5	128.5	128.5	126	125	120.5	116.5	116.5	116.5	113.5	113	111.5	111.5	108	107	107	106.5	106.5	106.5	106.5	106.5	106.5
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

```
Sequence 1, Application US/10025730
Fublication No. US20030045466A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
ITILE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REFRENCE: PF-0635 US
CURRENT APPLICATION NUMBER: US/10/025,730
CURRENT FILING DATE: 2001-12-18
FRICA PAPLICATION NUMBER: US/09/190,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: 3734805
US-10-025-730-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
US-10-025-730-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
```

.; 0 ö Query Match
Best Local Similarity 100.0%; Pred. No. 5.5e-147;
Matches 337; Conservative 0; Mismatches 0; Indels 0;

9 9 1 MKKMPLFSKSHKNPAEIVKILKDNIAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKE 1 MKKMPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKE ద ò 셤

121 AHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIA 180

ઠે

```
275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239
181 SDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLÖSENYVTKROSLKLLGELILDRH 240
                                                                                                                                       NFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPK 300
                                                                                                                                                             EPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 SAHPHILFMILKGYBAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276 CTQQNILFMLLKGYESPEIALNCGIMLRECIRHEPLAKIILWSEQFYDFFRYVEMSTFDI 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      336 ASDAFATFKDLLTRHKLLSAEFLEQHYDRFFSEYEKLLHSENYVTKROSLKLLGELLLDR 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      396 HNFILMIKKISKPENLKLMMNLLRDKSRNIQFEAFHVFKVFVANPNKTQPILDILLKNQA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 ASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDR
                                                             SDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 MPL-FSKSHKNPAEIVKILKDNLAILEKQ----DKKTDKASEEVSKSLQAMKEILCGTNEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Gal4-ANIC-BP-1 OTHER INFORMATION: fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.0%; Score 1381; DB 14; Length 496; 81.0%; Pred. No. 2.8e-117; cive 31; Mismatches 29; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      456 KLIEFLSKFONDRTEDEQFNDEKTYLVKQIRDLKRPA 492
                                                                                                                                                                                                                                                 LIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 KLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKKTA 336
                                                                                                                                                                                                                  301 LIBFLSSFQKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Merck Patent GmbH
TITLE OF INVENTION: ANTC-BP1-ligand
FILE REFERENCE: ANIC-BP-1-ligand
CURRENT APPLICATION NUMBER: US/10/239,079
CURRENT FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/10239079
Publication No. US20030148446A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 273; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 5
LENGTH: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
US-10-239-079-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-239-079-5
                                                                                                                                                                                                                                                                                                                                     US-10-239-079-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
                                                           181
                                                                                                                                       241
                                                                                                                                                                                                                                                         301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                            g
                                                                                                                                     à
                                                                                                                                                                          g
                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                       ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                           ò
```

Sequence 6, Application US/10239079
Publication No. US20330148446A1
GENERAL INFORMATION:
APPLICANT: Merck Parent GmbH
TITLE OF INVENTION: ANIC-BP1-ligand

```
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 BPQTEAVAQLAQELYNSGLESTLVADLQLIDFEGKKDVAQIFNNILRRQIGTRTFTVEYI 331
                                                                                                                                                                                                                                                                                                                                                                                                                                          271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 CTQQNILFMLLKGYESPEIALNCGIMLRECIRHEPLAKIILWSEQFYDFFRYVEMSTFDI 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP 299
                                                                                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 MPL-FSKSHKNPAEIVKILKDNLAILEKQ----DKKTDKASEEVSKSLQAMKEILCGTNEK 59
                                                                                                                                                                                                                                                                                                                                                                                                                          212 MPPFGKSHKSPADIVKNLKESMAVLEKQDISDKKAEKATEEVSKNLVAMKEILYGTNEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 SAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDI
                                                                                                                                                                                                                                                                                                                                                                                                 4 MPL-FSKSHKNPAEIVKILKDNLAILEKO---DKKTDKASEEVSKSLQAMKEILCGTNEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 ASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392 ASDAFATFKDLITRHKLLSAEFLEGHYDRFFSGYEKLLHSENYVTKROSLKLLGELLLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 EPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI
                                                                                                                                                                                               FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Lexa-ANIC-BP-1 OTHER INFORMATION: fusion protein
                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4,
                                                                                                                                                                                                                                                                                                            81.0%; Score 1381; DB 14; Length 552; 81.0%; Pred. No. 3.3e-117; Live 31; Mismatches 29; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.8%; Score 1376; DB 14; Length : 80.7%; Pred. No. 4.7e-117; Live 32; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 KLIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               512 KLIEFLSKFQNDRTEDEQFNDEKTYLVKQIRDLKRPA 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Gorgone, Gina A.
ITILE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REFERENCE: PF-0635 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/025,730 CURRENT FILING DATE: 2001-12-18 PRIOR APPLICATION NUMBER: US/09/190,965 PRIOR FILING DATE: 1998-11-13
FILE REFERENCE: ANIC-BP-1-ligand
CURRENT APPLICATION NUMBER: US/10/239,079
CURRENT FILING DATE: 2002-09-19
SUFFREE: PEQ ID NOS: 8
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10025730; Publication No. US20030045466A1; GENERAL INFORMATION:
                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                        Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: 9262934
US-10-025-730-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL Program
SEQ ID NO 3
LENGTH: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-10-025-730-3
                                                                                                                                      552
                                                                                                                                                                                                                                                                      US-10-239-079-6
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                      LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
US-10-425-114-54669
                                                                                      RESULT 6
US-10-025-730-5
                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 377
                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
     ò
                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                        61 EPQTEAVAQLAQELYNSGLLGTLVADLQLIDFEGKKDVAQIFNNILRRQIGTRTPTVEYI 120
                                                                                                                                                                                                               61 DYVVAQLSQELYNSNLLLILIQNLHRIDFEGKKHVALIFNNLLRRQIGTRSPTVEYT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 PHILFMLLKGYE--APQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 SDAFATFKOLLTRHKVLVADFLEQNYDTIF-EDYEKLLQSENYVTKRQSLKLLGELILDR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 SAHPHILFMILKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDI 179
                                                                                                                                        180 ASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLGSENYVTKRQSLKLLGELILDR 239
                                                                                                                                                                                                                                                        240 HNFAIMTKYISKPENLKLAMMILLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E-AVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISAH 122
                                                   60 EPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
1 MPPPGKSHKSPADIVKNLKESMAVLEKQDISDKKAEKATEEVSKNLVAMKEILYGTNEK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MPLFGKSOKSPVELVKSLKEAINALEAGDRKVEKAQEDVSKNLVSIKNMLHGSSDAEPPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 MPLFSKSHKNPABIVKILKDNLAILEKODKKTDKASEEVSKSLQAMKEILCGTNEKEPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65.1%; Score 1109; DB 14; Length 339; 65.0%; Pred. No. 1.1e-92; ive 59; Mismatches 54; Indels 4;
                                                                                                                                                                                                                                                                                                                           300 KLIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTA 336
                                                                                                                                                                                                                                                                                                                                               301 KLIEFLSKFONDRTEDEOFNDEKTYLVKOIRNLKRAA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/10025730;
Publication No. US20030045466A1;
GENERAL INFORMATION:
APPLICANT: Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Gorgone, Gina A.
TITLE OF INVENTION: CALCIUM BINDING PROTEIN;
FILE REFERENCE: PF-0635 US
CURRENT APPLICATION NUMBER: US/10/025,730;
CURRENT PILING DATE: 2001-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/09/190,965 PRIOR FILING DATE: 1998-11-13 NUMBER OF SEQ ID NOS: 5 SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: 91794137
US-10-025-730-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 65.0%
Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                               -10-025-730-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                   à
                                                                                                                                               Dp
                                                                                                                                                                                      à
                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                 ð
                                                                            - <del>Q</del>
                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                          \delta
                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
APPLICANT: Zhou, Yihua
APPLICANT: Xovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Waleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۳
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 KEILCGINEKEPPTE---AVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 KSFIYGNDSAEPSSEHVVQVAQLAQEVYNANILPMLIKMLPKFEFECKKDVGQIFNNLLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 ROIGTRSPTVBYISAHPHILFMLLKGYBAPQIALRCGIMLRECIRHEPLAKIILFSNOFR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 DFFKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKR 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSLKLIGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MPLLFGKSHKSPADVVKTLREVLTILDKLPPPKLDKDGNIQSDKKYDKALDEVSKNVAMI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 MP-LFSKSHKNPAEIVKILKDNLAILEK------QDKKTDKASBEVSKSLQAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 14; Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 PKPISDILNRNREKLVEFLSEFHNDRIDDEQFNDEKAYLIKQIQEMKSS 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 TOPIVEILLKNOPKLIEFLSSFOKERTDDEOFADEKNYLIKQIRDLKKT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68; Indels
300 KLIEFLSSFQKERTDDEQFADEXNYLIKQIRDLK 333
                              301 KLVDFLTNFHTDRSEDEQFNDEKAYLIKQIKELK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.4%; Score 1063.5; DB : 60.5%; Pred. No. 1.8e-88; tive 53; Mismatches 68
                                                                                                                                                                                          Sequence 5, Application US/10025730; Sequence 5, Application US/10025730; Publication No. US20030045466Al
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
TITLE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REFERENCE: PF-0635 US
CURRENT APPLICATION NUMBER: US/10/025,730
CURRENT FILING DATE: 2001-12-18
PRIOR PILING DATE: 2001-12-18
PRIOR PILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 5
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 54669, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: 91255838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 60.5% Matches 211; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Davi
APPLICANT: Screen, Steve
```

```
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                     à
                                                                                                     셤
                                                                                                                                                à
                                                                                                                                                                              qq
                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhou, Yhua Shenid K.
APPLICANT: Screen, Serven E
APPLICANT: Screen, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Wulleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRENCE: 38-21(53313)B
FILE REPRENCE: 38-21(53313)B
FILE REPRENCE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                         76 XMKGLFKTKPRTPVDIVRQTRECLVHLDLHSGSRSGDAKRDEKMTELSKNIRDMKSILYG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 NFDIASDASATFKELLITRHKATVAEFLSNNYDWFFEEFNSRLLSSTNYITKRQAIKLLGD 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 KMKGLFKSKPRTPVDIVRQTRECLVYLDLHSDSRSGDAKREEKMTELSKNIRDMKSILYG 169
                                                                                                                                                                                                                                                                                                                                                            56 TNEKEPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPT 115
                                                                                                                                                                                                                                                                                                                                                                                    116 VEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 SEYLESNKDLLDILILGYENMDIALHYGAMLRECIRHQSIARYVLESEHMKKFFDYIQLP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 TPDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDY-EKLLGSENYVTKRQSLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 LILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEIL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KKMPLFSKSHKNPAEIVKILKDNLAILE-----KQDKKTDKASEEVSKSLQAMKEILCG
                                                                                                                                                                                                                                                                                 2 KKMPLFSKSHKNPAEIVKILKDNLAILE-----KQDKKTDKASEEVSKSLQAMKEILCG
                                                                                                                                                                                                                                               ..
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.1%; Score 752; DB 12; Length 446; 45.0%; Pred. No. 5.9e-60;
                                                                                                                                                                                                        44.4%; Score 756; DB 12; Length 412; 45.3%; Pred. No. 2.3e-60; tive 67; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   376 VINRNKLLRFFAGFKIDK-EDEQFEADKEHVIKEISAL 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 IKNOPKLIEFLSSFOKERTDDEOFADEKNYLIKQIRDL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: LIB3912-007-H10_FLI.pep
US-10-425-114-52177
                                                                                                                                                OTHER INFORMATION: Clone ID: LIB3069-003-D7_FLI.per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67; Mismatches 111;
CURRENT APPLICATION NUMBER: US/10/425,114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
2.10-425-114-52177
Sequence 52177, Application US/10425114
Publication No. US20040034888A1
               CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 54669 LENGTH: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 45.0
Matches 152; Conservative
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays
                                                                                       TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                  US-10-425-114-54669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 52177
                                                                                                                                                                                                                                         Matches 153;
                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                   \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

```
US-10-424-599-224185.
US-10-424-599-224185.
US-20408.
US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 MILDRSNAAVMMRYVSSKDNIMILMNILKDSSKNIQIBAFHVFKLFAANKNKPPEVVNIL 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 QLAQELYSSGLLVTLIADLQLIDFECKKDVTQIFNNILRRQIGTRSPTVEYISAHPHILF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 QLVEBICKEDVLTLLIHKLPILGWBARKDLVHCWSILLKHKVBTNYYCVEYIEQHIELLD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIASDAFATF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 KOLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHNFAIMTK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 YILEVRYLKVMMTLLRDSSKNIQLSAFHIFKVFVANPNKPREVKIILSKNQEKLLDLLHN 311
TNEKEPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPT 115
                                                                  116 VEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELS 175
                                                                                                                                                                                                                                                                                                      230 SEYLESUKDILDILILGYENMDIALHYGAMLRECIRHQSIARYVLESEHMKKFFDYIQLP 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 TPDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDY-EKLLQSENYVŢKRQSLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 LILDRHNFAIMTKYISKPENLKLAMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEIL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 FLVVCYDNKDIALSCGIMLRECIKFPSLARYILESASFVLFFKFVELPNFDVASDAFSTF 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 YISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPKLIEFLSS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 KTPQEVAKSIKESLMALDTKTVVEVKALEKALEEVEKRPVTMRTMLSGDGESEPNLDQVS 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 KNPAEIVKILKDNLAILEKQD----KKTDKASEEVSKSLQAMKEILCGTNEKEPPTEAVA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.0%; Score 715.5; DB 12; Length
46.3%; Pred. No. 8.5e-57;
tive 61; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: PAT_MRT3847_44468C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 LKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 FOKER-TDDEQFADEKNYLIKQIRDL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; CIMER INFORMATION
US-10-424-599-224185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
```

```
US-10-424-599-209662
                                                     US-10-425-114-48872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                              à
                                                                                                                                                                                             셤
                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        입
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D
                                                                                                                   APPLICANT: Screen, Seven E.
APPLICANT: Screen, Seven E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Tabaska, Jack E.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 46025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 18-2113313)8
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 73128
LENGTH: 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 AQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISAHPHIL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 FMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDIASDAFAT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHNFAIMT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 FKDLLTKHEDAVSEFLSSHYEQFFGLYTKLLSSTNYVTRRÖSVKFLSEFLLEAPNAQIMK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 KYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPKLIEFLS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 SKSHKNPAEIVKILKDNLAILEKODKKTD-KASEEVSKSLQAMKEILCGTNEKEPPTEAV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 351;
                                                                                                                                                                                                                                                                                                                                                                                                                           38.1%; Score 649; DB 12; Length 3:
42.3%; Pred. No. 1e-50;
tive 67; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: 700170954_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 SFQKERTDDEQFADEKNYLIKQIRDL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48872, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                Sequence 46025, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                   Zhou, Yihua
Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhou, Yihua
Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 138; Conservative
                                                                  APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                     ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                       US-10-425-114-46025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-425-114-48872
US-10-425-114-46025
                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                    LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Shouth                                                                                                                                                                                                                                                                                                                                                                                         ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 CKEDVISLIVQDLPSLGWGVRKDLAICWCILLRQKVDETYCCVQYLENHLELLDFLVGCY 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 YSSGLLVTLIADLQLIDPEGKKDVTQIFNNILRRQIGTRSPTVEYISAHPHILFMLLKGY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 FLNIMINLLKOSSKNIRICAFHVFKVFVVANPNKPRCIVVALLDNRREVLKKLLHNLPSSKG 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 EAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 HKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHNFAIMTKYISKPE 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 HEVVVABFLSSHYEQFFELYSRLLSSTNYVTRRQAIKFLSEFLLETHNSQIMKRYIVEVR 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 NLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPKLIBFLSSFQKERT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PPTEAVA-QLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 PVLRSXCRQLTQLFFKEDTLRLLIKCLPKINLEARKDATQVVAN-LRKQHESMIMLSDYX 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 PAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPTEAVAQLAQEL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 LFKSKPRTPPDVVRQTRDLLLFVDRSPETRESKREEKAMSELFKNIRELKSILYGNSESE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LFSKSHKNPAELVKILKDNLAILE-----KQDKKTDKASEEVSKSLQAMKEILCGTNEKE
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                        э
Э
                                                                                                                                                                                                                                                                               DB 12; Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.2%; Score 514; DB 12; Length 33
35.4%; Pred. No. 2e-38;
tive 79; Mismatches 122; Indels
                                                                                                                                                                                                                                                                    37.0%; Score 630.5; DB 12; Length 42.0%; Pred. No. 4.9e-49; tive 69; Mismatches 113; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_31352C.1.pep
US-10-424-599-209662
                                                                                                         OTHER INFORMATION: Clone ID: LIB3637-244-E1_FLI.per
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)..(337)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 209662, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDE-LDEEKDLIIQEIQKL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 DDEQFADEKNYLIKQIRDL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (1)..(?
```

φ

```
71; Conservative 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: April 12, 2004, 10:33:56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 70029, Application US/10425114
; Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 38.1%
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Liu, Jingdong
           LENGTH: 184
TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                               Query Match
Best Local Similarity
Matches 71; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 TFK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 LLK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-425-114-70029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-425-114-70029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Job time : 47 secs
SEQ ID NO 149595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                      챵
                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Caro Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRESENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                76 SNSAVMTRYVSSRDNLRILMNLRESSKSIQIEAFHVFKLFAANQKKPADIISIFVANRS 135
                                                                                         233
                                                                                                             184 PIFDTAANVTA----ILTRHKSTEAAFLSENYEWFYABYNTKLLESSNYITRRQAVKILG 239
                                                                                                                                                                   234 ELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEI 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 SDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYE-KLLQSENYVTKRQSLKLLGELILDR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP 299
                                     240 DMLLDRSNSAVMTRYVSSRDNLRILMNLLRESSKSIQIEAFHVFKLFAANQHKPADIVSI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 SDAAATFKELLTRRKSTVAEFLSKNYEWFFAEYNTKLLESSNYITRRQAVKLLGDMLLDR 75
               120 SAHPHILFMLLKGYEAPQ--IALRCG-IMLRECIRHEPLAKIILFS-NQFRD-FFKYVEL 174
                                                                                         STFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYE-KLLQSENYVTKRQSLKLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.2%; Score 395.5; DB 12; Length 173; 50.0%; Pred. No. 5.1e-28; ive 35; Mismatches 37; Indels 7;
                                                                                                                                                                                                                                                                FVANKSKWIRLLEDFKIDK-EDEQFEADKAQVWREIEAL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_11371C.1.pep
US-10-424-599-158029
                                                                                                                                                                                                                                            294 LLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 KLIEFLSSFOKERTDDEQFADEKNYLIKQI-----RDL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 149595, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 158029, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.0%
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-10-424-599-158029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-424-599-149595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 158029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                           g
                                                                                                                                                                                                       g
                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Пb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽
                                               g
                                                                                       ò
                                                                                                                                                                 δ
```

```
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Serven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules Associated With
TITLE APPLICANT ASSOCIATED ASSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 IILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIF-EDYEKL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CAQLIQEFFADNTLRLLIQYLPKINLEARKDATQIVANLQRQQVQSKLIASDYLDTNLDL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 VAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISAHPHI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 LFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIASDAFA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 IILFYRRMDSCFTLFLL----LNTNAYFFHTDL-----LCTDVVEOREQKIFYQDSHVM 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LFKPKPRTPSDIVKQTRDLLLRLTSRD---DDNMPDLTKNLRDLKSILYGNSESERPVPEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LFSKSHKNPABIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPTEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 LQSENYVTKRQSLKLLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 FKVFVASPHKTOPIVEILLKNOPKLIEFLSSFOKERTDDEOFADEKNYLIKOIRDL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Gaps
                                                                                                                                                                                                                                                                                                                                          ж
•
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.2%; Score 275.5; DB 12; Length 161; 38.1%; Pred. No. 4.1e-17; ive 34; Mismatches 54; Indels 21;
                                                                                                                                                                                                       Length 184;
                                                                                                                                                                                          18.9%; Score 322.5; DB 12; Length
38.8%; Pred. No: 2.6e-21;
cive 37; Mismatches 72; Indels
; OTHER INFORMATION: Clone ID: PAT_MRT3847_106106C.1.pep
US-10-424-599-149595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: UC-ZMFLB73031E03_FLI.pep
```

```
70, Appl
30, Appl
30, Appl
30, Appl
4, Appli
4, Appli
5367, Appl
19, Appl
                                                                                                                                                                                                                                                                                                                              Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                             Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                App]
                                        April 12, 2004, 10:27:13 ; Search time 22 Seconds (without alignments) 790.816 Million cell updates/sec
                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Sequence 2, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 6, A
                                                                                    ....FADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                           Sequence 3,
Sequence 3,
Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                Sequence 4,
Sequence 5,
Sequence 5,
                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                          /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
/cgn2_6/prodata/2/iaa/5B_COMB.pep:*
/cgn2_6/prodata/2/iaa/6A_COMB.pep:*
/cgn2_6/prodata/2/iaa/6B_COMB.pep:*
/cgn2_6/prodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/prodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                            Potal number of hits satisfying chosen parameters:
                                                                                                                        389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                            model
                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                     US-10-025-730-1
1704
1 MKKMPLFSKSHKNPAEIVKI.
                            wa gniau
                                                                                                                                                                                                     Issued Patents AA:*
                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                       Query
Match Length
                                                                                                                                                                                                                                                                                                                                                  3349
1112
1128
1339
1112
1128
1128
1128
1128
1138
1138
1109
1109
11109
11109
11109
11109
11109
11109
11109
11109
                            protein search,
                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                 Scoring table:
                            protein
                                                                                    Sequence:
                                                                                                                       Searched:
                                                                                                                                                                                                    Database
                                          Run on:
                                                                                                                                                                                                                                                                                                                                    Result
```

```
ö
                                          2334, Ap
4, Appli
5, Appli
5, Appli
5, Appli
2, Appli
2, Appli
2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 AHPHILFWLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIA 180
                                                                                                                                                        6465, Ap
5420, Ap
6, Appli
1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 NFAIMTKYISKPENLKIMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPK 300
                                                                                                                        3133, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 SDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 NFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                     Appli
Appli
                                                                                                                                             5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKMPLFSKSHKNPABIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKMPLFSKSHKNPABIVKILKDNLAILEKQDKKTDKASEBVSKSLQAMKEILCGTNEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 SDAFATFXDLLTRHKVLVADFLEQNYDT1FEDYEXLLQSENYVYKRQSLKLLGELLDRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
          Sequence
Sequence
Sequence
                                          Sequence
Sequence
Sequence
                                                                            Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                         Sequence
Sequence
Sequence
                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 LIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 1704; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.7e-161;
Matches 337; Conservative 0; Mismatches 0;
                            US-08-923-924-6
US-08-923-924-6
US-08-870-216-234
US-08-470-260-5
US-08-470-491-5
US-08-477-451-5
US-08-922-928-2
US-09-134-0010-3133
US-09-134-0010-3133
US-09-134-0010-6465
US-09-134-0000-5426
US-09-134-0000-543-6465
US-09-134-0000-5430
                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Gorgone, Gina A.
TITLE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REPERENCE: PF-0635 US
CURRENT APPLICATION NUMBER: US/09/190,965
CURRENT FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL PROGram
SEQ ID NO 1
LENGTH: 337
                                                                                                                                                                               US-08-328-254-6
                                                                                                                                                                                          US-08-353-700-1
                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09190965 Patent No. 6071721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: 3734805
US-09-190-965-1
          ORGANISM: Homo sapiens
FEATURE: -
RESULT 1
US-09-190-965-1
102.5
102.5
102.5
101.5
101.5
101.5
101.9
99.5
99.5
99.5
97.5
97.5
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ਨੋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

301 LIEFLSSFOKERTDDEOFADEKNYLIKQIRDLKKTAP 337

Sequence 1 Sequence 8 Sequence 1 Sequence 2

Sequence Sequence Sequence

4

```
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                        엄
                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 SDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PPTBAVAQLAQBLYSSGLLVTLIADLQLIDFBGKKDVTQIFNNILRRQIGTRSPTVEYIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AHPHILFMLIKGYBAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 NFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 NFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKKMPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKKMPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1704; DB 4; Length 337; 100.0%; Pred. No. 1.7e-161; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 LIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 LIEFLSSFOKERTDDEOFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tang, Y Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorlone, Gina A.
ITTLE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REFERENCE: PF-0635 US
CURRENT APPLICATION NUMBER: US/09/190,965
CURRENT FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
LENGTH: 341
                                                                        APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorgone, Gina A.
TITLE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REFERENCE: PF-0635 US
CURRENT FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: 09/190,965
PRIOR PILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 3, Application US/09190965; Patent No. 6071721; GENERAL INFORMATION:
               Sequence 1, Application US/09470253
Patent No. 6365371
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 3734805
                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-09-190-965-3
US-09-470-253-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-470-253-1
                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
241 HNFTIMTKYISKPENLKLAMMLLRDKSRNIQFBAFHVFKVFVANPNKTQPILDILLKNQT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EPQTEAVAQLAQELYNSGLLGTLVADLQLIDFEGKKDVAQIFWNILRRQIGTRTPTVEY1 120
                                                                                                                                                                                                                                                                                                                                               60 EPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI 119
                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVPKVFVASPHKTQPIVEILLKNQP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 EPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 SAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MPFPPGKSHKSPADIVKNIKESMAVLEKQDISDKKAEKATEEVSKNIVAMKEILYGTNEK 60
                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 MPL-FSKSHKNPAEIVKILKDNLAILEKQ---DKKTDKASEEVSKSLQAMKEILCGTNEK 59
                                                                                                                                                                                                                                                                       1 MPFPPGKSHKSPADIVKNLKESMAVLEKQDISDKKAEKATEEVSKNLVAMKEILYGTNEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ASDAFATFKDLITRHKLLSAEFLEQHYDRFFSEYEKLIHSENYVTKRQSLKLIGELLLDR
                                                                                                                                                                                                                                        4 MPL-FSKSHKNPAEIVKILKDNLAILEKQ---DKKTDKASEEVSKSLQAMKEILCGINEK
                                                                                                                                                                                                                                                                                                                                                                             61 EPQTEAVAQLAQELYNSGLIGTLVADLQLIDFEGKKDVAQIFNNILRRQIGTRTPTVEYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 SAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 ASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                      4.
                                                                                                                                  DB 3; Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.8%; Score 1376; DB 4; Length 3
80.7%; Pred. No. 8e-129;
cive 32; Mismatches 29; Indels
                                                                                                                            80.8%; Score 1376; DB 3; Length 3 80.7%; Pred. No. 8e-129; tive 32; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300 KLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 KLIEFLSKFQNDRTEDEQFNDEKTYLVKQIRNLKRAA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Gorgone, Gina A.
AITLE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REPERENCE: PF-0635 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/470,253
CURRENT FILING DATE: 1999-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 1999-12-22
PRIOR APPLICATION NUMBER: 09/190,965
PRIOR FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL PROGRAM
SO ID NO. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-470-253-3; Sequence 3, Application US/09470253; Patent No. 6365371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: g262934
US-09-470-253-3
                                 ; FEATURE: -
; OTHER INFORMATION: g262934
US-09-190-965-3
                                                                                                                                                                                    Matches 272; Conservative
                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 272; Conserva
ORGANISM: Mus sp.
FEATURE: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                  Query Match
                                                                                                                                                           Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDAFATFKDLLTRHKVLVADFLEQNYDT1F-EDYEKLLQSENYVTKRQSLKLLGELILDR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 HNFTVMTRYISEPENLKLMMMMLKEKSRNIQFEAFHVFKVFVANPNKPKPILDILLRNQT 300
                                                                        181 ASDAFATFKDLITRHKLLSAEFLEQHYDRFFSEYEKLLHSENYVTKRQSLKLLGELLLDR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 E-AVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISAH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 PHILFMLLKGYE--APQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIA 180
180 ASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDR 239
                                                                                                                       240 HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP 299
                                                                                                                                           181 SDAFSTFKELLTRHKLLCAEFLDANYDKFFSQHYQRLINSENYTRRQSLKLLGELLLDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 MPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Indels
                                                                                                                                                                                          300 KLIEFLSSFOKERTDDEQPADEKNYLIKQIRDLKKTA 336
                                                                                                                                                                                                            301 KLIEFLSKFQNDRTEDEQFNDEKTYLVKQIRNLKRAA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.1%; Score 1109; DB 3; 65.0%; Pred. No. 3.1e-102; cive 59; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 KLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 KLVDFLINFHIDRSEDEQFNDEKAYLIKQIKELK 334
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorder, Meil C.
APPLICANT: Gorder, Gina A.
TITLE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REPERBRE: PP-0635 US
CURRENT APPLICATION NUMBER: US/09/190,965
CURRENT FILING DATE: 1998-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09470253
Patent No. 6365371
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09190965
Patent No. 6071721
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTHER INFORMATION: 91794137
US-09-190-965-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-470-253-4
                                                                                                                                                                                                                                                                                               US-09-190-965-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                    ð
                                                                                 g
                                                                                                                     à
                                                                                                                                                    g
                                                                                                                                                                                        à
                                                                                                                                                                                                                      셤
```

```
181 SDAFSTFKELLTRHKLLCAEPLDANYDKFFSQHYQRLINSENYYTRRQSLKLIGELLLDR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DYVVAQLSQELYNSNILLILILIQNIAHRIDFEGKKHVALIFNNELIRRQIGTRSPTVEYICTK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 HNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 HNFTVMTRXISEPENLKLMMMHLKEKSRNIQPEAFHVFKVFVANPNKPKPILDILLRNQT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 E-AVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISAH 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 PHILFMLLKGYE--APQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 SDAFATFKDLLTRHKVLVADFLEQNYDTIF-EDYEKLLQSENYVTKRQSLKLLGELILDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 MPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.4%; Score 1063.5; DB 3; Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.1%; Score 1109; DB 4;
65.0%; Pred. No. 3.1e-102;
tive 59; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 KLIEFLSSPOKERTDDEQFADEKNYLIKQIRDLK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 KLVDFLINFHIDRSEDEQFNDEKAYLIKQIKELK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/03190965
; Sequence 5, Application US/03190965
; Patent No. 6071721
; GENERAL INFORMATION:
   APPLICANT: Tang, Y. Tom
; APPLICANT: Gorgaler, Karl J.
; APPLICANT: Gorgaler, Karl J.
; APPLICANT: Gorgane, Gina A.
; TITLE OF INVENTION: CALCIUM BINDING PROTEIN
; FILE REPERENCE: PF-0635 US
; CURRENT APPLICATION NUMBER: US/09/190, 965
; CURRENT FILING DATE: 1998-11-13 **
; SOFIWARE: PERL PROGram
; SEQ ID NO 5
; SOFIWARE: PERL PROGram
; LENGTH: 377
APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
TITLE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REFERENCE: PP-0635 US
CURRENT FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: 09/190,965
PRIOR FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 5
SOFTHARE: PERL PROGram
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: 91794137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: 91255838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-190-965-5
                                                                                                                                                                                                                                                                                                                                        LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-09-190-965-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-470-253-4
                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
```

3

63

```
767 LEKOMKEKE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Beraud, Christophe APPLICANT: Freedman, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.5%,
Best Local Similarity 20.1%
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 DRHNFAIMTK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                           RESULT 9
US-09-914-259-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-914-259-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-724-517-2
 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                     ò
                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ਨੇ
                                 엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TFFLYVQSEVFDISSDAFSTFKELTTRHKAILAEFLDSNYDTFFAQYQNLLNSKNYVTRR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 KEILCGTNEKEPPTE---AVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KSFIYGNDSAEPSSEHVVQVAQLAQEVYNANILPMLIKMLPKFEFECKKDVGQIFNNLLR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 RQIGTRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROIGTRSPTVEYLGARPEILIQLVQGYSVPDIALTCGLMLRESIRHDHLAKIILYSDVFY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 DFFKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKR 226
                                                                                                                                                  61 KSFIYGNDSAEPSSEHVVQVAQLAQEVYNANILPMLIRMLPKFEFECKKDVGQIFNNLLR 120
                                                                                                                                                                                                                      181 TFFLYVQSEVFDISSDAFSTFKELTTRHKAIIAEFLDSNYDTFFAQYQNLLNSKMYVTRR 240
                                                                                                                                                                                                                                                                                                                                            QSLKLLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHK 286
                                                                                                                                                                                                                                                                                                                                                                 241 QSLKLIGELLLDRHNFNTMTKYISNPDNLRLMMELLRDKSRNIQYBAFHVFKVFVANPNK 300
                                                                                                                           KEILCGTNEKEPPTE---AVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILR 106
                                                                                                                                                                                                 RQIGTRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MPLLFGKSHKSPADVVKTLREVLTILDKLPPPKLDKDGNIQSDKKYDKALDEVSKNVAMI 60
                                                                         1 MPLLPGKSHKSPADVVKTLREVLTILDKLPPPKLDKDGNIQSDKKYDKALDEVSKNVAMI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDKKTDKASEEVSKSLQAM 49
                                                      -- QDKKTDKASEEVSKSLQAM 49
                                                                                                                                                                                                                                                                     DFFKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKR
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                    301 PKPISDILNRNREKLVEFLSEFHNDRTDDEQFNDEKAYLIKQIQEMKSS 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                287 IQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKKT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
 ; Pred. No. 1.2e-97;
53; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.4%; Score 1063.5; DB '60.5%; Pred. No. 1.2e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-09-470-253-5
; Sequence 5, Application US/09470253
; Patent No. 6365371
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Guegler, Karl J.
APPLICANT: Gregore, Gina A.
; TITLE OF INVENTION: CALCIUM
; FILE REFERENCE: PF-0635 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53; Mismatches
                                                    4 MP-LFSKSHKNPAEIVKILKDNLAILEK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/470,253
CURRENT FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: 09/190,965
PRIOR FILING DATE: 1988-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 MP-LFSKSHKNPAEIVKILKDNLAILEK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Caenorhabditis elegans
   60.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: 91255838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                    211; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Best Local Similarity
Matches 211; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 5
LENGTH: 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-470-253-5
                                                                                                                             20
                                                                                                                                                                                                 107
                                                                                                                                                                                                                                                                     167
                                                                                                                                                                                                                                                                                                                                            227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                      g
                                                                                                                                                         g
                                                                                                                                                                                             \delta
                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                           à
                                                                                                                                                                                                                                                                     ò
```

```
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264
                                241 QSLKLIGELLIDRHNFNTWTKYISNPDNLRLMMELLRDKSRNIQYEAFHVFKVFVANPNK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 LLVTLIADLQ--LIDFECKKDVTQIFNNILRRQI------GTRSPTVEYISAHPHI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 LFMLLKGYBAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIASDAFA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----NDLQEKFAQLEAEN-SILKDEKK 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 TPKDLLTRH------KVLVADFLE-QNYDTIFEDYEKLIQSENYVTKRQSLKLLGELIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         858 ORNTFSFAEKNFEVNYQELQEEYACLLKVKDDLEDSKNKQELEYKSKLKALNEELHLQRI 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   918 NPTIVKAKKSSVFDEDKTFVA---ETLEMGEVVEKDITELMEKLEUSVEKLELSQRLSDL 974
QSLKLLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHK 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----YISKPENLKLMMNLLRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 VKILKDNLAILEKODKKTDKASEEVSKSLQAMKEILCGTNEKEPPTEAVAQLAQELYSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             711 --ISKLKDLQOSLVNSKSEEMTLQI--NELQKEIEILRQEEKEKGTLEQEVQELQLKTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265 KSPNIQFEA--FHVFKVFVASPHKTQPIVEILLKNQPKLIBFLSSFQKERTD-DEQFAD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.5%; Score 128.5; DB 4; Length 3878;
20.1%; Pred. No. 0.0044;
Live 75; Mismatches 116; Indels 115;
                                                                                                                                                         301 PKPISDILNRNREKLVEFLSEFHNDRIDDEQFNDEKAYLIKQIQEMKSS 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: No. 6379941el motor proteins and methods for TITLE OF INVENTION: their use FILE REFERENCE: 1031 CURRENT APPLICATION NUMBER: US/09/724,517
                                                                                                                      287 TQPIVEILLKNOPKLIEFLSSFOKERTDDEGFADEKNYLIKQIRDLKKT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STACED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT APPLICATION NUMBER: US/09/914,259
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 3878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                975 SEQLKQKHGEISFLNEEVKSLKQ 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 -----EKNYLIKQIRDLKK 334
                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/09914259
Patent No. 6495336
GENERAL INFORMATION:
APPLICANT: Makowski, Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/09724517; Patent No. 6379941
```

1

```
1027 RELESALDHIKLQCDRRLTLQQKEHEQKMQLLLHHFKEQDGEGIMETFKTYEDKIQQLEK 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    967 NLSRGEANVLEKLACLSPVEIRTILFRYFNKVVNLREAERKQQLYNEEMKMKVLERDNMV 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------ RHKVLVAD--- 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 ------FEDYEXLLOS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TKYISK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 -------HPHILFMLKGYEAPQIALRCGIMLRECIRHEPLAKIILFS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            910 KRRHDVDEKLKNGRVLSPEEEHVLFQLEEGIEALEAAIE---YRNESIQNRQKSLRASFH 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 PENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPKLIEFLSSF--- 308
                                                                                                                                                                                                                                                                                                                                                                                     23 DNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPTEAVAQLAQELYSSGLLVTL 82
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) Sequence 2, Application US/09641807A
) Patent No. 6440731
) GENERAL INFORMATION:
) APPLICANT: Beradu, Christophe
) APPLICANT: Breedman, Richard
) TITLE OF INVENTION: No. 6440731e1 motor proteins and methods for ITLE OF INVENTION: their use
) TITLE OF INVENTION: their use
) TITLE OF INVENTION: 1031
CURRENT APPLICATION NUMBER: US/09/641,807A
) CURRENT FILING DATE: 2000-08-17
) NUMBER OF SEQ ID NOS: 4
) SOFTWARE: FRAESEQ for Windows Version 4.0
) SEQ ID NO 2

LENGTH: 1279
                                                                                                                                                                                                                                                                                                                                              61; Mismatches 137; Indels 165;
                                                                                                                                                                                                                                                                                                         Length 1279;
                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 NOFRDFFKYVE---LSTFDIASDAFATFKDLLT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 IADLOLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 ENYVTKRQS------LKLLGELILDRHNFAIM----
                                                                                                                                                                                                                                                                                                       6.7%; Score 113.5; DB 19.3%; Pred. No. 0.028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1191 SGHMLGNENKTETDDNQFTKSHSRLSSQIQ 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 -----QKERTDDEQFADEKNYLIKQIR 330
CURRENT FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: US/09/641,807
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                        LOCATION: (409) ... (436)
OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                                                                                                                                       Local Similarity 19.39
nes 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human
FEATURE:
NAME/KEY: VARIANT
LOCATION: (409)...(446)
                                                                                                                                                                                                     NAME/KEY: VARIANT
                                                                                                                                             TYPE: PRT
ORGANISM: Human
                                                                                                   SEQ ID NO 2
LENGTH: 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-641-807A-2
                                                                                                                                                                                                                                                               US-09-724-517-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               日
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \stackrel{>}{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
```

```
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    967 NISRGEANVLEKLACLSPVEIRTILFRYFNKVVNLREAERKQQLYNEEMKMKVLERDNMV 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1027 RELESALDHLKLQCDRRLTLQQKEHEQKMQLLLLHHFKEQDGEGIMETFKTYEDKIQQLEK 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | |: | : | : |: | : |: | : |: | DLYFYKKTSRDHKKKLKELVGEAI---RRQLAPSEYQEAGDGVLKPEGGGMLSEELKWASR 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                           852 LRSSQALNTDSLKISTRL--NLLEQELSEKNVQLQTSTAEEKTKISEQVEVLQKEKDQLQ 909
                                                                                                                                                                                                                                                                                          910 KRRHDVDEKLKNGRVLSPEEEHVLFQLEEGIEALEAAIE---YRNESIONRQKSLRASFH 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENYVIKROS-----IKLIGELILDRHNFAIM--------TKYISK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPKLIEFLSSF--- 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 DNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPTEAVAQLAQELYSSGLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                        NQFRDFFKYVE----LSTFDIASDAFATFKDLLT------RHKVLVAD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------FEDYBKLLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 DNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPTEAVAQLAQELYSSGLLVTL
                                                                                              Indels 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Beraud, Richard
TITLE OF INVENTION: No. 6448026el motor proteins and methods for TITLE OF INVENTION: their use
FILE REFERENCE: 1031
CURRENT APPLICATION NUMBER: US/09/723,096
FURRENT PLING DATE: 2000-11-27
PRIOR FILING DATE: 2000-08-17
                                                       DB 4; Length 1279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1279;
                                                     6.7%; Score 113.5; DB 4;
19.3%; Pred. No. 0.028;
live 61; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.7%; Score 113.5; DB 4;
Best Local Similarity 19.3%; Pred. No. 0.028;
Matches 87; Conservative 61; Mismatches 137;
                                                                                                                                                                                                              83 IADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1191 SGHMLGNENKTETDDNOFTKSHSRLSSQIQ 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 -----QKERTDDEQFADEKNYLIKQIR 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOCATION: (409)...(436)
CTHER INFORMATION: Xaa = any amino acid
US-09-723-096-2
OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 2, Application US/09723096
; Patent No. 6448026
                                                                                              87; Conservative
                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1279
  ; US-09-641-807A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-09-723-096-2
                                                                                                                                                                                                                                                                                                                                                                      163
                                                                                                                                                                                                                                                                                                                                                                                                                                                  201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252
                                                                                                                                                                                                                                                                                          122
                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                            Matches
                                                                                                                                   à
                                                                                                                                                                     엄
                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
Sequence 70, Application US/08630822A
Patent No. 5840695
GENERAL INFORMATION:
APPLICANT: FRANK, GLENN R.
APPLICANT: WALLENFELS, LYNDA
ITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 KNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI---RDL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69; Mismatches 124;
                                                                                                                                                                                                             Sequence 6286, Application US/09543681A, Patent No. 6605709; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 19.83
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Frocev
US-09-543-681A-6286
                                                                                                                                                                                RESULT 14
US-09-543-681A-6286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-630-822A-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                               엄
                                                                                    à
                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ठ
               à
                                                                                                                                                                                                                                                                                                                                                                                       DLYFYKKTSRDHKKKLKELVGEAI--RRQLAPSEYQEAGDGVLKPEGGGMLSEELKWASR 1144
                                                                                                                                                                          967 NLSRGEANVLEKLACLSPVEIRTILFRYFNKVVNLREAERKQQLYNEEMKMKVLERDNMV 1026
                                                                                                                                                                                                                                                   1027 RELESALDHIKLQCDRRITLQQKEHEQKMQLLLHHFKEQDGEGIMETFKTYEDKIQQLEK 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            309 LPEIDFFSEDRKEKSSSVGYDXKKKOXSNIKRFHNKINRTKEEKKKKWN--KIIINRNNI 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 LQHNT--TNKCKTFLFNKHIIFDKİENNNIPLFIYDLLNYIFKSDQTYFYHNNFIDEYKQ 424
                   910 KRRHDVDEKLKNGRVLSPEEEHVLFQLEEGIEALEAAIE---YRNESIQNRQKSLRASFH 966
                                                                                                                                                                                                                                                                                         -----TKYISK 251
                                                                                                                                                                                                                                                                                                                                                              PENLKLMMNLLRDKSPNIOFEAFHVFKVFVASPHKTQPIVEILLKNQPKLIEFLSSF--- 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 KEPPTEAVAQLAQELYSSGLLVTLIAD-----LQLIDFEGKKDVTQIFNN------ 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 ILRRQI--GTRSPTVEYI--SAHPHILFMLLK---GYEAPQIALRCGIMLRECIRHEPLA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425 KICKQIKCSTKKNDISHIITSRKENHLFHVQKLENNYKHPNI------NKQLRKTKIL 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- 197
                                                                     -HPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKMPLFSKSHKNPAEIV--KILKDNLAILEKODKKTDKASEEVSKSLQAMKEILCGTNE 58
                                                                                                                                           ----RHKVLVAD---
                                                                                                                                                                                                                  --FLEQNYDTI-----FEDYEKLLOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Long, David M.
APPLICANT: Metz, Anneke M.
APPLICANT: Metz, Anneke M.
TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Genes FILE REPERENCE: 47714-5009-US
CURRENT APPLICATION NUMBER: US/09/417,485D
CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.6%; Score 113; DB 4; Length 2184;
21.9%; Pred. No. 0.068;
iive 58; Mismatches 140; Indels 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 KIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTR-HKV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa at position 330 = Leu or Ile;
OTHER INFORMATION: Xaa at position 335 = Asp or Gly.
IADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISA-
                                                                                                                                           NQFRDFFKYVE----LSTFDIASDAFATFKDLLT----
                                                                                                                                                                                                                                                                                         ENYVTKROS-----LKLLGELILDRHNFAIM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1191 SGHMLGNENKTETDDNOFTKSHSRLSSOIQ 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                     309 -----QKERTDDEQFADEKNYLIKQIR 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09417485D Patent No. 6541202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 21.9*
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:
--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . (335)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: unsure LOCATION: (330)..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-09-417-485D-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2184
                                                                                                                                                                                                                                                                                       220
                                                                                                                                                                                                                                                                                                                            1087
                                                                                                                                                                                                                                                                                                                                                                252
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                   g
                                                                                                                                                                    g
                                                                                                                                                                                                               \stackrel{>}{\circ}
                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                          g
                                                                 ð
                                                                                                                                      à
```

```
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT PILING DATE: 109/9/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                         151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : : | |: : : | | |: : : | | | 368 ---ILFEEQIELPDD--IFINKLPDKIADLRLEQFEINKQRDQIF------QPNLYI-- 413
                                                             198 VADFLEQN-YDTIFEDYE-----KLLQSENYVTKR-QSLKLLGELILDRHNFAIMT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 ALNKSSADKAQMRŠSSVQLLQLEQYYLQQQNSFQKRTLQSNVQLQSLLQLQLQRDYSSAYID 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264 LSQEHAQLLQEILSDKRLDS----SEEVAKEAQTAELSNQAIKNNAFYLAQADINKKLSD 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----ATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 HNFAIMTKYISKPENLKLAMMILLRDKSPNIQFEAFHVFK----VFVASPHKTQPIVEILL 295
KYVY--NYFKEFINNVINTKFGKIYRKFFPRKHILNKIHKIFKIIRLQIIXKYRIINIRM 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 LESQLEEVLQSLAKAQEDLANYSNELIV-----LQTQPERAQSVLFNNSERLQQIRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 KLIITTQNNNELNRHSLMVKNRL------DRAIQSERNL-KEQIDVLKGSLLLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 ----EPPTEAVAQLAQEL--YSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                          247 KYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKN 297
                                                                                                                                                                                                                                      Indels 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.3%; Score 107; DB 4; Length 1155; 19.8%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 L--RCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIASDAF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 ILKDNLAILEKODKKTDKASEEVSKSLOAMKEILCGTNEK-----
   477
```

```
400 EKKAKTLPLEAPRSATETQELDVRKERGEILIDELMDAIXKVKVNVPDENRLKLIENILGR 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 IDTDKDRHIKVE--DVLKVIDIVEKEDGIMSTKQLDELVQLLKKEE--VIELEEKKEKQE 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 -----TPVATEVDKNADEVEFTK-KDLEVVEDALDTLSKDKNNLVIEKEVIKDI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----- NYDTIFEDYEKL-- 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 KEEIADYQEDVEELKEAIVAAEKPKDEIKETKGAQRLLKXVNKMITKMDTVVQEIESKES 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 -----LQSENYVTKRQSL---KLLGELILDRHNFAI-MTKYISKPENLKLMMNLL-- 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 LIADLOLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISAHPHILFMLLKGYEAPQIALR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255 LIDTAPVIDAEKTPKV------ATSP-VESPLAPPEVLIM-----GAPK---- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 CGIMLRECIRHEPLAKIILFSNQFRDFRKYVELSTFDIASDAFATFKDLLTRHKVLVADF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 --RDKSPNIQFEAFHVFKVF-----VASPHKTQPIVEILLKNQPKLIEFLSSFQKER 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 KDNLAILEKODKKTDKASEEVSKSLQAMKEILCGTNEKEPPTEAVAQLAQELYSSGLLVT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.2%; Score 105; DB 2; Length 586;
Best Local Similarity 20.0%; Pred. No. 0.064;
Matches 77; Conservative 54; Mismatches 136; Indels 118; Gaps
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin Release #1.0, Version #1.25
                                  NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPETIGEN ROSS P.C.
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FATERILIA RELEASE #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,822A
FILING DATE: 11-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-17-C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEPHONE: CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 586 amino acids
TYPE: amino acids
TYPE: Amino acids
TYPE: Amino acids
TOWNEY TELEPHONE: TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL TENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               516 SQQKSFVPPSETLHLESSQQKSTVP 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313 TDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Xaa = any amino acid
LOCATION: 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                               ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                      STREET: 1700 Linc
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-630-822A-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

Search completed: April 12, 2004, 10:32:58 Job time: 24 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

April 12, 2004, 10:33:03; Search time 20 Seconds (without alignments) 1620.827 Million cell updates/sec

probable transposa probable transposa ribosomal protein polyporopepsin (EC probable transcrip probable carbamoyl ornithine cyclodea amino acid ABC tra protein FINI 9.7 [i

endoglucanase prec endoglucanase prec

hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical outer hypothetical outer hypothetical outer hypothetical prote Fe-S oxidoreductas

8-amino-7-oxononan

hypothetical prote virulence-mediatin

probable resistanc

1 MKKMPLFSKSHKNPAEIVKI.....RADEKNYLIKQIRDLKKTAP 337 US-10-025-730-1 337 Title: Perfect score:

OFIGO Scoring table: Sequence:

Gapop 60.0 , Gapext 60.0

283366 seqs, 96191526 residues Searched:

0

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 300 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	hypothetical calci		hypothetical prote		н	hypothetical prote	ρ	hypothetical prote			υ	hypothetical prote		ဌ	hypothetical profe	₩			Ψ	probable desA2 pro	probable methyltra	hypothetical prote		_	hypothetical prote	- 1	hypothetical prote		
	ΙΩ	157997	T50117	T27129	T16651	203900	S72925	G89814	AG2552	AH2522	F71407	AB1605	C64300	G95316	G70325	AB2247	S19734	T22075	T23866	C87153	D70896	E96937	G98020	90668H	T40402	G71441	E64762	D90679	H85529	T17557
	DB	į N	N	7	~	N	~	N	~	~1	N	~	~	~	0	2	~	N	7	N	~	7	~	N	~	~	-	~		
	Length	341	329	338	377	923	103	122	134	134	135	154	156	171	179	191	229	241	264	275	275	282	283	299	301	305	309	309	309	309
A 0	Query	6.8	4.7	4.2	4.2	2.4	2.1	2.1	2.1		2.1	•	2.1	2.1	2.1	•			•	2.1	2.1	•	2.1	2.1			•	2.1	•	2.1
	Score	23	16	14	14	89	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
	Result No.		7	3	4	ហ	9	7	œ	Φ	10	11	12	13	14	15	16	17		19	20	21	22		24	25	26	27		29

744332 744332 746990333 746990331 746964360 746964360 746964360 746964360 746964360 746964960 746964	2827772 2832 2822 2822 2822 2822 2822 28
000000000000000000000000000000000000000	000000000000000000000000000000000000000
11111111111111111111111111111111111111	1288812444666777788
	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛๛	

myocilin - mouse myocilin - human methyl-accepting c hypothetical prote hypothetical prote hypothetical prote hypothetical prote auxin-regulated pr hypothetical prote probable dropgluco hypothetical prote probable dropgluco hypothetical prote ferrous iron trans

probable micochond
ND-40 repeat-prote
mannosidase famor
mannose-l-phosphat
probable wirulence
probable membrane
N-methyl D-asparta
OmpA-related prote
Ca2+-transporting
hypothetical prote
glutamate receptor
N-methyl-D-asparta
probable RAS GTPas
probable RAS GTPas

utrophin human lysosomal traffick beige protein homo fibrinogen alpha c homeotic protein M beta-defensin-7

toxin-co-regulated

reticulocyte-bindi

Dbx homeobox (home hypothetical prote hypothetical prote probable ribosomal hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote

All protein - vari hypothetical prote VITF-2, late gene hypothetical prote uncharacterized pr H transfer deterni protein gp35 from hypothetical prote hypothetical prote small protein - He	fibr protein [impo conserved hypothet replication-associ interleukin-2 prec conserved hypothet hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein ribosomal protein	phase protein (imporbable poly(3-hy probable poly(3-hy hypothetical protein hypothetical protein propolymer transpoblopolymer protein hypothetical protein hypothetical protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein protein	hypothetical prote superoxide dismuta hypothetical prote NBS-IRR type resis hypothetical prote NBS-IRR type resis hypoxanthine phosp hypothetical prote HupB hydrogenase r syd protein [impor thioredoxin f prec thioredoxin f prec hypoxanthine phosp hypoxanthine phosp hypoxanthine phosp hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote
6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8 150 2 6 1.8	6 1.8 152 2 2 6 1.8 153 2 6 1.8 155 2 6 1.8 155 2 6 1.8 155 2 6 1.8 155 2 6 1.8 155 2 6 1.8 155 2 6 1.8 155 2 6 1.8 157 2 6 1.8 157 2 6 1.8 157 2 6 1.8 157 2 6 1.8 157 2 6 1.8 157 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.8 158 2 6 1.	6 1.8 161 2 2 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	219 6 1.8 173 2 F70112 220 6 1.8 174 2 A35383 221 6 1.8 174 2 A35383 222 6 1.8 176 2 E90006 223 6 1.8 176 2 T02217 224 6 1.8 178 2 AH05217 225 6 1.8 178 2 AH0521 226 6 1.8 178 2 A705217 229 6 1.8 180 2 A20558 231 6 1.8 181 2 A70861 232 6 1.8 182 2 A5052 233 6 1.8 182 2 A5052 234 6 1.8 182 2 A5052 235 6 1.8 182 2 A5052 236 6 1.8 182 2 A5052 237 6 1.8 182 2 A5052 238 6 1.8 182 2 A5052 239 6 1.8 182 2 A5052 235 6 1.8 182 2 A5052 236 6 1.8 182 2 A5052 237 6 1.8 182 2 A5052 238 6 1.8 182 2 A5052 239 6 1.8 183 2 C71072 240 6 1.8 186 2 J02181 241 6 1.8 186 2 J02181 242 6 1.8 186 2 J02181 243 6 1.8 188 2 A3335 244 6 1.8 189 2 A63395 245 6 1.8 189 2 A63395 247 6 1.8 192 2 A75506 248 6 1.8 192 2 A75506 248 6 1.8 192 2 A75506
hypothetical prote ribosomal protein hypothetical prote hypothetical prote hypothetical prote erythrocyte membra hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote	hypothetical prote gene 3 protein-rel NADH2 dehydrogenas 11K protein - cani carboxypeptidase B hypothetical mutan hypothetical prote conserved hypothet hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote sensorin A - Calif hypothetical prote	hypothetical prote conserved hypothet probable type II s hypothetical prote type I restriction hypothetical prote conserved hypothetical prote hypothetical prote hypothetical prote sugar transport ho ribosomal protein ribosomal protein s sugar transport ho ribosomal protein ribosomal protein s sugar transport ho ribosomal protein ribosomal protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein	translation initia hypothetical prote hypothetical prote hypothetical prote probable translati probable translati probable translati hypothetical prote hemoglobin alpha c orf US426 - infect heat shock protein RNA-binding protein RNA-binding protein probable membrane ribosomal protein hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypothetical hypo
11.88888222211.8888883222222222222222222	1.8 98 2 1.8 100 2 1.8 100 2 1.8 100 2 1.8 100 2 1.8 100 2 1.8 110	1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8 1.8	6 1.8 135 2 B69103 6 1.8 135 2 B69842 6 1.8 135 2 B69842 6 1.8 137 2 T17944 6 1.8 137 2 T17944 6 1.8 140 2 D71002 6 1.8 140 2 D71004 6 1.8 140 2 D71004 6 1.8 142 2 148552 6 1.8 144 2 T16961 6 1.8 144 2 T16961 6 1.8 145 2 G69011 6 1.8 145 2 G69011 6 1.8 145 2 G69010 6 1.8 148 2 B95641 6 1.8 148 2 B95641 6 1.8 148 2 B95641 6 1.8 148 2 D90143 6 1.8 150 2 F72163

C; Keywords: calcium binding

3-dehydroquinate d development relate hypothetical prote NNF1 protein - yea hypothetical prote probable heme bind conserved hypothet related to BET1 pr gene T protein - E hypothetical prote phasphoribosylglyc ARC transporter, A hypothetical prote transcription regu DNA repair protein phosphoribosylglyc BC transporter, A hypothetical prote phosphoribosylglyc probable permease hypothetical prote probable permease hypothetical prote conserved hypothet conserved hypothet conserved hypothet conserved hypothet conserved hypothet conserved hypothet conserved hypothet conserved hypothet conserved hypothet conserved hypothet conserved hypothet coll division ATP- cell division AT	change 19-May-2000 ssed in cleavage stage mouse em
A84191 HG7106 HG7106 HG7106 C81282 C85778 S52837 S52837 S18884 A43322 H94354 AC2301 S0686 F90048 F90048 F90048 F90048 G95238 C98933 C71653 C7162 C98933 C7162 C98933 C7162 C98933 C7162 C98933 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C7162 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C98093 C9809	ALIGNMENTS  protein - mouse  revision 02-Aug-1996 #text_chang  .; Nozaki, M. a novel mRNA sequence expressed (UID:93119656; PMID:8418809  ated from GB/EMBL/DDBJ
	or _r
2000 2000 2000 2000 2000 2000 2000 200	nding see) capency into, into, into capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency capency ca
	ical calcium-binding s: Mus sp. (mouse) 100: 157997 to, H.; Matsushiro, rod. Dev. 34, 1-7, 1 Molecular cloning o nce number: 157997; ion: 157997 ion: 157997
<u> </u>	callus Institute Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Device Control Devi
9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 157997 hypothetical calcium-bic; species: Mus sp. (mou C; Date: 0.02-Aug-1997 C; Accession: 157997 R; Miyamoto, H.; Matsush Mol. Reprod. Dev. 34, 1 A; Title: Molecular clora, Reference number: 157 A; Reference number: 157 A; Ratus: preliminary; A; Molecula: type: mRNA A; Residues: 1341 A; RESA

```
C;Genetics:
A;Gene: SPDB:SPAC1834.06c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
T16651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                  ठे
                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Cross-references: GB:S51858; NID:g262933; PIDN:AAB24801.1; PID:g262934 C; Superfamily: Saccharomyces hypothetical protein YKL189w
```

```
A;Cross-references: EMBL:AL157734; PIDN:CAB75774.1; GSPDB:GN00066; SPDB:SPAC1834.06c
A;Experimental source: strain 972h(-); cosmid c1834
                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-338 <WIL>
A;Cross-references: EMBL:Z99277; PIDN:CAB16486.1; GSPDB:GN00020; CESP:Y53C12A.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                           mo25 homolog [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Bate: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 28-Jul-2000
C;Accession: T50117
R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, February 2000
A;Reference number: Z55039
A;Reference number: Z55039
A;Reference number: J55039
A;Reference number: DNA
A;Molecule type: DNA
A;Residues: 1-329 <SEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Y53C12A.4 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Cacession: T27129
R; Kershaw, J.; Lennard, N. submitted to the EMBL Data Library, September 1997
A; Reference number: Z20315
A; Accession: T27129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                   Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Query Match 6.8%; Score 23; DB 2; Length 341; Best Local Similarity 100.0%; Pred. No. 1e-15; Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
4.2%; Score 14; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Map position: 2
A,Introns: 29/3; 103/3; 136/2; 215/1; 282/3
C,Superfamily: Saccharomyces hypothetical protein YKL189w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 1
A;Introns: 34/3; 185/3
C;Superfamily: Saccharomyces hypothetical protein YKL189w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
4.7%; Score 16; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                          244 IMTKYISKPENLKLMMNLLRDKS 266
                                                                                                                                                       245 IMTKYISKPENLKLMMNLLRDKS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: clone Y53Cl2A C;Genetics:
A;Gene: CESP:Y53Cl2A.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 SENYVTKRQSLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 SENYVTKRÓSLKLIGE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 LRRQIGTRSPTVEY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 LRRQIGTRSPTVEY 122
                                                                                                                          ò
                                                                                                                                                                                 q
```

```
hypothetical protein alr8014 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120. C;Species: Nostoc sp. PCC 7120 a synonym of Anabaena sp. strain PCC 7120 c;Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 c;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002 c;Accession: AG2552 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Natanabe, A.; Iriguc: Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein SA0444 [imported] - Staphylococcus aureus (strain N31 C;Species: Staphylococcus aureus (strain N31 C;Species: Staphylococcus aureus (cipate: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: G89814 T; Uchiyama, T; Wabay, T; Waran, T; Yuzawa, H; Kobayashi, I; Rskurcda, M; Ohla, T; Hattori, M; Ggasawara, N; Hayashi, H; Hiramatsu, K. Sakiho, C; Shiba, T; Hattori, M; Ogasawara, N; Hayashi, H; Hiramatsu, K. Lancet 357, 1225-1240, 2001 A;Fitle: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-122 «KUR»
A;Cross-references: GB:BA000018; PID:g13700376; PIDN:BAB41674.1; GSPDB:GN00149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-134 «KUR»
A;Cross-references: GB:AP003603, PIDN:BAB77344.1; PID:g17134787; GSPDB:GN00182
A;Experimental source: strain PCC 7120
                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-103 <SMI>
A;Cross-references: EMBb:U00018; NID:g467037; PIDN:AAA17261.1; PID:g467077
                                                                                                                                                                                                                                                                                                                                                                Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 2;
100.0%; Pred. No. 21;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.1%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 24; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.1%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 27; Matches 7; Conservative 0; Mismatches
                  A; Description: Mycobacterium leprae cosmid B2168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain N315
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100....
7; Conservative
                                                                   A; Reference number: S72586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 AEIVKIL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 AEIVKIL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 KDNLAIL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 KDNLAIL 91
                                                                                                   A;Accession: S72925
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: G89814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: AG2552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: alr8014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: SA0444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ⋩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Substitute torso protein precursor - fruit fly (Drosophila melanogaster)

Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 24-Sep-1999
C; Accession: 803900
R; Spreanger, F: Stevens, L.M.; Nuesslein-Volhard, C.
R; Stranger, F: Stevens, L.M.; Nuesslein-Volhard, C.
R; R; Reserven umber: 803900; MUID:89181943; PMID:2927509
A; Title: The Drosophila gene torso encodes a putative receptor tyrosine kinase.
A; Recession: 803900; MUID:89181943; PMID:2927509
A; Status: not compared with conceptual translation
A; Residues: 1-923 cspr.
A; Status: not compared with conceptual translation
A; Residues: 1-923 cspr.
A; Cross-references: GB:X15150; NID:g8712; PIDN:CAA33247.1; PID:g603810
A; Cross-references: FlyBase:FBgn0003733
A; Map position: 2R 4313.er
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein; transmembr F; 1-2070bmain: signal sequence #status predicted csr.
C; Keywords: AFP; growth factor receptor; kinase-related transforming protein; transmembr F; 1-2070bmain: signal sequence #status predicted csr.
F; 1-321/Product: gene torso protein #status predicted cwMT>
F; 413-880/Domain: protein kinase homology ckIN>
F; 413-880/Domain: protein kinase ATP-binding motif
                               Cipacies: Caenorhabditis elegans
Cipate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
Cipate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
Cipate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
Cipate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
Riberabach.
Cipate: Tides1
Aireston: Tides2
Aireston: Tides2
Aireston: Tides2
Aireston: Tides2
Aireston: Tides2
Aireston: Tides2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
hypothetical protein R02E12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C;Accession: T16651
R;Leimbach, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein B2168 Cl_182 - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 4.2%; Score 14; DB 2; Length 377; Best Local Similarity 100.0%; Pred. No. 3.2e-06; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.4%; Score 8; DB 2; Length 923; 100.0%; Pred. No. 15; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Accession: 872925
R,Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 LRRQIGTRSPTVEY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 LRROIGTRSPTVEY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449 SSGLLVTL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 SSGLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
```

ö

Gaps

. 0

ö

Gaps

. 0

g.

ö

Gaps

. 0

NLAILEK 30

```
Cidate: 2.7Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 Cidate: 2.7Nov-2001 #sequence_revision 27-Nov-2001 #sequence_revision 27-Nov-2001 Cidate: 2.2Nov-2001 #sequence_revision 27-Nov-2001 Figure 29-Nov-2001 Figure 20-Nov-2001 Figure 20-Nov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CiSpecies: Methanococcus jannaschii.
CiSpecies: Methanococcus jannaschii.
CiDate: 13.5ep-1996 #sequence_revision 13-5ep-1996 #text_change 21-Jul-2000
CiDate: 13.5ep-1996 #sequence_revision 13-5ep-1996 #text_change 21-Jul-2000
CiAccession: C64300
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake
Rsich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
A;Atitle: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasch
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: C64300
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: G95316
R;Barnett, M.J; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Borror, Ralman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.! Aproc. Natl. Acad. Sci. US.A. 98, 9883, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melil: A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA A;Residues: 1-156 <BUL>
A;Residues: 1-156 <BUL>
A;Cross-references: GB:U67459; GB:L77117; NID:g2826236; PIDN:AAB97990.1; PID:g1498760; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein SMa0809 [imported] - Sinorhizobium meliloti (strain 1021) magapla
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein MJ0003 - Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.1%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 30; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
2.1%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: FOR4911-5381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 NNILRRO 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 NNILRRO 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 VEILLIN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 VEILLKN 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: G95316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  요
                                                                                                                                                                                                                                                                  AH3522
hypothetical protein all7360 [imported] - Nostoc sp. (strain PCC 7120) plasmid pcC7120al
C; Species: Nostoc sp. PcC 7120
A;Note: Nostoc sp. PcC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AH3522
R;Kaneko, T.; Makamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Accession: AH3522
A;Status: preliminary
A;Molecule type: DNA
A;Crossion: AH352
A;Crossion: AH352
A;Crossion: AH352
A;Crossion: AH352
A;Crossion: AH352
A;Crossion: AH353
A;Cross references: GB:BA000020; PIDN:BAB77118.1; PID:g17134559; GSPDB:GN00180
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all7360
A;Geneme: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety.
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety.
C;Species: Columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000
C;Accession: F71407
R;Bevan. M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pens, A.; Puigdomenech
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
C; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Reterence number: DNA
A;Ret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
AB1605
B. subtilis comG operon protein 6 homolog lin1379 [imported] - Listeria innocua (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C'Genetics:
A;Map position: 4COP9-4G3845
C;Superfamily: Arabidopsis thaliana 15.6K hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB: Z97336; NID: g2244788; PID: g2244809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 2
100.0%; Pred. No. 27;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 2
100.0%; Pred. No. 27;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.1
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                           104 NLAILEK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OLIDFEG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 NLAILEK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 QLIDFEG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

ö

Gaps

ö

Length 156; 0; Indels

..

Gaps

; 0

Length 154; 0; Indels A;Gene: alr3529

ö

Gaps

..

```
Glutathione transferase (EC 2.5.1.18) - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 18-Jun-1999
C;Accession: S19734
R;Chang, L.H.; Fan, J.Y.; Liu, L.F.; Tsai, S.P.; Tam, M.F.
Biochem, J. 281, 545-551, 1992
Biochem, J. 281, 545-551, 1992
A;Title: Cloning and expression of a chick liver glutathione S-transferase CL 3 subunit A;Reference number: S19734; MUID:92143826; PMID:1339283
A;Accession: S19734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: Z68106; PIDN: CAA92125.1; GSPDB: GN00028; CESP: F41E7.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CiSpecies: Caenorhabditis elegans
CiDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T22075
Fsilennard, N.
submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T23866
R;Steward, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-229 <CHA>
A;Cross-references: BMBL:M38219; NID:g211529; PIDN:AAA62731.1; PID:g211530
C;Superfamily: glutathione transferase
C;Keywords: transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 241;
                                                                      Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F41E7.2 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein R03C1.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                2.1%; Score 7; DB 2;
100.0%; Pred. No. 37;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 2;
100.0%; Pred. No. 46;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 2;
100.0%; Pred. No. 44;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: X
A:Introns: 27/2; 54/1; 126/3; 161/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: clone F41E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity luv...
7; Conservative
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z19509
A; Accession: T22075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 YEKLLQS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 PIVEILL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 PIVEILL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 YEKLLOS 47
                                                                                                                                                                                    82 LIADLQL 88
                                                                                                                                                                                                                                       44 LIADLOL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 7; Conserv
                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-241 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP: F41E7.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Genetics:
                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T23866
                                                                                                                                                                                    ò
                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: G70325
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Rolecule type: DNA
A;Residues: 1-179 <AQF>
A;Experimens: 1-179 <AQF>
A;Experimental source: GB:AE000682; NID:g2982979; PIDN:AAC06593.1; PID:g2982980; GB:AE00065
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gispecies: Nostoc sp. PCC 7120
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Accession: AB2247
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. S. (205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:2159285; PMID:11759840
A; Residues: 1-171 < KUR>
A; Cross-references: GB: AE006469; PIDN: AAK65097.1; PID: G14523533; GSPDB: GN00165
A; Cross-references: GB: AE006469; PIDN: AAK65097.1; PID: G14523533; GSPDB: GN00165
A; Experimental source: strain 1021, megaplasmid pSymA
R; Galbert, F:; Finan, T.W.; Long, S.R.; Publer, A. Abola, P.; Ampe, F.; Barloy-Hubbler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: G70325
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-191 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB75228.1; PID:g17132662; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription regulator TetR/AcrR family - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May.1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: G70325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein alr3529 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 2;
100.0%; Pred. No. 33;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
2.1%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.1
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 LAKIILF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 LAKILLF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 PTEAVAQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PTEAVAG 67
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: SMa.0809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: acrR3
                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gg
```

ö

Gaps .; 0 ; 0

Gaps

. 0

```
A;Gene: desA2
C;Superfamily: delta-9 acyl-ACP desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39
                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Genetics:
                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                           ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C'Species: Mycobacterium leprae
C'Species: Mycobacterium leprae
C'Species: Mycobacterium leprae
C'Species: Mycobacterium leprae
C'Species: Mycobacterium leprae
C'Species: Mycobacterium leprae
C'Species: Mycobacterium leprae
C'Species: Mycobacterium leprae
C'Species: Mycobacterium leprae
C'Species: Mycobacterium leprae
C'Species: Mycobacterium leprae
C'Species: Mycobacterium leprae
R'Cole, S.T.; Esglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
R; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Accession: C87153
A;Accession: C87153
A;Accession: C87153
A;Accession: C87153
A;Accession: C87153
A;Accession: C87154
A;Molecule type: DNA
A;Residues: 1-275 c8TO>
A;Cross-references: GB:AL450380; NID:g13093607; PIDN:CAC30907.1; GSPDB:GN00147
C;Genetics:
A;Genetics:
submitted to the EMBL Data Library, November 1996
A; Reference number: Z19810
A; Accession 123866
A; Accession 123866
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-264 <MILs
A; Cross-references: EMBL: Z82279; NID: e1062116; PIDN: CAB05260.1; GSPDB: GN00020; CESP: R03C
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cipate: 1,-0u1-1998 #sequence_revision 17-0u1-1998 #text_change 04-Aug-2003
Cipate: 1,-0u1-1998 #sequence_revision 17-0u1-1998 #text_change 04-Aug-2003
Cipaccesion: D70896
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70897
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D70896
A;Accession: D7086
A;Accession: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 04-Aug-2003
C;Accession: D70896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable desA2 protein - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 2
100.0%; Pred. No. 50;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.1%; Score 7; DB 2
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 AQLAQEL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 AQLAQEL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 ILKDNLA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 ILKDNLA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: CESP:R03C1.3
A,Map position: 2
A:Introns: 104/3; 128/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 19
C87153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
R.H.; Jaskunas, S.R
                                                                                                                                                                                                                                          Pypothetical protein appC [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Accession: G90020
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.;
e, R; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Mateushima, P.; McAhren, S.; P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, & A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-282 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK78288.1; PID:g15023150; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-283 «KUR»
A;Cross-references: GB:AE007317; PIDN:AAK99995.1; PID:g15458825; GSPDB:GN00174
                                                   Gabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 283;
    Length 275;
                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 7; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Superfamily: oligopeptide permease protein oppB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.1%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 54; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0%; Pred. No. 54; Matches 7; Conservative 0; Mismatches
/ Match 2.1%; Score 7; DB 2
Local Similarity 100.0%; Pred. No. 52;
nes 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: CAC0307
C,Superfamily: precorrin methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 RQSLKLL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 IFNNILR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 IFNNILR 106
                                                                                               20 ILKDNLA 26
                                                                                                                                        74 ILKDNLA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROSLKLL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: G98020
```

Ü

Ļ

```
2.1%; Score 7; DB 2; Length 309; 100.0%; Pred. No. 59;
A; Reference number: A71400; MUID: 98121113; PMID: 9461215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: tropinesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 ENLKLMM 259
                                                                                                                                                                                                                                                                                                                                                                                                                          272 EAFHVFK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 EAFHVFK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 ENLKLMM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-309 < HAY>
                                                                                                                        A; Residues: 1-305 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: ECs0404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                         hypothetical protein SA1156 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Accession: H89906
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
C; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.;
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Recession: H89906
A;Retacus preliminary
A;Molecule type: DNA
A;Residues: 1-299 «KUR>
A;Coss-references: GB:BA000018; PID:g13701117; PIDN:BAB42412.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: G71441
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel
avanadh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans C.; Chalwatzis, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          forkhed nuclear signaling protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-bec-1999 #sequence_revision 03-bec-1999 #text_change 07-bec-1999
C;Accession: T40402
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.
Submitted to the EMBL Data Library, August 1998
A;Reference number: Z21926
A;Reference number: Z21926
A;Reference number: T40402
A;Reference number: DAN
A;Recession: T40402
A;Reference number: DAN
A;Recession: T310 - (LNN
A;Redues: 1-301 - (LNN
A;Reperimental source: EMBL:AL031261; PIDN:CAA20309.1; GSPDB:GN00067; SPDB:SPBC3H7.13
A;Experimental source: strain 972h-; cosmid c3H7
C;Gene: SPDB:SPBC3H7.13
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein - Arabidopsis thaliana ("cuse-ear cress)
C;Species: Arabidopsis thaliana ("cuse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 2;
100.0%; Pred. No. 57;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 2
100.0%; Pred. No. 57;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.(
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 EEVSKSL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 KLLQSEN 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 EEVSKSL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 KLLOSEN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

```
C;Accession: E64762

C;Accession: E64762

R; Blattner, F. R., Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; (A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: E64762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable 2,6-dioxo-6-phenylhexa-3-enoate hydrolase (EC 3.7.1.8) - Escherichia coli (sti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-309 <BLAT>
A;Cross-references: GB:AE000142; GB:U00096; NID:g1786542; PIDN:AAC73452.1; PID:g178654;
A;Experimental source: strain K-12; substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:BA000007; PIDN:BAB33827.1; PID:g13359861; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
A,Accession: G71441
A,Status: preliminary, nucleic acid sequence not shown, translation not shown
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Escherichia coli
C.Date: 10-Sep.1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: mhpC
C,Superfamily: tropinesterase
C,Keywords: aromatic hydrocarbon catabolism; hydrolase; PCB biodegradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                            A,Cross-references: GB:Z97343; NID:g2245073; PID:e327051; PID:g2245086
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.1%; Score 7; DB 1; Length 309; Best Local Similarity 100.0%; Pred. No. 59; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    Length 305;
                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                              A,Map position: 4COP9-4G3845
C,Superfamily: Saccharomyces hypothetical protein YKL189w
                                                                                                                                                                                                                                                                 Query Match 2.1%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 58; Matches 7; Conservative 0; Mismatches
```

```
A;Reference number: Z22314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 RDFFKYV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 RDFFKYV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 ADLOLID 109
                                                                                                                                                                                                                                                                                                                     A; Genome: plasmid pMRC01
A; Note: ORF00061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 ADLQLID 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-320 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                         C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-teferences: GB:AE005174; NID:912513185; PIDN:AAG54700.1; GSPDB:GN00145; UWGP:Z04
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                              hypothetical protein mhpC [imported] - Escherichia coli (strain 0157:H7, substrain ED193
                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Bscherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: H85529
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T43132

hypothetical protein - Lactococcus lactis plasmid pMRC01

hypothetical protein - Lactococcus lactis

c.Speciese: Lactococcus lactis

c.Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C.Accession: T43132

R.Pougherty, B.A.; Hill, C.; Weidman, J.F.; Richardson, D.R.; Venter, J.C.; Ross, R.P.

R.Pougherty, B.A.; Hill, C.; Weidman, J.F.; Richardson, D.R.; Venter, J.C.; Ross, R.P.

Mol. Microbiol. 29, 1029-1038, 1998

A.Title: Sequence and analysis of the 60 kb conjugative, bacteriocin-producing plasmid
            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CySpecies: Chlorella virus PBCV-1
CySpecies: Chlorella virus PBCV-1
CySpecies: Chlorella virus PBCV-1
CySpecies: Chlorella virus PBCV-1
CySpecies: Chlorella virus PBCV-1
CySpecies: Chlorella virus PBCV-1
CySpecies: Cott-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
RyCraves, M.V.; Van Etten, J.L.
Submitted to the BMBL Data Library, May 1999
A;Reference number: Z18806
A;Reference number: Z18806
A;Recession: T1755
A;Accession: T1755

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96435.1
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Gene: A677R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 309;
        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
        .,
o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; Score 7; DB 2;
100.0%; Pred. No. 59;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 2
100.0%; Pred. No. 59;
tive 0; Mismatches
        Mismatches
        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Lac 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 7; Conservative
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: tropinesterase
                                                                         253 ENLKLMM 259
                                                                                                                                                  189 ENLKLMM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENLKLMM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 ENLKLMM 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 TFDIASD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 TFDIASD 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-309 <GRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: mbpC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues:
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 30
                                                                         à
                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
C'Accession: F70034

R;Kunst, F: Ogasawara, N: Moszer, I: Albertini, A.M.; Alloni, G.; Azevedo, V.; Berti.
C; Bron, S: Broullet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cl.
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A,Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galli.
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.]
Koetter, P.; Koningstein, G.; Kroph, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinoi!
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauee,
Y, M.; Ogawar, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanloi
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ouche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanloi
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Tognoni, A.; Tosato, V.; Uchiyam,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasta, K.; Yasta, K.; Yoshida,
A;Ritle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Reference number:
A,Refer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rishe, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Char. Jongy, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett. R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001

#/Description: Sulfolobus solfataricus complete genome.

#/Reference number: A99139

#/Accession: G90221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15458.1; PID:g2635960
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein yvdO - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Accession: G90291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endoglucanase precursor [imported] - Sulfolobus solfataricus
A;Accession: T43132
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                  A;Residues: Î-314 <DOU>
A;Cross-references: EMBL:AE001272; PIDN:AAC56050.1
A;Experimental source: strain DPC3147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 2;
100.0%; Pred. No. 59;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; Score 7; DB 2
100.0%; Pred. No. 60;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Sulfolobus solfataricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
```

```
C;Species: Enterobacter aerogenes
C;Jotes 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T08494
R;Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.
R;Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.
R;Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, R.; Thomas, C.M.
A;Trile: Conservation of the genetic switch between replication and transfer genes of A;Reference number: Z16434; MUID:97118926; PMID:8954881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kobayashi, H.; Sekibata, S.; Shibuya, H.; Yoshida, S.; Kusakabe, I.; Murakami, K. Agric. Biol. Chem. 53, 1927-1933, 1989
A;Title: Cloning and sequence analysis of CDNA for Irpex lacteus aspartic proteinase. A;Reference number: UT0057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-340 <KOB>
A;Note: the amino-terminal 24 residues were sequenced on the isolated proteinase
                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U67194; NID:g1572520; PIDN:AAC64438.1; PID:g1572543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ribosomal protein var1 - yeast (Candida glabrata) mitochondrion
C.Species: mitochondrion Candida glabrata
C.Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyporopepsin (EC 3.4.23.29) - Irpex lacteus
C;Species: Irpex lacteus
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Dec-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RiAinley, W.M.; Macreadie, I.G.; Butow, R.A.
J. MOL. Biol. 184, 565-576, 1985
A.fitle: varl gene on the mitochondrial genome of Torulopsis glabrata.
A.Reference number: S04681; MUID:86011564; PMID:3900417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Genome: mitochondrion
A;Gentic code: SGC2
C;Superfamily; Saccharomyces cerevisiae ribosomal protein varl
C;Superfamily; Saccharomyces protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                           probable transposase - Enterobacter aerogenes plasmid R751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Cross-references: EMBL:X02893
A,Note: the source is designated as Torulopsis glabrata
                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-334 <THO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 2;
100.0%; Pred. No. 63;
rative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; Score 7; DB 2;
100.0%; Pred. No. 63;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100...
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 IMTKYIS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 IMTKYIS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-336 < AIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Genome: plasmid R751
                                                                                                                                                                                                                                                                            A; Accession: T08494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: S04682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S04682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: JU0057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: JU0057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: tnpA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: varl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                 C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S04682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               endoglucanase precursor [imported] - Sulfolobus solfataricus
c;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Accession: G90360
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A,Description: Sulfolobus solfataricus complete genome.
A,Reference number: A99139
A,Accession: G90360
A,Status: preliminary
A,Residues: 1-334 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Enterpolacter aerogenes

C; Date: 11-Un-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C; Accession. T08491

R; Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.

Plasmid 36, 95-111, 1996

A; Title: Conservation of the genetic switch between replication and transfer genes of In

A; Reference number: Z16434; MUID:97118926; PMID:8954881

A; Statutus: preliminary; translated from GB/EMBL/DDBJ

A; Residues: 1-334 <THO>
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE006641; NID:g13815224; PIDN:AAK42142.1; GSPDB:GN00155 C;Genetics:
A;Gene: SSO1949
                                                                            A;Cross-references: GB:AE006641; NID:gl3814564; PIDN:AAK41590.1; GSPDB:GN00155 C;Genetics:
A;Gene: SSO1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U67194; NID:g1572520; PIDN:AAC64435.1; PID:g1572540
C;Genetics:
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 2; Length 334; 100.0%; Pred. No. 63; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 334;
                                                                                                                                                                                          DB 2; Length 332;
. 63;
                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T08491
probable transposase - Enterobacter aerogenes plasmid R751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
2.1%; Score 7; DB 2;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                          2.1%; Score 7; DB 2
100.0%; Pred. No. 63;
tive 0; Mismatches
                                                                                                                                                              Ouery Match
Best Local Similarity 100.0
المورية 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                184 FDIASDA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                   177 FDIASDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 FDIASDA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 FDIASDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 PKLIEFL 42
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-332 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Genome: plasmid R751
                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QC
                                                                                                                                                                                                                                                                                                      8
```

ó,

ö

RESULT 38

à ď

```
Eitheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonsc Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, (
                                                                                                                                      RibelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova .; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Lete: Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melite: A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid ABC transporter, permease protein VC1360 [imported] - Vibrio cholerae (stra: C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: F82210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE004215; GB:AE003852; NID:g9655842; PIDN:AAF94518.1; GSPDB:GNO0
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Erwolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.S.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                         ornithine cyclodeaminase (EC 4.3.1.12) [imported] - Brucella melitensis (strain 16M)
                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-359 <KUN>
A;Residues: 1-359 <KUN>
A;Cross-references: GB:AL0008918; PIDN:AAL53639.1; PID:g17984556; GSPDB:GN00191
A;Experimental source: strain 16M
                                                          C.Species: Brucella melitensis
C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein FIN19.7 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 01-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 7; DB 2;
100.0%; Pred. No. 67;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.1%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 68; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: ornithine cyclodeaminase
C;Keywords: ammonia-lyase; carbon-nitrogen lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: Î-365 <HEI>
A;Cross-references: GB:AE004215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity luu...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 EKLLQSE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 EKLLOSE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 GLLVTLI 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLLVTLI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                  C; Accession: AD3559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: F82210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Accession: G96668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: BMEII0397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: VC1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: C72746
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah Awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; BDNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-357 <KAM>
A;Cross-references: DDBJ:AP000059; NID:g5103911; PIDN:BAA79463.1; PID:d1043249; PID:g510
A;Experimental source: strain Kl
                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable carbamoylphosphate synthetase APE0498 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
C;Superfamily: pepsin
C;Keywords: aspartic proteinase; glycoprotein; hydrolase
F;32,212/Active site: Asp #status predicted
F;192,238/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 7; DB 2; Length 357;
100.0%; Pred. No. 67;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                      DB 1;
                                                                                                                                Query Match
2.1%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 2;
100.0%; Pred. No. 65;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.co
Process 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
                                                                                                                                                                                                                                          179 IASDAFA 185
                                                                                                                                                                                                                                                                                             220 IASDAFA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 IVEILLK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 İVEİLLK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335 EIVKILK 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 EIVKILK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: C72746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: CAC0708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: APE0498
```

Db

ò

ö

Query Match

Matches

RESULT 40

qq

à

C;Genetics:

ò

```
A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diffunctional endo-1,4-beta-xylanase homolog - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 07-Dec-1999
C;Accession: 164223
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
C.A.; Venter, J.C.
Science 270, 337-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200, MUID:96026346; PMID:7569993
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-372 < TIGR>
A;Residues: 1-372 < TIGR>
A;Residues: 1-372 < TIGR>
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8-amino-7-oxononanoate synthase (EC 2.3.1.47) - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: Ose-May-1998 #sequence_revision 08-May-1998 #text_change 05-May-2000
C;Accession: G70355
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
Nature 392, 353-358
Nature 392, 353-358
Nature 392, 353-358
Nature 392, 353-358
Nature 392, 353-358
Nature 392, 353-358
Nature 392, 353-358
Nature 392, 353-358
Nature 392, 353-358
Nature 392, 353-358
Nature 392, 353-358
Nature 392, 353-358
Nature 392, 353-358
Nature 392, 353-358
Nature 392, 353-358
Nature 393-358
Nature 392, 353-358
Nature 392, 363-368
Nature 392, 363-368
Nature 393, 363-368
Nature 393, 363-368
Nature 393, 363-368
Nature 393, 363-368
Nature 393, 363-368
Nature 393, 363-368
Nature 393, 363-368
Nature 393, 363-368
Nature 393, 363-368
Nature 393, 363-368
Nature 393, 363-368
Nature 393, 363-
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A,Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A,Accession number: A86141; MUID:21016719; PMID:11130712
A,Accession G96668
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-368 <STO>
A;Cross-references: GB:AE005173; NID:g6633811; PIDN:AAF19670.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: F1N19.7
A;Map position: 1
C;Superfamily: Arabidopsis thaliana hypothetical protein T4F9.90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 2; Length 368; 100.0%; Pred. No. 69; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 2
100.0%; Pred. No. 70;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.1'
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 7; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 LMMNLLR 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 LMMNLLR 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 EEVSKSL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 EEVSKSL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
```

```
A,Cross-references: EMBL:U40939; NID:g1073175; PID:g1072179; PIDN:AAA81703.1; CESP:F13I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EWBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-270 <DUZ>
A;Residues: 1-270 <DUZ>
A;Residues: EMBL:AF038613; PIDN:AAB92046.1; GSPDB:GN00022; CESP:F42A6.1
A;Experimental source: strain Bristol N2; clone F42A6
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AF100675; PIDN:AAC69002.1; GSPDB:GN00022; CESP:F42A6.1
A;Experimental source: strain Bristol N2; clone Y55H10A
C;Superfamily: 5-aminolevulinate synthase; glycine C-acetyltransferase homology C;Keywords: acyltransferase; coenzyme A; phosphoprotein; pyridoxal phosphate F;229-363/Domain: glycine C-acetyltransferase homology <GCA>F;223/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Typechers.ca. process. Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 01-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F13D11.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 23-Mar-2001
C;Accession: T16059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: CESP:F13D11.4
A;Introns: 25/2; 43/1; 80/3; 108/2; 137/3; 227/2; 252/3; 304/1; 344/3
C;Superfamily: dihydrokaempferol 4-reductase
                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 376;
                                                                                                                                    Length 373;
                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rirulton, L. submitted to the EMBL Data Library, November 1995 A; Description: The sequence of C. elegans cosmid F13D11. A; Reference minner: $69020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Du, Z.; Scheet, P.; Andrews, S.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid F42A6.
A;Reference number: Z21201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F42A6.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                    2.1%; Score 7; DB 2;
100.0%; Pred. No. 70;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 2;
100.0%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                             Query Match
Best Local Similarity 100..
Tr Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                    299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                     274 PKLIEFL 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 VEILLKN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEILLKN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-381 <ANT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-376 <FUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CESP: F42A6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T32624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: T33761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
```

õ QQ

en

```
A; Residue: 1,400 < KUR>
A; A; Residues: 1.400 < KUR>
A; A; Residues: 1.400 < KUR>
A; A; Cross-references: GB: AL591985; PIDN: CAC49159.1; PID: g15140644; GSPDB: GN00167
A; Experimental source: strain 1021, megaplasmid pSymB bits of the psymB source: strain 1021, megaplasmid pSymB bits of the psymB source: T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Huble: pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L; Hyman, R.W.; Jones, T.
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaurr hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, IA; Reference number: A96039; WUID: 21368234; PMID: 11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nypothetical protein P65 - Mycoplasma pneumoniae (strain ATCC 29342)

NyAlternate names: hypothetical protein F10_orf405

Sispeciaes: Mycoplasma pneumoniae

A;Variety: ATCC 29342

C;Date: 27-Feb-1997 #sequence revision 25-Apr-1997 #text_change 07-Dec-1999

C;Accession: S73853; S49068; S49069

R;Himmelreich, R; Hilbert, H; Plagens, H; Pirkl, E; Li, B.C.; Herrmann, R.

Nucleic Acids Res: 24, 4420-4449, 1996

A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-405 < HIM.
A; Residues: 1-405 < HIM.
A; Residues: 1-405 < HIM.
A; Cross-recences: EMBL: AB000051; GB: U00089; NID: g1674211; PIDN: AAB96175.1; PID: g1674;
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
K; Proft, T.; Herrmann, R.
Mol. Microbiol. 13, 337-348, 1994
A; Title: Identification and characterization of hitherto unknown Mycoplasma pneumoniae
A; Reference number: 849059; MUID: 95075318; PMID: 7984111
                    A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing A;Reference number: A95842; MUID:21396508; PMID:11481431 A;Accession: G95936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:Z32653; NID:g474085; PIDN:CAA83574.1; PID:g474086
A;Experimental source: clone F10-2B
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: clone F10-2D
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: Z32655; NID: 9474087; PIDN: CAA83576.1; PID: 9474088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: 873853
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
             9889-9894, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 2
100.0%; Pred. No. 75;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Keywords: duplication
F,57-96/Region: 40-residue repeat <DUP1>
F,122-161/Region: 40-residue repeat <DUP2>
      Natl. Acad. Sci. U.S.A. 98,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 KASEEVS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37 KASEEVS 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40-75 <PRO1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83-95 <PRO2>
                                                                                                                                        A, Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S49068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S49069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: SMb21255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AjExperimental Bource: strain $288C.

Richeret, G.; Mattheakis, L.C.; Sor, F.

Yeast 9. (61-667, 1993

Ajritle: DNA sequence analysis of the YCN2 region of chromosome XI in Saccharomyces cere
Ajreference number: $33960; MUD: 93348778; PMID: 8394042

Ajreference number: $33960; MUD: 93348778; PMID: 8394042

Ajreference number: $33960; MUD: 93348778; PMID: 8394042

Ajreference number: $33960; MUD: 93296985; PIDN: CAA49422.1; PID: 9296989

Richardnu, S.; Voss, H.; Schwager, C.; Rupp, T.; Grothues, D.; Sensen, C.; Stegemann, J.

Submitted to the Protein Sequence Database, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G95936

hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymE C:Species: Sinorhizobium meliloti
C:Species: Sinorhizobium meliloti
C:Species: 24-Aug-2201 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: G95936
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
                                                                                                                                                                                                                                                                                                                                                                           RESULT 47
S34681
hypothetical protein YKL189w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: 534681; S33963; S38021; S38026
R;Wieman, S.; Voss, H.; Schwagaer, C.; Rupp, T.; Stegemann, J.; Zimmermann, J.; Grothues submitted to the EMBL Data Library, July 1993
A;Bescription: Sequencing and analysis of 51.5 kilobases on the left arm of chromosome X A;Accession: S34681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-399 <WI2>
A;Cross-references: EMBL:Z28189; NID:G486334; PIDN:CAAB2032.1; PID:G486335; MIPS:YKL189w
A;Experimental source: strain S288C
A;Experimental source: strain S288C
B;Maia e Silva, A.; Bossier, P.; Vilela, C.; Fernandes, L.; Soares, H.; Guerreiro, P.; R submitted to the Protein Sequence Database, March 1994
A;Reference number: S38024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Cross-references: EMBL: 228189; NID: 9486334; PIDN: CAA82032.1; PID: 9486335; MIPS: YKL189w
                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-399 <WIE>
A;Residues: 1-399 <WIE>
A;Cross-references: EMBL:X74151; NID:9450365; PIDN:CAA52249.1; PID:9395236
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gарв
A;Introns: 14/1; 73/1; 133/1; 263/3; 323/3
C;Superfamily: Caenorhabditis elegans hypothetical protein Y55H10A.2
                                                                                                                                                                       ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 399;
                                                                                                        Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: Saccharomyces hypothetical protein YKL189w
                                                                                              2.1%; Score 7; DB 2;
100.0%; Pred. No. 71;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 2;
100.0%; Pred. No. 74;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Experimental source: strain S288C
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: SGD:S0001672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: S37825
A;Accession: S38021
                                                              Query Match
Best Local Similarity
Tr Conserva
                                                                                                                                                                                                                                   306 SSFOKER 312
                                                                                                                                                                                                                                                                                              317 SSFOKER 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 YVTKRQS 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 YVTKROS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-399 <MAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S38026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 11L
C; Superfamil:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: SGD: HYM1
```

Query Match

g

ö

ö

```
C)Accession: B90563
R;Chambaud, I:; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I. Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                    Cypate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
Cypatession: F97058
Rybolling, Jr. Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Let, J. Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4832-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium ClayReference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein MYPU 4130 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-436 «KUR»
A;Cross-references: GB:AE001437; PIDN:AAK79257.1; PID:g15024215; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AL445566; PID:g14089827; PIDN:CAC13586.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                               Fe-S oxidoreductases CAC1286 [imported] - Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 436;
                                                     Length 430
                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: conserved hypothetical protein b0835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 virulence-mediating protein - Vibrio anguillarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.1%; Score 7; DB 2 Best Local Similarity 100.0%; Pred. No. 81; Matches 7; Conservative 0; Mismatches
                                                  2.1%; Score 7; DB 2
100.0%; Pred. No. 80;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. No. 82;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Clostridium acetobutylicum
                                               Query Match 2.15
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C, Species: Vibrio anguillarum
                                                                                                                                                                      261 LLRDKSP 267
                                                                                                                                                                                                                              362 LLRDKSP 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 LLGELIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428 LLGELIL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVKILKD 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 IVKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-440 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: F97058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: MYPU 4130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: CAC1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
                                                                                                                                                                                                                                                                                                                          25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 54
                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                   hypothetical outer membrane protein, similar to Wza, OMA family exoFI [imported] - Sinor C; Species: Sinorhizobium meliloti
C; Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C; Accession: D55975
R; Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9884, 2001
A; Title: Natl. Acad. Sci. U.S.A. 98, 9889-9884, 2001
A; Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A; Reference number: A95842; MUID:21396508; PMID:11481431
A; Accession: D59975
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-421 «KUR>
A; Residues: 1-421 «KUR>
A; Residues: 1-421 «KUR>
A; Residues: 1-421 «KUR>
A; Residues: T. Ain 1021, megaplasmid pSymB
A; Experimental source: strain 1021, megaplasmid pSymB
B; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
L.; Hyman, R.W.; Jones, T.
L.; Hyman, R.W.; Jones, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pypothetical protein T6C23.6 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: D5719
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Roney, T.; Rohey, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-430 <STO>
A;Cross-references: GB:AE005173; NID:g6665542; PIDN:AAF22911.1; GSPDB:GN00141
C;Genetics:
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 421;
                  Length 405;
                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                  DB 2;
. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
. 78;
2.1%; scc...
100.0%; Pred. No. , v.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 2
100.0%; Pred. No. 78;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: T6C23.6
A;Map position: 1
C;Superfamily: porphobilinogen synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
                                                                           7; Conservative
                                                                                                                                   257 LMMNLLR 263
                                                                                                                                                                                            354 LMMNLLR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336 AQLAQEL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 AQLAQEL 73
               Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: exoF1; SMb20945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Contents: annotation C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Genome: plasmid
```

Dp ð

ö

ö

```
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable resistance protein YBR293w - yeast (Saccharomyces cerevisiae)
C;pspecies: Saccharomyces cerevisiae
C;Bate: 26-Aug-1994 #Sequence_revisiae
C;Bate: 26-Aug-1994 #Sequence_revisiae
C;Bate: 26-Aug-1994 #Sequence_revisian
C;Accession: 846175
R;Fritz, C; Hollenberg, C.P.; Kirchrath, L.; Ramezani Rad, M.
A;Refacernce number: 846175
A;Accession: 846175
A;Accession: 846175
A;Residues: 1-474 <-RID.
A;Residues: 1-474 <-RID.
A;Residues: 1-474 <-RID.
A;Residues: 1-474 <-RID.
A;Residues: 1-474 <-RID.
A;Coss-references: EMBL:336162; NID:9536749; PIDN:CAA85258.1; PID:9536750; GSPDB:GNOOG
C;Genelics:
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293w
A;Gene: MIPS:YBR293
virC, from Vibrio anguillarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myocilin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: JE0096; JE0198
R;Tomarev, S.I.; Tamm, E.R.; Chang, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.1%; Score 7; DB 2 Best Local Similarity 100.0%; Pred. No. 82; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 2
100.0%; Pred. No. 88;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 AQELYSS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 ILKDNLA 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 AQELYSS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 ILKDNLA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JE0096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
A;Title: Characterization of the mouse Myoc/Tigr gene.
A;Reference number: JE0096; MJID:98249809; PMID:9588210
A;Reference number: JE0096; MJID:98249809; PMID:9588210
A;Accession: JE0096
A;Accession: JE0096
A;Robecule type: mRNA
A;Residues: 1-490 <TON>
A;Cross-references: GB:AF039869; NID:g3115382; PIDN:AAC40112.1; PID:g3115383
B;Takahashi, H; Noda, S; Imamura, Y; Nagasawa, A; Kubota, R; Mashima, Y; Kudoh, IB:Ochem. Biophys. Res. Commun. 248, 104-109, 1998
A;Title: Mouse myocilin (Myoc) gene expression in ocular tissues.
A;Reference number: JE0198; MJID:98340858; PMID:9675094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. Accession: JC5830
R; Kubota, R.; Kudoh, J.; Mashima, Y.; Asakawa, S.; Minoshima, S.; Hejtmancik, J.F.; Ogn Biochem. Biophys. Res. Commun. 242, 396-400, 1998
A;Title: Genomic organization of the human myocilin gene (MYOC) responsible for primar; A;Reference number: JC5830; MUID:98113364; PMID:9446806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-504 «KUB»
A;Cross-references: DDBJ:AB006686
C;Comment: This cytoskeletal protein is involved in the morphogenesis of the basal bod;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: E82508
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methyl-accepting chemotaxis protein VCA0031 [imported] - Vibrio cholerae (strain N1696]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A§2035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                     A;Wolecule type: mRNA
A;Residues: 1-490 <TAK>
A;Cross-references: DDBJ:AB013592; NID:g3374583; PIDN:BAA32031.1; PID:g3374584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 2;
100.0%; Pred. No. 90;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
'
ochem. Biophys. Res. Commun. 245, 887-893, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2
93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 2
100.0%; Pred. No. 93;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity luu...
Asa 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 NLLRDKS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: myoc
A; Introns: 202/1; 244/1
                                                                                                                                                                                                                                                                                                              A, Accession: JE0198
A, Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: E82508
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Gene: Myoc/Tigr
A, Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myocilin - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 57
```

```
A; Experimental source: clone Y55D9A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity luv.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: Z20325
A;Accession: T27191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518 NEKEPPT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            518 NEKEPPT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 NEKEPPT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 NEKEPPT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Gene: CESP: Y55D9A.2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CESP: Y55D9A.2a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: F86244
                                                                                                                                                                                                                                           C; Accession: T27190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypochetical protein ECS0472 [imported] - Escherichia coli (strain O157:H7, substrain RI C; Species: Escherichia coli (c; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Rawara, N.; Vasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7, and genoma; Reference number: A99629; MUID:21156231; PMID:11258796 A; Accession: H90687 A; Reference DNA Res. Dreliminary A; Molecule type: DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence DNA A; Rederence D
A;Residues: 1-521 <HEL>
A;Cross-references: GB:AE004347; GB:AE003853; NID:g9657411; PIDN:AAF95945.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession. D85538
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Atture 409, 529-533, 2001
A;Title: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-523 <STO>
A;Residues: 1-523 <STO>
A;Cross-references: GB:AE005174; NID:g12513274; PIDN:AAG54768.1; GSPDB:GN00145; UWGP:Z05
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein 20521 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o;
                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:BA000007; PIDN:BAB33895.1; PID:g13359929; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 2.1%; Score 7; DB 2; Length 523; Local Similarity 100.0%; Pred. No. 96; Pred. 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.1%; Score 7; DB 2; Length 523; Best Local Similarity 100.0%; Pred. No. 96; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                         Length 521;
                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 2;
100.0%; Pred. No. 96;
tive 0; Mismatches
                                                                                                                                                                                                                                   154 PLAKIIL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 PLAKIIL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 LLVTLIA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 PLAKIIL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            356 PLAKIIL 362
                                                                                                                                                                                                                                                                                                                                                                                                                      78 LLVTLIA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: D85538
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                 A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: ECs0472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: Z0521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                          ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
```

```
Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonsc Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Lii, J.H.; Lin, X.; Liu, X.; Liu, Z.X.; Liu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AL032649; PIDN:CAA21702.1; GSPDB:GN00022; CESP:Y55D9A.2a
A;Experimental source: clone Y55D9A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-552 <WIL>
A;Cross-references: EMBL:AL032649; PIDN:CAA21703.1; GSPDB:GN00022; CESP:Y55D9A.2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein Y55D9A.2b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                           C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 2; Length 543; 100.0%; Pred. No. 1e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 2; Length 552;
100.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
hypothetical protein Y55D9A.2a - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 4
A;Introns: 1/3; 44/3; 76/1; 160/3; 209/1; 314/1; 541/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-543 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                            R;Wallis, J.
submitted to the EMBL Data Library, October 1998
A;Reference number: 220325
A;Accession: T27190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Wallis, J. submitted to the EMBL Data Library, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Preq. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 4
A;Introns: 1/3; 44/3; 76/1; 160/3; 209/1; 314/1
```

```
Conservative
                                                                                                                 356 KKTDKAS 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 KVLVADF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         519 KVLVADF 525
                                                             33 KKTDKAS 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 LLVTLIA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLVTLIA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-624 <NAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 1
        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B82122
                                                               ò
                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unxin_regulated protein GH3 homolog At2g46370 - Arabidopsis thaliana C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Face: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 18-Jul-2001
C,Accession: A84902
R,Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A.; Reference and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A,Reference number: A84420; MUID:20083487; FMID:10617197
A,Accession: A84902
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F86244
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-554 <STO>
A;Cossereferences: GB:AE005172; NID:g22525630; PIDN:AAB65493.1; GSPDB:GN00141
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: AE002093; NID: 94559380; PIDN: AAD23040.1; GSPDB: GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A)Reference number: 219841
A)Reference number: 219841
A)Reference number: 219841
A)Reference number: 219841
A)Reture: preliminary; translated from GB/EMBL/DDBJ
A)Rolecule type: DNA
A)Residues: 1-587 <WIL>
A)Residues: 1-587 <WIL>
A)Residues: 1-587 <WIL>
A)Residues: 1-587 <WIL>
A)Residues: 1-587 <WIL>
A)Residues: 1-587 <WIL>
A)Residues: 1-587 <WIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           724103

hypothetical protein R102.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Cact-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24103
R;Berks, M.
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 2; Length 554; 100.0%; Pred. No. 1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 7; DB 2; Length 576; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 2; Length 587; 100.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 4
A;Introns: 19/2; 111/3; 147/1; 270/2; 407/1; 481/3; 529/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. Superfamily: soybean auxin-regulated protein GH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: clone R102
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 AILEKOD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 EILLKNQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       26 AILEKQD 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EILLKNO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-576 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, Genetics:
A, Gene: CESP:R102.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: At2g46370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A84902
                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

```
C,Accession: T44840
R;Nakar, D.; Gutnick, D.L.
submitted to the EMBL Data Library, July 1999
A;Description: Genomic organization of the wce region of Acinetobacter lwoffii RAG-1 r. A;Reference number: 222856
A;Accession: T44840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chaccession: B86369
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons: Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, (A.A.; J.H.; Li, Y.; Lin, X.; Liu, Z.H.; Li, Y.; Lin, X.; Liu, Z.H.; Liu, Z.B.; Maiti, R.; Marzial: Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: B86369
                                                                                                                                                                                                                                                                          probable dTDPglucose 4,6-dehydratase (EC 4.2.1.46) [imported] - Acinetobacter lwoffii
C;Species: Acinetobacter lwoffii
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: Î-731 <STO>
A;Cross-references: GB:AE005172; NID:g4056437; PIDN:AAC98010.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F508.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 2; Length 624; 100.0%; Pred. No. 1.1e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 7; DB 2; Length 731;
100.0%; Pred. No. 1.3e+02;
ive 0; Mismatches 0; Indels
   Indels
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AJ243431; PIDN:CAB57208.1
A;Experimental source: strain RAG-1
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: weeK
C;Superfamily: trsG protein
C;Keywords: carbon-oxygen lyase; hydro-lyase
   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.(
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity luv...
7; Conservative
```

```
C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AG2375
WD-40 repeat-protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, B. Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A,Accession: B82122
A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-758 <HEI>
A,Cross-references: GB:AE004281; GB:AE003852; NID:g9656616; PIDN:AAF95223.1; GSPDB:GN001
A,Experimental source: serogroup 01; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: VC2077
A;Map position: 1
C;Superfamily: ferrous iron transport protein B; translation elongation factor Tu homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable mitochondrial intermediate peptidase precursor - fission yeast (Schizosaccharom C; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 17-Mar-2003 C; Accession: T38081 R; Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: 221767
A;Reference number: 221767
A;Recession: T38081
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Ratus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-762 <CON>
A;Cross-references: EMBL: Z70690; PIDN:CAA94628.1; GSPDB:GN00066; SPDB:SPACIF3.10c
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 2; Length 762;
100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 2; Ler 100.0%; Pred. No. 1.4e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Map position: 1
C,Superfamily: thimet oligopeptidase
C,Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity luv...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 LVTLIAD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 Abiolip 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
hes 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 ADLQLID 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 LVTLIAD 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: SPDB: SPAC1F3.10c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: A97668
C;Accession: A97668
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldmar
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.
Science 294, 232-2322, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A;Reference number: A97359; MUID:2160851; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mannosidase AGR_C_4665 (AF126472) [imported] - Agrobacterium tumefaciens (strain C58, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel, Kargence, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٥.
                                                                                                                                                                                                                                                                                                                                                                ö
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-786 <KUR>
A;Residues: 1-786 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76258.1; PID:g17133695; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr4559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-818 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK88298.1; PID:g15157768; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: GB:AE008688; PIDN:AAL43556.1; PID:g17741069; GSPDB:GN00186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mannosidase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·.
                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.1%; Score 7; DB 2; Length 818; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 818;
                                                                                                                                                                                                                                                                                       Query Match 2.1%; Score 7; DB 2; Length 786; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 2; Ler
100.0%; Pred. No. 1.5e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Gene: AGR C 4665
A,Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 KLLGELI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 NLAILEK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 KLLGELI 245
                                                                                                                                                                                                                                                                                                                                                                                                                                      24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-818 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: AF2892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A97668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: AF2892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: Atu2575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
```

셤

ò

```
A;Title: The complete sequence of the 8.2 kb segment left of MAT on chromosome III revenue number: S12916; MUID:91181345; PMID:1964349
A;Accession: S12919
                                                                                                                                                                                                                                                                                                              A,Molecule type: DNA
A,Residues: 1-923 <DUJ>
A,Cross-references: EMBL:X59720; NID:g1907116; PIDN:CAA42304.1; PID:g1907179; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rimonyer, H.; Sprengel, R.; Schoepfer, R.; Herb, A.; Higuchi, M.; Lomeli, H.; Burnasher Schence 256, 1217-1221, 1992
A;Title: 156, 1217-1201, NWDA receptors: molecular and functional distinction of subtypes. A;Reference number: A43274; MUID:92271257; PMID:1350383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-methyl D-aspartate receptor (NMDR) glutamate-gated ion channels subtype NR2C - rat C,Species: Rattus norvegicus (Norway rat)
C,Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Experimental source: brain
A.Note: sequence extracted from NCBI backbone (NCBIP:103274)
C.Superfamily: N-methyl-D-aspartate receptor 2C; glutamate receptor homology
C.Keywords: transmembrane protein
F;425-852/Domain: glutamate receptor homology <GRH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                            A;Molecule type: DNA
A;Residues: 1-923 <THI>
A;Residues: 1-923 <THI>
A;Crosarreferences: EMBL:X56909; NID:g4489; PIDN:CAA40229.1; PID:g4493
R;Herbert, C.J.; Jia, Y.; Slonimski, P.P.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Accession: C43274
A, Status: preliminary; not compared with conceptual translation
A, Molecule type: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 1; Le...
No. 1.6e+02;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 2; Length 962;
100.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OmpA-related protein [imported] - Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;799-836/Domain: transmembrane #status predicted <TM10>
F;846-868/Domain: transmembrane #status predicted <TM11>
F;891-919/Domain: transmembrane #status predicted <TM12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <TM5><TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <TM8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <PMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F)538-554/Domain: transmembrane #status predicted F;583-603/Domain: transmembrane #status predicted F;628-64/Domain: transmembrane #status predicted F;675-694/Domain: transmembrane #status predicted F;708-735/Domain: transmembrane #status predicted F;708-755/Domain: transmembrane #status predicted F;739-755/Domain: transmembrane #status predicted F;735-759/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: probable membrane protein YCR037C
C;Keywords: transmembrane protein
F;458-479/Domain: transmembrane #status predicted
F;501-518/Domain: transmembrane #status predicted
F;538-564/Domain: transmembrane #status predicted
F;583-603/Domain: transmembrane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 1
100.0%; Pred. No. 1.60
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. ....
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: SGD:PHO87; MIPS:YCR037c
A;Cross-references: SGD:S0000633; MIPS:YCR037c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      784 SSGLLVT 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 TEAVAOL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 TEAVAQL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 SSGLLVT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-962 < MON>
                                                                                                                                                                                                                                                                              A;Accession: S19449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: C43274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Map position: 3R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;766-784/Domain:
F;799-836/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                             Nature 392, 353-358, 1998

A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A,Reference number: A70300; MUID:98196666; PMID:9537320
A,Accession: A70363
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Molecule type: DNA
A,Forestidus: 1-831 cAQF>
A,Cross-references: GB:AEO00704; NID:g2983301; PIDN:AAC06893.1; PID:g2983302; GB:AE00065
A,Experimental source: strain VF5
C,Genetics:
A,Gene: mpg
                                                                                                                                                                                                                                                                    C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: A70363
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable virulence factor YPO2291 [imported] - Yersinia pestis (strain C092)
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: O2.Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AD0779
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Cinllingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Kutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Accession: AD0279
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB:AL590842; PIDN:CAC91096.1; PID:g15980287; GSPDB:GN00175 C; Genetics:
A; Gene: YP02291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable membrane protein YCR037c - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YCR524
C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 16-Jun-2000
C;Accession: S12919; S;9449
R;Thierry, A.; Fairhead, C.; Dujon, B.
Yeast 6, 521-534, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 2; Length 846;
100.0%; Pred. No. 1.5e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                           mannose-1-phosphate guanyltransferase - Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 2
100.0%; Pred. No. 1.5
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100...
7; Conservative
                                                                                     239 KLLGELI 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 SENYVTK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                533 SENYVTK 539
                               230 KLLGELI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        564 IVEILLK 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 IVEILLK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-846 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues:
```

g

ð

RESULT 75

셤

à

```
C; Superfamily: chromosome segregation protein SMC1
              A;Gene: TM1182
                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A72287

Sypothetical protein TM1182 - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C;Datesion: A72287

C;Accession: A72287

C;Accession: A72287

C;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUD:99287316; PMID:10360571
A;Accession: A72287
A;Accession: A72287
A;Molecule type: DNA
A;Residues: 1-1170 <ARN>
A;Residues: 1-1170 <ARN>
A;Residues: 1-1170 <ARN>
Crosser-references: GB:AE001774; GB:AE000512; NID:g4981717; PIDN:AAD36257.1; PID:g498173
C;Genetics:
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession. A87364
R;Niterman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.
B.; Aub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
D.J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87364
A;Accession: A87364
A;Accession: Loss of Caulobacter crescentus.
A;Residues: 1-1055 of Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulobacter Caulo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Molecule type: DNA
A.Residues: 1-1115 <MUR>
A.Croser-references: GB:X55197; NID:g10097; PIDN:CAA38982.1; PID:g10098
C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C;Keywords: hydrolase
F;689-866/Domain: ATPase nucleotide-binding domain homology <AIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Plasmodium yoelii
C;Date: 03-Unr-1993 #sequence_revision 03-Jun-1993 #text_change 19-Apr-2002
C;Accession: A45761
R;Murakami, K.; Tanabe, K.; Takada, S.
J. Cell Sci. 97, 487-495, 1990
A;Title: Structure of a Plasmodium yoelii gene-encoded protein homologous to the Ca(2+)-A;Reference number: A45761; MUID:91161669; PMID:2150071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE005673; NID:g13422195; PIDN:AAK22909.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ca2+-transporting ATPase (EC 3.6.3.8) - Plasmodium yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 7; DB 2; Ler 100.0%; Pred. No. 1.9e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 2;
Local Similarity 100.0%; Pred. No. 2e+02
Les 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   784 IVKILKD 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 LRDKSPN 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 LRDKSPN 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
Glutamate receptor channel subunit epsilon 3 - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: 149705
R;Kutsuwada, T.; Kashiwabuchi, N.; Mori, H.; Sakimura, K.; Kushiya, E.; Araki, K.; Megu Nature 358, 36-41, 1992
A;Fitle: Molecular diversity of the NMDA receptor channel.
A;Reference number: 149705
A;Accession: 149705
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: B45219
R;Ishii, T.; Moriyoshi, K.; Sugihara, H.; Sakurada, K.; Kadotani, H.; Yokoi, M.; Akazav
R;Ishii, T.; Moriyoshi, K.; Sugihara, H.; Sakurada, K.; Kadotani, H.; Yokoi, M.; Akazav
Biol. Chem. 268, 2886-2843, 1993
A;Title: Molecular characterization of the family of the N-methyl-D-aspartate receptor
A;Reference number: A45219; MUID:93155102; PMID:8428958
A;Accession: B45219
A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:124263)
C;Superfamily: N-methyl-D-aspartate receptor 2C; glutamate receptor homology
F;438-865/Domain: glutamate receptor homology <GRH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Superfamily: N-methyl-D-aspartate receptor 2C; glutamate receptor homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable RAD50 DNA repair protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 01-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-methyl-D-aspartate receptor chain NMDAR2C - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-1239 <RES>
A;Cross-references: GB:D10694; NID:g538239; PIDN:BAA01536.1; PID:g538240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1250;
   Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
2.1%; Score 7; DB 1; Ler
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
2.1%; Score 7; DB 2; Ler
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0;
                               2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: neurotransmitter receptor F;425-852/Domain: glutamate receptor homology <GRH>
2.1%; Score 7; DB 2;
100.0%; Pred. No. 2.1e+
             100.0%; Pred. ...
                    Best Local Similarity 100.1
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 TEAVAÇE 120
                                                                                                                             170 KYVELST 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 TEAVAOL 107
                                                                                                                                                                                                310 KYVELST 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1250 <ISH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 TEAVAQL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 TEAVAOL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Molecule type: mRNA
```

```
A; Molecule type: mRNA
A; Residues: 27-246;2839-3343 <TIN2>
A; Cross-references: EMBL:X69086
A; Cross-references: EMBL:X69086
R; Love, D.R.; Hill, D.F.; Dickson, G.; Spurr, N.K.; Byth, B.C.; Marsden, R.F.; Walsh, I
Nature 339, 55-58, 1989
A; Title: An autosomal transcript in skeletal muscle with homology to dystrophin.
A; Reference number: S03966; MUID:89238543; PMID:2541343
A; Accession: S03966
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 2944-3433 <LOV>
A;Cross-references: EMBL:X15488; NID:g30933; PIDN:CAA33515.1; PID:g930062
C;Comment: This protein is found primarily at the neuromuscular junctions in adult musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Reference number: S28381
A.Accession: S28381
A.Accession: S28381
A.Accession: S28381
A.Accession: S28381
A.Residues: 1-3433
A.Cross-references: EMBL:X69086; NID:g34811; PIDN:CAA48829.1; PID:g34812
A.Cross-references: EMBL:X69086; NID:g34811; PIDN:CAA48829.1; PID:g34812
B.Tinslay, J.M.; Blake, D.J.; Roche, A.; Fairbrother, U.; Riss, J.; Byth, B.C.; Knight, A.Title: Primary structure of dystrophin-related protein.
A.Reference number: S28914; MUID:93096045; PMID:1461283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:119851; OMIM:128240
A;Map position: 6q24-6q24
C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrc
                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: A42771
R;Galinski, M.R.; Medina, C.C.; Ingravallo, P.; Barnwell, J.W.
R:Galinski, M.R.; Medina, C.C.; Ingravallo, P.; Barnwell, J.W.
A;Title: A reticulocyte-binding protein complex of Plasmodium vivax merozoites.
A;Reference number: A42771; MUID:92315338; PMID:1617731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CiSpecies: Homo sapiens (man)
CiDate: 17-Apr-1993 #sequence revision 03-Oct-1995 #text_change 16-Jul-1999
CiAccession: 528381; S28914; $03966
RiTinsley, J.M.
submitted to the EMBL Data Library, November 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                           reticulocyte-binding protein 1 - Plasmodium vivax
C;Species: Plasmodium vivax
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA *
A;Residues: 1-2819 <GAL>
A;Residues: 1-2819 <GAL>
A;Experimental source: Belem strain, merozoites
A;Note: sequence extracted from NCBI backbone (NCBIN:108114, NCBIP:108115)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.1%; Score 7; DB 2; Length 2829; Best Local Similarity 100.0%; Pred. No. 4.7e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                  Length 2013;
                                                                                                                         Indels
                                                      DB 2; Le:
                                                  2.1%; Score 7; DB 2
100.0%; Pred. No. 3.44
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: dystrophin-related protein
                                               Query Match
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                    100 IFNNILR 106
                                                                                                                                                                                                                                                                              539 IFNNILR 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 SLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 SLKLLGE 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB: UTRN; DMDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d regenerating muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S28914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        utrophin - human
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 86
                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C75610

probable membrane associated protein PFB0615c - malaria parasite (Plasmodium falciparum)

probable membrane associated protein PFB0615c - malaria parasite (Plasmodium falciparum)

C;Species: Plasmodium falciparum

C;Accession: C71610

C;Accession: C71610

C;Accession: C71610

C;Accession: C71610

C;Accession: C71610

C;Accession: C71610

C;Accession: C71610

Science 282, 1126-1132, 1938

A;Atitle: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.

A;Accession: C71610

A;Accession: C71610

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Actus: DNA

A;Accession: C71610

A;Actus: DNA

A;Accession: C71610

A;Actus: DNA

A;Accession: C71610

A;Actus: DNA

A;Accession: C71610

A;Actus: DNA

A;Accession: C71610

A;Actus: DNA

A;Accession: C71610

A;Actus: DNA

A;Accession: C71610

A;Actus: DNA

A;Accession: C71610

A;Actus: DNA

A;Accession: C71610

A;Actus: DNA

A;Accession: C71610

A;Actus: DNA

A;Accession: C71610

A;Actus: DNA

A;Accession: C71610

A;Actus: DNA

A;Accession: C71610

A;Actus: DNA

A;Accession: C71610

A;Actus: DNA

A;Accession: C71610

A;Actus: DNA

A;Accession: C71610

A;Actus: DNA

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Accession: C71610

A;Acc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-2013 <GAR>
A;Cross-references: GB:AE001406; GB:AE001362; NID:g3845230; PIDN:AAC71912.1; PID:g384523
A;Cross-references: clone 3D7
C;Genetics:
A;Gene: PFB0615c
C;Accession: D84727
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A64420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Residues: 1-1489 <GEN>
A)Cross-references: EMBL:Z98530; PIDN:CAB11059.1; GSPDB:GN00066; SPDB:SPAC4F8.13c
A)Experimental source: strain 972h-; cosmid c4F8
C;Genetics: A)Gene: SPDB:SPAC4F8.13c
A)Gene: SPDB:SPAC4F8.13c
A)App position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: AE002093; NID: 94263721; PIDN: AAD15407.1; GSPDB: GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 7; DB 2; Ler 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 7; DB 2; Ler
100.0%; Pred. No. 2.6e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.1 Best Local Similarity 100. Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 2
C;Superfamily: RAD50 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1058 AEİVKİL 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 HKVLVAD 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       925 HKVLVAD 931
                                                                                                                                                                                                                                                              A; Accession: D84727
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1292 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 AEIVKIL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Genetics: A;Gene: At2g31970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
```

```
Matches
                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
lysosomal trafficking regulator, long splice form - mouse
NyAlternate names: beige protein homolog
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 24-Nov-1999
C;Accession: T30851
R;Barbosa, M.D.F.S.; Tchernev, V.T.; Kingsmore, S.F.
R;Barbosa, M.D.F.S.; Tchernev, V.T.; Kingsmore, S.F.
B;Description: Two bg or not two bg? Longest isoform of mouse Lyst (beige) gene.
A;Recession: T30851
A;Accession: T30851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3788 CARA>
A;Residues: 1-3788 CARA>
A;Cross-references: EMBL:U70015; NID:g1813541; PID:g1813542; PIDN:AAC53011.1
A;Experimental source: strain C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
2.1%; Score 7; DB 2; Length 3788;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 1; Length 3433; 100.0%; Pred. No. 5.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              F;2812-2849/Domain: WW repeat homology <WWl>
F;2837-3117/Region: cysteine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;3263-3284/Region: leucine zipper motif F;3328-3349/Region: leucine zipper motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Map position: 1
C,Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1182 VKILKDN 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 SLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 VKILKDN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: Lyst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

T13960 beige protein homolog - rat

RESULT 88

1204 SLKLIGE 1210

```
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T13960
B;Mori, M.; Nishikawa, T.; Higuchi, K.; Nishimura, M.
Submitted to the EMBL Data Library, November 1998
A;Description: Deletion in the beige gene of the beige rat due to recombination between A;Reference number: Z17837
A;Accession: T13960
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T13960
A;Status: mRNA
A;Residues: 1-3788
A;Cross-references: EMBL:AB020019; NID:d1241953; PID:d1035670; PIDN:BAA34688.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: B41606
A,Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr A,Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr A,Molecule type: DNA A,Molecule type: DNA A,Molecule type: 1-25 < MUJ2>
C,Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Œ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fibrinogen alpha chain - duck (fragment)
N;Contains: fibrinopeptide A
N;Contains: fibrinopeptide A
C;Species: Anas platyrhynchos (domestic duck)
C;Date: 30-Jun-1987 #sequence_revision 28-Dec-1987 #text_change 26-Jan-1996
C;Accession: JP0101
R;Min, Y; Ping, Z; Yaoshi, Z.
R;Min, Y; Ping, Z.
Si.: Sin. B Chem. Biol. Agric. Med. Barth Sci. 28, 31-35, 1985
A;Title: Purification and primary structures of duck fibrinopeptides A and B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: Mus musculus (house mouse)
C.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Molecule type: protein
A.Residues: 1-15 <MIN>
C.Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
C.Superfamily: blood coagulation; plasma; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: E41606
R;Murtha, M.T.; Leckman, J.F.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S. 88, 10711-10715, 1991
A;Title: Detection of homeobox genes in development and evolution.
A;Reference number: A41606; MUID:92073357; PMID:1720547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 2; Length 3788;
100.0%; Pred. No. 6.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

1.8%; Score 6; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.8%; Score 6; DB 2; Length 15; Best Local Similarity 100.0%; Pred. No. 38; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homeotic protein MoxC - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1203 SLKLIGE 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A94238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 SLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 SSFQKE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 SSFOKE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: beige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
```

ò

4

```
A,Title: Comparison of the promoter proximal regions of the toxin-co-regulated tcp gen. A,Reference number: JC4719; MUID:96200848; PMID:8621096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dbx, displays extreme spatial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Crose-references: EMBL:AL109972; PIDN:CAB53272.1; GSPDB:GN0070; SCOEDB:SCJ9A.11c A;Experimental source: strain A3(2)
                                       С; Accession: PC4162; S37097
R;Ogierman, M.A.; Voss, E.; Meaney, C.; Faast, R.; Attridge, S.R.; Manning, P.A.
Gene 170, 9-16, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SCJ9A.11c - Streptomydes coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T3147
R;Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the BMBL Data Library, August 1999
A;Reference number: Z21622
A;Accession: T37147
   C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 17-Oct-1997
C;Accession: A46257
                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-46 < OGI>
A;Cross-references: EMBL:X74730; NID:g398396; PIDN:CAA52748.1; PID:g398403
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: 13.5 day embryonic telencephalon
A;Note: sequence extracted from NCBI backbone (NCBIP:112797)
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;2-58/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-61 <LU1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 6; DB 2; Length 61; 100.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.8%; Score 6; DB 2; Length 61; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R,Lu, S.; Bogarad, L.D.; Murtha, M.T.; Ruddle, F.H. Proc. Natl. Acad. Sci. U.S.A. 89, 8053-8057, 1992.
A,Titlel: Expression pattern of a murine homeobox gene, L.A,Reference number: A46257; MUID:92390387; PMID:1355604.
A,Accession: A46257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 2; Ler
100.0%; Pred. No. 1.1e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
A;Residues: 1-61 <HAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Local Similarity 100.0%; Pred. No. 1.4
Best Local Similarity 0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dbx homeobox (homeodomain) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247 KYISKP 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Gene: SCOEDB: SCJ9A.11c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 LKDNLA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 LKDNLA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYISKP 29
                                                                                                                                                                                                                                      A; Accession: PC4162
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: tcpC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                  RESULT 91
645455
beta-defensin-7 - bovine
N;Alternate names: peptide BNBD-7
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 25-Oct-1996
C;Accession: 645495
R;Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens
J. Biol. Chem. 268, 6641-6648, 1993
A;Title: Purification, primary structures, and antibacterial activities of beta-defensin
A;Reference number: 45495; MUID:93203264; PMID:8454635
A;Molecule type: protein
A;Residues: 1-40 <SEL>
A;Note: sequence modified after extraction from NCBI backbone
C;Keywords: antibacterial; disulfied bond; pyrroglutanic acid
F;1-40/Product: beta-defensin-7 #status experimental
F;1-40/Product: beta-defensin-7 #status experimental
F;9-38,16-31,21-39/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deta-defensin-9 - bovine

NyAlternate names: poptide BNBD-9

NyContains: beta-defensin-8

C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 22-Apr-1995

C;Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 22-Apr-1995

C;Accession: 144495, H45495, Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens

N;Telle: Purification, primary structures, and antibacterial activities of beta-defensin

A;Reference number: A45495; MUID:93203264; PMID:8454635

A;Rolecule type: protein

A;Residues: 1-40 <SEL>

A;Molecule type: protein

B;A-40 <SEL>

A;Molecule type: protein

A;Residues: 1-40 <SEL>

A;Molecule type: protein

B;A-40 <SEL>

A;Molecule type: protein

B;A-40 <SEL

A;Molecule type: protein

A;Residues: 1-40 <SEL>

A;Molecule type: protein

B;A-40 <SEL

A;Molecule type: protein

B;A-40 <SEL

A;Molecule type: protein

B;A-40 <SEL

A;Molecule type: protein

B;A-40 <SEL

A;Molecule type: protein

B;A-40 <SEL

A;Molecule type: protein

B;A-40 <SEL

A;Molecule type: protein

B;A-40 <SEL

A;Molecule type: protein

B;A-40 <SEL

A;Molecule type: protein

B;A-40 <SEL

A;Molecule type: protein

B;A-40 <SEL

A;Molecule type: protein

B;A-40 <SEL

A;Molecule type: protein

B;A-40 <SEL

A;Molecule type: protein

B;A-40 <SEL

A;Molecule type: protein

B;A-40 <SEL

A;Molecule type: protein

A;Residues: 1-40 <SEL

A;Molecule type: protein

A;Residues: 1-40 <SEL

A;Molecule type: protein

A;Residues: 1-40 <SEL

A;Molecule type: protein

A;Residues: 1-40 <SEL

A;Molecule type: protein

A;Residues: 1-40 <SEL

A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                toxin-co-regulated protein chain C - Vibrio cholerae (fragment)
C;Species: Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 2; Length 40;
100.0%; Pred. No. 95;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 2; Length 40; 100.0%; Pred. No. 95; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
247 KYISKP 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRQIGT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 RRQIGT 30
                                                                       α
                                                                       KYISKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 93
```

ò

Й

ö

Gaps

ö

Gaps

ö

ò 셤

ö

Gaps

. 0

67 PTEAVA 43 PTEAVA

62 38

g ð

S.

```
C;Accession: A64600
R;Tomb, J.F.; Mhite, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.I. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, I Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, (A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
Kassidues: 1-75 <TOM>
A;Cross.references: GB:AE000578; GB:AE000511; NID:g2313759; PIDN:AAD07716.1; PID:g2313
                                                                                                      R.H.; Jaskunas, S.R.
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A,Authors Yang, Y.; Young-Bllido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A;Attler Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A,Reference number: A97872; MUD:21429245; PMID:11544234
A,Accession: H97956
A,Status: preliminary
A,Rolecule type: DNA
A,Rolecule type: DNA
A,Residues: 1-73 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE007317; PIDN:AAX99484.1; PID:g15458268; GSPDB:GN00174 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Helicobacter pylori
C.Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C, Accession: T42944

K,Albrecht, J.C.; Fleckenstein, B.
submitted to the EMBL Data Library, August 1998
A, Description: Primary structure of the herpesvirus ateles genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein HP0641 - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 2; Length 75; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 2; Length 75;
100.0%; Pred. No. 1.7e+02;
:ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 6; DB 2; Length 73; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein 30 - ateline herpesvirus 3 (strain 73)
C;Species: ateline herpesvirus 3
A;Variety: strain 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z22274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 LSSFQK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 EVSKSL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVSKSL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 LSSFOK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T42944
                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: spr0680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable ribosomal protein L29 (rpmC) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Species: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C;Accession: G71355
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDc they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: G7135
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Nolecule type: DNA
A;Residues: 1-72 <COL>A;COL>A;COL>A;COL>A;COL>A;COL>A;COL>A;COLS-references: GB:AE001202; GB:AE000520; NID:93322446; PIDN:AAC65182.1; PID:9332246
C;Genetics:
A;Gene: TP0197
                                                                                                                                                                                                                              hypothetical protein SP0772 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: O3-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: E95089
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
On, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Aitle: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Accession: E95089
A;Accession: E95089
A;Accession: E95089
A;Residues: 1-67 < KURA, A;Accession: E95080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDN:AAK74910.1; PID:g14972247; GSPDB:GN00164; TIGR:SP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CiSpecies: Streptococcus pneumoniae
CiDate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
CiAccession: H97956
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein spr0680 [imported] - Streptococcus pneumoniae (strain R6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 2; Length 72; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 6; DB 2; Length 67;
100.0%; Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Prec.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE005672; PII
A;Experimental source: strain TIGR4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 6; Conservative
```

305 LSSFQK 310

à g

A; Gene: SP0772

Query Match

LSSFOK 47

RESULT 97

Query Match Best Local Similarity Matches 6; Conserva

104 ILRRQI 109

à g

45 ILRRQI 50

RESULT 98

```
DNA Res. 3, 109-136, 1996
A, Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: rat ribosomal protein L31
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: REV50469-50206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.(
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          66 VAQLAQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 VAQLAQ 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 AEIVKI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 AEIVKI 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: C86200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A64306
                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tilo329

hypothetical protein 60 - Orgyia pseudotsugata nuclear polyhedrosis virus

C;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV

C;Dete: 16-Uul-1999 #sequence_revision 16-Uul-1999 #text_change 11-May-2000

C;Accession: Tilo329

R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.

A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis

A;Reference number: Z17011; MUID:97271300; PMID:9126251

A;Recession: Tilo329

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-82 <AHR>

A;Cross-references: EMBL:U75930; NID:g2934903; PID:g1911306
                                                                                                                                                                                                                     hypothetical protein Atu2118 [imported] - Agrobacterium tumefaciens (strain CS8, Dupont) ("Species: Agrobacterium tumefaciens C'Species: Agrobacterium tumefaciens C'Species: Agrobacterium tumefaciens C'Sacesion: AF2836

R'Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I R'Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

Alauthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Symechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08.Oct-1999
C;Accession: 875083
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: AF2836
A;Status: preliminary
A;Residues: UPO KUR>
A;Residues: 1-80 KUR>
A;Residues: B-80 KUR>
A;Residues: B-80 KUR>
C;Genetics: C:Cs KUR>
A;Residues: CS KUR>
A;Residues: CS KUR>
A;Cross references: GB-AE008688; PIDN:AAL43108.1; PID:G17740580; GSPDB:GN00186
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              875083
hypothetical protein ssl0461 - Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 2; Length 80; 100.0%; Pred. No. 1.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.8%; Score 6; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.8
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 EQFADE 321
                           75
                                                                               46 AQELYS 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 LQLIDF 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 LQLIDF 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 EQFADE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: Atu2118
                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 103
                                                                         ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
A,Accession: S75083
A;Status: preliminary
A;Holecule type: DNA
A;Residues: 1-83 < KAN>
A;Residues: 1-83 < KAN>
A;Cross-references: EMBL:D90910; GB:AB001339; NID:g1652956; PIDN:BAA17945.1; PID:d10186
A;Cross-references: EMBL:D90910; GB:AB001339; NID:g1652956; PIDN:BAA17945.1; PID:d10186
A;Cross-references: EMBL:D90910; GB:AB001339; NID:g1652956; PIDN:BAA17945.1; PID:d10186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, D.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A. Senon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, A;Authors: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi A;Reference number: A64300; WUID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Firheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonsc Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Y.; Liu, X.; Liu, S.X.; Liu, S.; Khaykin, E.; Kim, C.C.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: GB:U67463; GB:L77117; NID:g1590846; PIDN:AAB98030.1; PID:g1590847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-87 <BUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: A64306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C86200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 2; Length 87;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 6; DB 2; Length 83; 100.0%; Pred. No. 1.9e+02; tive 0; Mismatches 0; Indels
A; Reference number: S74322; MUID: 97061201; PMID: 8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ribosomal protein L31 - Methanococcus jannaschii
```

RESULT 106

g

8

Best Loca Matches

ö

```
Cyaccesion: 10.7 10.0 moduled Leviblum 19-NOV-1988 #text_cnange 13-Aug-1999
Cyaccesion: A27056
R;Ngai, J; Stack, J.H.; Moon, R.T.; Lazarides, E.
Proc. Natl. Acad. Sci. U.S.A. 84, 4432-4436, 1987
A;Title: Regulated expression of multiple chicken erythroid membrane skeletal protein 4
A;Reference number: A27056; MUD:87260822; PMID:3474611
A;Accession: A27056
A;Molecule type: mRNA
A;Residues: 1-90 cNGA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R.Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.C. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, I. Nature 388, 539-547, 1997

A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. Strain PCC 7120
A;Note: Nostoc sp. Strain PCC 7120
A;Note: Nostoc sp. Strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AH1987
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. B, 205-213, 2001
A;Aritle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE000590; GB:AE000511; NID:g2313907; PIDN:AAD07833.1; PID:g23139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A; Reference number: A64520; MUID:97394467; PMID:9252185
A; Accession: D64617
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-90 < TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: GB:M16962; NID:g211745; PIDN:AAA48762.1; PID:g211746
C.Superfamily: membrane protein 4.1; protein 4.1 membrane-binding domain homology
C.Keywords: alternative splicing; cytoskeleton; membrane protein
F;1-90/Domain: protein 4.1 membrane-binding domain homology (fragment) <B41>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: BA000019; PIDN: BAB73408.1; PID: 917130798; GSPDB: GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein HP0780 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
                                                                           erythrocyte membrane protein 4.1 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 13-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein asr1451 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 2; Length 90;
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.8%; Score 6; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 IRDLKK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 SSGLLV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRDLKK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 SSGLLV 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-93 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: D64617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 110
AH1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein jhp0717 - Helicobacter pylori (strain J99)

C;Special protein jhp0717 - Helicobacter pylori (strain J99)

C;Special Helicobacter pylori

A;Variety: strain J99

A;Variety: strain J99

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999

C;Accession: E71896

B;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.;

Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A;Reference number: A71800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cipedies: Escherichia coli

Cipade: Becherichia coli

Cipade: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001

Cipade: 18-Jul-2001

Cipade: 18-Jul-2001

Cipade: 18-Jul-2001

Cipade: 18-Jul-2001

Cipade: 18-Jul-2001

Cipade: 18-Jul-2001

Cipade: 18-Jul-2001

Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: Cipade: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - Escherichia coli (strain 0157:H7, substrain RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: DNA
A,Residues: 1-88 <ARN>
A;Cross-references: GB:AE001503; GB:AE001439; NID:g4155275; PIDN:AAD06300.1; PID:g415528
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:BA000007; PIDN:BAB34614.1; PID:g13360651; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Cross-references: GB:AE005172; NID:g8927680; PIDN:AAF82171.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 2; Length 89;
100.0%; Pred. No. 2e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2e+02;
0; Indels
                                                                                                                                                                                                            Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 88;
                                                                                                                                                                                                                                                    2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 2;
100.0%; Pred. No. 2e+02
tive 0; Mismatches
                                                                                                                                                                                                       1.8%; Score 6; DB 2;
100.0%; Pred. No. 2e+02
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G90777
hypothetical protein ECs1191 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.8
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                            290 IVEILL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 IRDLKK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 LAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRDLKK 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAILEK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 IVEILL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: E71896
A; Status: preliminary
                                                                                                                       A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: ECs1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ø
                                                                                                                                                                                                                Query Match
```

RESULT 107

ð g ö

RESULT 108

Matches

ò д

```
A;Gene: Atu0448
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Gene: AGR C 795
A,Map position: circular chromosome
                                                                                                                 Best Local Similarity 100.0
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.8
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                        289 PIVEIL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 PIVEIL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 LLKNOP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 LLKNOP 63
                                                                                                                                                                                                                                                                6 PIVEIL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 PIVEIL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-97 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA A;Residues: 1-98 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: G97413
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: as13656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                           ⋩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hize31

hypothetical protein Atu0448 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

hypothetical protein Atu0448 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

c, Species: Agrobacterium tumefaciens

c, Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002

c, Accession: AE2631

c, Accession: AE2631

Frade, D.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CiSpecies: Sinchtizobium meliloti
CiDate: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
CiAccession: P95332
R;Barnett, M.J; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
F.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A/Cross-references: GB. AE006469; PIDN: AAK65224.1; PID: g14523672; GSPDB:GN00165
A/Experimental source: strain 1021, megaplasmid psyma
B/Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Weils, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
                                                                                                                                                                                                                                                                                                                                                                                                    F95332
hypothetical protein SMa1045 [imported] - Sinorhizobium meliloti (strain 1021) magaplasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577, MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE008688; PIDN:AAL41467.1; PID:g17738792; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                          ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                              1.8%; Score 6; DB 2; Length 93;
100.0%; Pred. No. 2.1e+02;
Artive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 2; Ler
100.0%; Pred. No. 2.2e+02;
cive 0; Mismatches 0;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asr1451
                                                                             Query Match
Best Local Similarity 100.00
Lag 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 LLVTLI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 LLVTLI 86
                                                                                                                                                                                                                                                                                     17 VKILKD 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-95 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Contents: annotation C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-97 < KUR>
                                                                                                                                                                                                                            18 VKILKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: F95332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: AE2631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: SMa1045
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 112
                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

```
hypothetical protein as13656 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: A12262
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, A.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein AGR_C_795 [imported] - Agrobacterium tumefaciens (strain CS8, Cere C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: G97413
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:BA000019; PIDN:BAB75355.1; PID:g17132789; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: AE007869; PIDN: AAK86264.1; PID: 915155372; GSPDB: GN00169
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 2; Length 97; 100.0%; Pred. No. 2.2e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 2; Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
1.8%; Score 6; DB 2; Ler
100.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No. 2.2e+02; ative 0; Mismatches 0;
```

```
A; Residues: 1-101 < VEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene: NDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B44056
IN protein - canine coronavirus (strain K378)
N;Alternate names: 6a protein
C;Species: canine coronavirus
C;Species: canine coronavirus
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: B44056
R;Vennema, H.; Rossen, J.W.A.; Wesseling, J.; Horzinek, M.C.; Rottier, P.J.M.
R;Vennema, H.; Rossen, J.W.B.;
R;Vennema, H.; Rossen, J.W.B.; Wesseling, J.; Horzinek, M.C.; Rottier, P.J.M.
A;Title: Genomic organization and expression of the 3' end of the canine and feline ente
A;Reference number: A44056; MuID:93033103; PMID:1329312
A;Accession: B44056
A;Molecule type: genomic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A,Reference number: A70300, MUID:98196666; PMID:9537320
A,Accession: H70413
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residuas: 1-100 <AQF:
A,Cross-references: GB:AE000734; NID:g2983733; PIDN:AAC07302.1; PID:g2983741; GB:AE00065
A,Experimental source: strain VF5
gene 3 protein-related protein VC0197 [imported] - Vibrio cholerae (strain N16961 serogic C,Species: Vibrio cholerae
C,Species: Vibrio cholerae
C,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C,Accession: F82351
C,Accession: F82351
C,Accession: R92351
C,Accession: R92351
C,Accession: R92351
C,Accession: R92351
C,Accession: R92351
C,Accession: R92351
C,Accession: R92351
C,Accession: R92351
C,Accession: R92351
C,Accession: R92351
C,Accession: R92351
C,Accession: R92351
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Accession: R92361
C,Acce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 03-Jun-2002
C;Accession: H70413
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: F82351
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <HEL>
A;Cross-references: GB:AE004110; GB:AE003852; NID:g9654600; PIDN:AAF93373.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
A;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) I chain nuoK1 - Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 100.0%; Pred. No. 2.3e+02; 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
1.8%; Score 6; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A)Gene: nuoK1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C;Keywords: membrane-associated complex; NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 LKGYEA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 LKGYEA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 LIDFEG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 LibřěG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
carboxypeptidase B (EC 3.4.17.2) precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 09-May-1997
C;Accession: A38354; B29181
R;Burgos, F.J.; Salva, M.; Villegas, V.; Soriano, F.; Mendez, E.; Aviles, F.X.
Biochemistry 30, 4082-4089, 1991
A;Title: Analysis of the activation process of porcine procarboxypeptidase B and determ.
A;Reference number: A38354; MUID:91208150; PMID:2018774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Accession: A38354
A, Status: preliminary
A, Molecule type: protein
A, Residues: 1-103 < RUR>
R, Aviles, F.X.; Vendrell, J.; Burgos, F.J.; Soriano, F.; Mendez, E.
R, Aviles, F.X.; Vendrell, J.; Burgos, F.J.; Soriano, F.; Mendez, E.
A, Title: Sequential homologies between procearboxypeptidases A and B from porcine pancre
A, Reference number: A29181; MUID:85279427; PMID:4026847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyporhetical mutant NADH dehydrogenase (ubiquinone) chain 5 - rat mitochondrion (fragme C,Species: mitochondrion Rattus norvegicus (Norway rat)
C,Date: 23-Jul-1998 #sequence_revision 23-Jul-1998 #text_change 20-Apr-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ricoral, M.; Paris, B.; Baffet, G.; Tichonicky, L.; Guguen-Guillouzo, C.; Kruh, J.; De Exp. Cell Res. 184, 158-166, 1989
A;Title: Increased level of the mitochondrial ND5 transcript in chemically induced rat A;Reference number: A60600; MUID:90005714; PMID:2507335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Residues: 1-107 <COR>
A, Experimental source: artifical carcinogen induced hepatoma cell line Morris 7288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
A,Cross-references: GB:X66717; NID:958849; PIDN:CAA47247.1; PID:958851 C;Superfamily: feline infectious peritonitis virus 11K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: B29181
A;Molecule type: protein
A;Residues: 'SS',3-13,'H',15-23,'Q',25-26,'A',28-30,'HXX',34-38 <AVI>
C;Superfamily: carboxypeptidase
C;Keywords: hydrolase; metallo-carboxypeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.8%; Score 6; DB 4; Length 107; Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 2; Length 103; 100.0%; Pred. No. 2.3e+02;
                                                                                                    Length 101;
                                                                                                    1.8%; Score 6; DB 1; Length 101;
llarity 100.0%; Pred. No. 2.3e+02;
Conservative 0; Mismatches 0; IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. worther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: liver; mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 DFLEQN 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Genome: mitochondrion A; Genetic code: SGC1
                                                                                                                                                                                                                                                                                                          96 LLVTLI 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 LVTLIA 84
                                                                                                                                                                                                                                             78 LLVTLI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 DFLEON 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: A60600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A60600
```

```
hypothetical protein 1 (165-23S rRNA spacer region) - Chlorella ellipsoidea chloroplast Cispecies: chloroplast Chlorella ellipsoidea Cispecies: chloroplast Chlorella ellipsoidea Cispecies: chloroplast Choression: 324444

R;Yamada, T.; Shimaji, M.
R;Yamada, T.; Shimaji, M.
R;Yamada, T.; Shimaji, M.
R;Yamada, T.; Shimaji, M.
R;Yamada, T.; Shimaji, M.
R;Yamada, T.; Shimaji, M.
R;Yamada, T.; Shimaji, M.
R;Yamada, T.; Shimaji, M.
R;Yamada, T.; Shimaji, M.
R;Yamada, T.; Shimaji, M.
R;Yamada, T.; Shimaji, M.
R;Yamada, T.; Shimaji, M.
R;Yamada, T.; Shimaji, M.
R;Yamada, T.; Shimaji, M.
R;Yamada, T.; Shimaji, M.
R;Yamada, T.; Shimaji, M.
R;Yamada, T.; Shimaji, M.
R;Reference number: A93622; MUID:86232622; PMID:3714498
A;Rccssion: A24444
A;Molecule type: DNA
A;Residues: 1-110 < YaMs
A;Note: the authors translated the codon ATT for residue 6 as Asn, CAA for residue 35 z
                                                                                                                                                                                                                A;Cross-references: GB:AE004729; GB:AE004091; NID:g9949143; PIDN:AAG06428.1; GSPDB:GN0(A;Experimental source: strain PA01 C;Genetics: A;Gene: PA3040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cispecies: Staphylococcus aureus
Cispecies: Staphylococcus aureus
Cispecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
Ciscession: A89999
Ciscession: A89999
Cistecssion: A89999
May, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:BA000018; PID:g13701789; PIDN:BAB43082.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein SA1802 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 1.8%; Score 6; DB 2; Length 109; Local Similarity 100.0%; Pred. No. 2.5e+02; Nes 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.8%; Score 6; DB 2; Length 110; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.8%; Score 6; DB 2; Length 109; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels
         A; Reference number: A82950; MUID; 20437337; PMID: 10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: conserved hypothetical protein b2672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 EKLLQS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 IRDLKK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 IRDLKK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 KLIEFL 305
                                                                                                                                                                                       A; Residues: 1-109 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 EKLLQS 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-109 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Genome: chloroplast
C;Keywords: chloroplast
                                                     A;Accession: A83265
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A89990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                Cispecies: Aeropyrum pernix
Cispecies: Aeropyrum pernix
Cispecies: Aeropyrum pernix
Ciscossion: 1998 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
Ciscossion: E72494
Rikawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Vamazaki, J.; Kudoh, Res. Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A; Reference number: A72450; MUID:99310339; PMID:10382966
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein YPO0742 [imported] - Yersinia pestis (strain CO92)
hypothetical protein YPO0742 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AF0091
B;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. and mon-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Title: Genome sequence of Yersinia pestis, pMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conserved hypothetical protein PA3040 [imported] - Pseudomonas aeruginosa (strain PA01) (Species: Pseudomonas aeruginosa (Species: Pseudomonas aeruginosa (Species: Pseudomonas aeruginosa (Species: Pseudomonas aeruginosa (Species: Pseudomonas aeruginosa (Species: Pseudomonas aeruginosa (Species: Chacesion: A83265 (Species: Chacesion: A83265 (Species: Chacesion: A83265 (Species: Chacesion: A83265 (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chacker) (Species: Chac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-108 <KAW>
A;Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BAA81613.1; PID:d1045399; PID:g510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-108 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC89593.1; PID:g15978825; GSPDB:GN00175 C;Genetics: A;Gene: YP00742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.8%; Score 6; DB 2; Length 108; Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 6; DB 2; Length 108;
100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: APE2596
C;Superfamily: Aeropyrum pernix hypothetical protein APE2596
                                                                                                                                                                                                                         hypothetical protein APE2596 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Perional 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 QSLKLL 232
73 LVTLIA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 YSSGLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 YSSGLL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 QSLKLL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: AF0091
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 122
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

à

Ř.

ö

ö

```
A;Cross-references: EMBL:X56770; NID:95589; PIDN:CAA40089.1; PID:95590
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1990
                                                                                                            Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 TVEYIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 IRDLKK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 IRDLKK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 TVEYIS 75
                                                                                                                                                                                           26 AILEKO 31
                                                                                                                                                                                                                                            83 AILEKO 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: C86636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: C86636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A99504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: SSO3188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: yajB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                              ò
                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sensorin A - California sea hare
(;Species: Aplysia californica (California sea hare)
(;Species: Aplysia californica (California sea hare)
(;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
(;Accession: 823653
(R;Brunet, J.F.; Shapiro, E.; Foster, S.A.; Kandel, E.R.; Iino, Y.
(Science 252, 865-8859, 1991
(A;Title: Identification of a peptide specific for Aplysia sensory neurons by PCR-based A;Reference number: 823653; MUID:91227915; PMID:1840700
A;Accession: 823653
A;Accession: 823653
A;Accession: Ransa A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-113 <BRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein c0630 - Sulfolobus solfataricus C; Species: Sulfolobus solfataricus C; Species: Sulfolobus solfataricus C; Species: Sulfolobus solfataricus C; Accession: S74015 #sequence_revision 24-Oct-1997 #text_change 20-Jun-2000 C; Accession: S74015 R; Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S Mol. Microbiol. 22, 175-191, 1996 A; Title: Organizational characteristics and information content of an archaeal genome: A; Reference number: S73076; MUID:97055432; PMID:8899719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Cross-references: EMBL:Y08256; NID:g1707679; PID:g1707709
A, Experimental source: strain P2
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996
C,Superfamily: Sulfolobus solfataricus hypothetical protein c0630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                         RESULT 125
T12499
T12499
T12499
C19491
C29becias: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C;Accession: T12499
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
S;Doustka, A.; Klein, Sequence Database, June 1999
A;Reference number: Z17525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Accession: S74015
A, Status: nucleic acid sequence not shown; translation not shown
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 2; Length 112; 100.0%; Pred. No. 2.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: EMBL:AL080178
A;Experimental source: adult testis; clone DKFZp434Kl71
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.8%; Score 6; DB 2; Ler
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 NILRRQ 108
                                                                                                                                                                                                                                                                                                                                                     A;Accession: T12499
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-110 <POU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 NILRRO 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-112 <SEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 EIVKIL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s Eivkil 10
                            KLIEFL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: DKFZp434K171.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                               26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                823653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                               g
```

```
hypothetical protein SSO3188 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Accession: A99504 C;Accession: A99504 C;Accession: A99504 C;Accession: A99504 C;Accession: A99504 C;Accession: A99504 C;Accession: A,C;A;Confalonieri, F;Shc, V; Allard, G;Awayez, M.J.; Chan Jong, I; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. Submitted to GenBank, April 2001 A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein yajB [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-122 <STC>A;Residues: 1-122 <STC>A;Cross-references: GB:AE005176; PID:g12722935; PIDN:AAK04189.1; GSPDB:GN00146
A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-123 <KUR>
A; Cross-references: GB: AE006641; NID: 913816623; PIDN: AAK43288.1; GSPDB: GN00155
C; Genetics:
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein AF0905 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n 1.8%; Score 6; DB 2; Length 123; Similarity 100.0%; Pred. No. 2.7e+02; 6; Conservative 0; Mismatches 0; Indels
                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0: Indels
1.8%; Score 6; DB 2; Ler
100.0%; Pred. No. 2.5e+02;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 2; Let Local Similarity 100.0%; Pred. No. 2.7e+02; nes 6; Conservative 0; Mismatches 0;
```

```
A;Genome: cyanelle
C;Superfamily: uncharacterized conserved protein ycf35
C;Keywords: cyanelle
                                                                                                                                Query Match
Best Local Similarity luv...
...as 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                          82 LIADIO 87
                                                                                                                                                                                                                                                                                                                               68 LIADLO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-128 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 LIADLQ 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 LIADLO 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 LYSSGL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetica:
A;Gene: NMB0833
                    A; Gene: ycf35
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 133
A81153
                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Jun-2003
C;Accession: A69363
R;Klenk, "H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelon, K.E.; Ketchum, K.A.; Dodson.; Fleatschmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. adducts, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Adducts 390, 364-370, 1397
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Atitle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaech, R.; Accession: A69363
A;Accession: A69363
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-124 <KLE>
A;Cross-references: GB:AE001041; GB:AE000782; NID:g2689364; PIDN:AAB90335.1; PID:g264969
C;Superfamily: uncharacterized conserved protein MJ1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable type II secretion system protein PA0680 [imported] - Pseudomonas aeruginosa (st C;Species: Pseudomonas aeruginosa (st C;Species: Pseudomonas aeruginosa (c;Species: Pseudomonas aeruginosa (c;Species: Pseudomonas aeruginosa (c;Species: Pseudomonas aeruginosa (st C;Species: Pseudomonas aeruginosa (st C;Species: Pseudomonas (st C;N; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID: 20437337; PMID: 10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE004503; GB:AE004091; NID:99946553; PIDN:AAG04069.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein yof35 - Cyanophora paradoxa cyanelle C;Species: cyanelle Cyanophora paradoxa C;Species: cyanelle Cyanophora paradoxa C;Baccies: a0-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 12-Jun-2003 C;Accession. V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A. submitted to the EMBL Data Library, July 1995 A;Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-128 <STI>
A;Cross-references: EMBL:U30821; NID:g1016083; PIDN:AAA81309.1; PID:g1016222
A;Experimental source: strain Pringsheim LB555
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 2; Length 124; 100.0%; Pred. No. 2.8e+02; iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 1; Ler 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Experimental source: strain PAO1
C, Genetics:
A, Gene: PAO680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: Z15840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261 LLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 EGKKDV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGKKDV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLRDKS 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-124 <STO>
                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T06966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 131
F83560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

```
Rifettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherry, B.A. ri, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V. A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58, A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Accession: HT1046
R;Kawarabayasi, Y; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch.
DNA Res: 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: this accession replaces an interim accession for a sequence replaced by GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE002436; GB:AE002098; NID:g7226062; PIDN:AAF41244.1; PID:g7226(
A;Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                      type I restriction enzyme-related protein NMB0833 [imported] - Neisseria meningitidis
                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: H71046
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-129 <KAW>
A;Cross-references: GB:AP000006; NID:g3236133; PIDN:BAA30776.1; PID:g3258093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: A81153
                                                                                        Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: PH1664
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     th Similarity 100.0%; Pred. No. 2.9e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 2; Length 128; 100.0%; Pred. No. 2.9e+02; tive 0; Mismatches 0; Indels
        Length 128;
                                                                                        Indels
1.8%; Score 6; DB 2; Lei
100.0%; Pred. No. 2.9e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein PH1664 - Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: strain OT3
```

```
A;Cross-references: DDBJ:AP000059; NID:g5103911; PIDN:BAA79276.1; PID:g5103960 A;Experimental source: strain Kl C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 5
A;Introns: 40/1; 53/2; 98/1; 118/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 IFEDYE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 EAVAOL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 EAVAQL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 IFEDYE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-131 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: CESP:T27E4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: D84401
                                                                                                                                         A; Gene: APE0321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     948814

Pypothetical protein 2 - turkey herpesvirus

C;Species: turkey herpesvirus

C;Species: turkey herpesvirus

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999

R;Smith, G.G.; Zelnik, V.V.; Ross, N.N.

submitted to the EMBL Data Library, October 1994

S;Description: Gene organization in herpes virus of turkey: identification of a novel OR

A;Accession: S48814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CiSpecies: Aeropyrum pernix
CiSpecies: Aeropyrum pernix
CiDate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
CiDate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
CiDate: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-199
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiDate: 20-Aug-1999
CiD
                                                                                                                                                                                                                                                                                                                                                       C;Accession: H90161
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.G.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Moreldues: 1-129 «KDR»
A; Cross-references: GB:AE006641; NID:g13813343; PIDN:AAK40551.1; GSPDB:GN00155
C;Genetics:
A;Gene: SS02006
C;Superfamily: Aeropyrum pernix hypothetical protein APE0505
                                                                                                                                                                                                                           conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1.129 <SMI>
A;Cross-references: EMBL:Z46371; NID:g562788; PIDN:CAA86494.1; PID:g562790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 129;
5. 2.9e+02;
cches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 2; Length 129;
100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 137
H72722
hypothetical protein APE0321 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 2
100.0%; Pred. No. 2.9
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Reference number: A99139
A)Accession: H90161
A)Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 ECIRHE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 DIASDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIASDA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-130 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 ECIRHE 69
                  19 LYSSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

```
30S Tibosomal protein S6E [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Accession: D84401
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, J. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl Jung, K.H.; Alam, M.; Freattas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L. A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE004437; NID:g105B1909; PIDN:AAG20576.1; GSPDB:GN00138 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Accession: T25924
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-13
A,Residues: 1-13
A,Cross-references: EMBL-U64837; PIDN:AAB04836.1; GSPDB:GN00023; CESP:T27E4.5
A,Experimental source: strain Bristol N2; clone T27E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Appointational protein T27E4.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T2524
R;Bradshaw, H.
Submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid T27E4.
A;Reference number: Z20111
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 6; DB 2; Length 131;
100.0%; Pred. No. 2.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.8%; Score 6; DB 2; Length 131; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                Query Match 1.8%; Score 6; DB 2; Length 130; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 6; Conservative 0; Mismatches 0; Indels
C;Superfamily: Aeropyrum pernix hypothetical protein APE0321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: Haloarcula ribosomal protein HS13
```

```
C; Accession: G86569
R; Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I Rucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: G86569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-133 <AQP>
A;Coss-references: GB:AE000687; NID:g2983050; PIDN:AAC06665.1; PID:g2983057; GB:AE0006
A;Experimental source: strain VF5
C;Genetics:
A;Gene: aq_384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A,Reference number: A70300; MUID:98196666; PMID:9537320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:BA000008; NID:g8979006; PIDN:BAA98841.1; GSPDB:GN00142
A;Experimental source: strain J138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: E70334
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Aquifex aeolīcus
C.Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata)
C;Species: Pyrobotrys stellata
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 13-Aug-1999
02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X68202; NID:g18266; PIDN:CAA48289.1; PID:g18267 A;Note: the source is designated as Chlamydobotrys stellata C;Superfamily: rat ribosomal protein L27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 2; Length 133; 100.0%; Pred. No. 3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                A,Gene: rs8
C,Superfamily: Escherichia coli ribosomal protein S8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
1.8%; Score 6; DB 2; I
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein aq 384 - Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 KNYLIK 327
                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-133 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 IVKILK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 İVKİLK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 KNYLIK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: S26612
A;Molecule type: mRNA
A;Residues: 1-134 <WOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                      C, Genetics;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ribosomal protein S8 CP0113 [imported] - Chlamydophila pneumoniae (strains CWL029 and AB C.Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C.Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C.Accession: D72054; B81612
S.A.Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
A.Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A.Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: DNA
A,Residues: 1-133 <ARN>
A,Residues: 1-133 <ARN>
A,Residues: 1-133 <ARN>
A,Cross-references: GB:ARO01647; GB:AE001363; NID:g4376920; PIDN:AAD18773.1; PID:g437693
A,Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406; 2000
A,Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A,Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE002173; GB:AE002161; NID:g7189033; PIDN:AAF37996.1; PID:g718904
A;Experimental source: strain AR39, HL cells
                                                                                                                                                              N.Alternate names: PCZA361.28
C.Species: Amycolatopsis orientalis
C.Species: Amycolatopsis orientalis
C.Species: Amycolatopsis orientalis
C.Species: Amycolatopsis orientalis
C.Species: Amycolatopsis orientalis
C.Species: Amycolatopsis orientalis
C.Species: Amycolatopsis orientalis
C.Species: Table 1. 3. 185-162
B.Yun Wageningen, A.; Kirkpatrick, P.; Williams, D.; Harris, B.; Kershaw, J.; Lennard, S.Yun Wageningen, A.; Estachingen, A.; Estachingen, B.; Sequencing and analysis of genes involved in the biosynthesis of a vancomycin A;Reference number: Z18804
A;Reference number: Z18804
A;Recession: T30595
A;Retaute: preliminary
A;Molecule type: DNA
A;Residues: 1-132 <VAN>A;Residues: EMBL:AJ223998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 142
G86569
S8 ribosomal protein [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 2; Length 133; 100.0%; Pred. No. 3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 2; Ler 100.0%; Pred. No. 2.9e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
A;Gene: rs8; CP0113
C;Superfamily: Escherichia coli ribosomal protein S8
                                                                                                                                          sugar transport homolog - Amycolatopsis orientalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 ILFMLL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 ILFMLL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-133 <REA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 IVKILK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVKILK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: D72054
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: E81612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
```

à

à

g

Pred. No. 3e+02; 0; Mismatches

100.08;

Best Local Similarity 100. Matches 6; Conservative

223 VTKRQS 228

à

53 VTKRQS 58

```
C. Accession: E69842

E. Kunst. F.; Ogaawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte (C.; Bron, S.; Brouillet, S.); Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch. A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A.; Althors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle ich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Kohingstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois A.; Authors: Lauber, J.; Lazarevic, V.; Ley. B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell Rieger, M.; Rivolta, A.; Cudega, B.; Roche, B.; Roshe, M.; Sadaie, Y.; Sato, T.; Scanlon A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sato, T.; Scanlon A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sato, T.; Scanlon A.; Winters, P.; Wipat, A.; Taraka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Ochiyama T.; Winters, P.; Wipat, A.; Taraka, T.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Uchiyama A.; Altle: The complete genome sequence of the Gram-Positive bacterium Bacillus subtilis. A.; Reference number: A69580; MUID:98044033; PMID:9384377

A.; Residues: preliminary; nucleic acid sequence not shown; translation not shown A.; Residues: 1-135 «KUN

A.; Residues: 1-135 «KUN

A.; Resperimental source: strain 168

A.; Resperimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SSO2684 [imported] - Sulfolobus solfataricus CiSpecies: Sulfolobus solfataricus CiSpecies: Sulfolobus solfataricus CiDate: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 CiAccession: B90443
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; J.; Jeffriss, A.C.; Kozera, C.J.; Modina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-136 <KUR>
A;Cross-references: GB:AE006641; NID:g13816004; PIDN:AAK42801.1; GSPDB:GN00155
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein A441L - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #Bequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T17944
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 2; Length 135;
100.0%; Pred. No. 3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: yjaV
C,Superfamily: Bacillus subtilis hypothetical protein yjaV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Description: Sulfolobús solfataricus complete genome.
A,Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 6; DB 2; L
100.0%; Pred. No. 3e+02;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Graves, M.V.; Van Etten, J.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 ONYDTI 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 QNYDTI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 LVTLIA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 LVTLIA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: SSO2684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #text_change 09-Jun-2000
C;Date: 20-Aug-1999 #tequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: F72638
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
R;Kawarabayasi, Y.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; N
DNA, Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyz
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation initiation factor eIF-2, beta subunit - Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Species: Methanobacterium thermoautotrophicum C; Date: O5-Dec-1997 #text_change 08-Oct-1999 C; Accession: B69103 R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S. Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J.; Bacteriol. 179, 7135-7155, 1997 A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID:98037514; PMID:9371463 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-135 <MTH>
A;Residues: 1-135 <MTH>
A;Cross-references: GB:AE000932; GB:AE000666; NID:g2622894; PIDN:AAB86235.1; PID:g262289
A;Cross-references: strain Delta H
C;Genetics:
A;Gene: MTH1769
C;Superfamily: Methanococcus jannaschii probable translation initiation factor eIF-2 bet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: F72638
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-134 «KAN»
A;Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79510.1; PID:d1043296; PID:g510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 2; Length 135; 100.0%; Pred. No. 3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 1.8%; Score 6; DB 2; Length 134; Local Similarity 100.0%; Pred. No. 3e+02; les 6; Conservative 0; Mismatches 0; Indels
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: Aeropyrum pernix hypothetical protein APE0542
                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein APE0542 - Aeropyrum pernix (strain K1)
```

A; Experimental source: strain Kl

A;Gene: APE0542

Query Match

Matches

ð

hypothetical protein yjav - Bacillus subtilis C;Species: Bacillus subtilis

RESULT 147

E69842

Best Local Similarity 100. Matches 6; Conservative

Query Match

212 DYEKLL 217

ð

```
C;Accession: D71104
R;Kawarabayasi, Y; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                             A;Accession: D71104
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-140 <KAW>
A;Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29694.1; PID:g3257011
A;Experimental source: strain OT3
A;Experimental source: strain OT3
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: Methanococcus jannaschii probable translation initiation factor eIF-2 be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          System, hypothetical protein 140 - Rhizobium sp.
C;Species: Rhizobium sp.
C;Species: Rhizobium sp.
C;Species: Rhizobium sp.
C;Species: Rhizobium sp.
C;Stecies: Rhizobium sp.
C;Accession: S34667
R;Rochepeau, P.; Fellay, R.; Broughton, W.
Submitted to the BMBL Data Library, July 1993
A;Reference number: S34667
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-140 <ROC>
A;Cross-references: BMBL:X74068; NID:g395149; PIDN:CAA52196.1; PID:g581535
C;Genetics:
A;Start codon: GTG
C;Superfamily: Rhizobium plasmid pNGR234a protein y4h0
                                                                                                                                                  C.Species: Pyrococcus horikoshii
C.Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable translation initiation factor eIF-2 beta - Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 2; Length 140; 100.0%; Pred. No. 3.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 2; Length 140;
100.0%; Pred. No. 3.1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 DYEKLL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 RCGIML 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 DYEKLL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 RCGIML 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: PH0605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S34667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HASH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein (orf in Lhca3.St.1 promoter) - potato
C;Species: Solanum tuberosum (potato)
C;Species: Solanum tuberosum (potato)
C;Species: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999
C;Accession: T07027
R;Nap, J-P, van Spanje, M.; Dirkse, W.G.; Baarda, G.; Mlynarova, L.; Loonen, A.; Grondh Plant Mol. Biol. 23, 605-612, 1993
A;Title: Activity of the promoter of the Lhca3.St.1 gene, encoding the potato apoprotein
A;Reference numbers: S39557; MUID:94033339; PMID:8219093
A;Accession: T07027
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: L137 cAnd.
A;Residues: 1-137 cAnd.
A;Residues: 1-137 cAnd.
A;Residues: EMBL:S66876; NID:9440964; PIDN:AAB28865.1; PID:9440965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable translation initiation factor aif-2, subun it beta PAB0959 - Pyrococcus abyssi Cispecies: Pyrococcus abyssi Cispecies: Pyrococcus abyssi Cispecies: Pyrococcus abyssi Cispecies: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000 CiAccession: E75056
Examonymous, Genoscope Submitted to the EMBL Data Library, July 1999
Albescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru Aixcession: E75056
Aixcession: E75056
Aixcession: E75056
Aixclain: preliminary
Aixclain: Dreliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Residues: 1-140 <KAM>
A,Cross-references: GB:AZ748287; GB:AL096836; NID:g5458657; PIDN:CAB50346.1; PID:g545885
A,Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: PAB0959
C;Superfamily: Methanococcus jannaschii probable translation initiation factor eIF-2 bet
                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                Superfamily: Chlorella virus PBCV-1 hypothetical protein A441L
                                                                                                                                                                    A.Cross-references: EMBL:U42580, NID:g402896, PIDN:AAC96809.1
A:Experimental source: specific host Chlorella strain NC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.8%; Score 6; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                         Query Match 1.8%; Score 6; DB 2; Length 137; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                  Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
1.8%; Score 6; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
submitted to the EMBL Data Library, May 1999
                          A;Reference number: Z18806
A;Accession: T17944
                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 ILFMLL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 LLGELI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 DYEKLL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 LLGELT 122
                                                                                                              A; Molecule type: DNA
A; Residues: 1-137 <GRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 İLFMLL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 DYEKLL 12
                                                                                                                                                                                                                             C;Genetics:
A;Note: A441L
C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
```

. 0

Gaps

..

Gaps

```
A. Accession: A38884
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Candido, E. P. M.
M. Molecule type: MRNA
A. Candido, E. P. M.
A. Candido, E. P. M.
A. Molecule type: MRNA
A. Reference number: A39467; MUID: 83220736; PMID: 6190129
A. Accession: A02917
A. Molecule type: mRNA
A. Reference number: A39467; MUID: 83220736; PMID: 6190129
A. Accession: A02917
A. Molecule type: mRNA
A. Residues: 'KLCSFRQ', 47-143 < RUS>
A. Coss-references: GB: K01864; NID: 9156331; PIDN: AAA28065.1; PID: 9156332
A. Cross-references has been revised in reference A38884
C. Superfamily: alpha-crystallin
C. Keywords: heat shock; stress-induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: T15047
R; Morigudah, K; Sugiura, M.
R; Morigudah, K; Sugiura, M.
Plant J. 12, 215-221, 1997
A; Title: Structure and subcellular localization of a small RNA-binding protein from tob:
A; Reference number: Z18278; MUID:97408943; PMID:9263462
A; Accession: T15047
A; Molecule type: mRNA
A; Residuae; preliminary; translated from GB/EMBL/DDBJ
A; Residuaes: 1-144 < MORA
A; Cross-references: EMBL:D28862; NID:92366749; PIDN:BAA22083.1; PID:92366750
A; Experimental source: young leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA-binding protein RGP-3 - wood tobacco (fragment)
C;Species: Nicotiana sylvestris (wood tobacco)
C;Date: 20-8p-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T16961
R;Moriguchi, K.; Sugita, M.; Sugiura, M.
Plant J. 12, 215-21, 1997
A;Title: Structure and subcellular localization of a small RNA-binding protein from tob.
A;Reference number: Z18278; MUID:97408943; PMID:9263462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology C;Keywords: RNA binding F;39-106/Domain: ribonucleoprotein repeat homology <RRM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA binding protein 3 - wood tobacco
C;Species: Nicotiana sylvestris (wood tobacco)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 1; Length 143;
100.0%; Pred. No. 3.2e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 2; Ler 100.0%; Pred. No. 3.2e+02; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
                                            R;Candido, E.P.M.
submitted to GenBank, November 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.8*
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.0
                                                                                                                  A, Reference number: A38884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 KPENLK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 DAFATF 187
           A; Residues: 1-143 <JON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 KPENLK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 DAFATF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: T16961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: RGP-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T15047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HHKW41

heat shock protein 16-41 - Caenorhabditis elegans
NyAlternate names: heat shock protein 16 2
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: A25199; A38884; A02917
Cispecies: A25199; A38884; A02917
Cispecies: Dispecies: A25199; A38884; A15188
Cispecies: Caenorhabditis A25199
Ainclecule type: DNA

Ainclecule type: DNA
                                                                                                                                                                                                                                                                         A Molecule type: protein

A;Residues: 1-103, T',105-123,'S',125-141 < WIL>

A;Residues: 1-103, T',105-123,'S',125-141 < WIL>

B;Experimental source: Rambouillet breed

R;Huisman, T.H.J.; Dozy, A.M.; Wilson, J.B.; Efremov, G.D.; Vaskov, B.

Biochim. Biophys. Acta 160, 467-469, 1968

A;Title: Sheep hemoglobin D, an alpha-chain variant with one apparent amino acid substit

A;Reference number: A90574; MUID:69004666; PMID:5680274

A;Accession: A90574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: protein
A,Residues: 1-14,'D',16-141 <HUI>
C;Superfamily: globin, globin homology
C;Keywords: blood; chromoprotein; erythrocyte; heme; iron; metalloprotein; oxygen carrie
F;2-141/Domain: globin homology <GLB>
F;2-141/Domain: globin homology <GLB>
F;88/Binding site: oxygen (His) (distal axial ligand) #status predicted
F;87/Binding site: heme iron (His) (proximal axial ligand) #status predicted
A; Experimental source: Soay and Clan breeds
A, Experimental source: Soay and Clan breeds
A, Note: only the composition was determined for the insoluble core region (residues 100-
B; Wilson, J.B.; Brandt, G.; Huisman, T.H.J.
J. Biol. Chem. 243, 3687-3692, 1968
A; Title: The structure of sheep hemoglobins. III. Structural studies of the alpha chain
A; Reference number: A92036; MUD: 68313124; PMID: 5658545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      orf US426 - infectious laryngotracheitis virus
Orf US426 - infectious laryngotracheitis virus
C;Species: infectious laryngotracheitis virus
C;Species: infectious laryngotracheitis virus
C;Accession: 14852
R;Sakaguchi, M.; Urakawa, T.; Hirayama, Y.; Miki, N.; Yamamoto, M.; Hirai, K.
Nyirus Genes 6, 355-378, 1992
A;Title: Sequence determination and genetic content of an 8.9-kb restriction fragment
A;Reference number: A48552, MUID:93118245; PMID:1282282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA,
M. Residues: 1-142 <SAK.
A;Kesidues: 1-142 <SAK.
A;Cross-references: GB:M80595; NID:g291557; PIDN:AAB59898.1; PID:g291567
A;Note: sequence extracted from NCBI backbone (NCBIN:121622, NCBIP:121633)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.8%; Score 6; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 142;
5. 3.1e+02;
cches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.8%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 3.1
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 GLLVTL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 SLKLLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 GLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 SLKLLG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
```

ö

Gaps

. 0

Length 143;

ò.

Gaps

.. 0

0; Indels

Length 144;

ò CD

 $\Xi$ 

```
C; Accession: G69011
S; Smith, D. R.; Doucette-Stamm, L. A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Oiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, I ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. A. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func A; Reference number: A69000; MUID: 98037514; PMID: 9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-145 <MTH>
A;Cross-references: GB:AE000801; GB:AE000666; NID:g2621145; PIDN:AAB84615.1; PID:g26211
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mer operon ORF2 hypothetical protein - Serratia marcescens plasmid pDU1358 (fragment) C;Species: Serratia marcescens C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 08-Oct-1999 C;Accession: E29010 R;Griffin, H.G.; Foster, T.J.; Silver, S.; Misra, T.K. A;Coc. Natl. Acad. Sci. U.S.A. 84, 3112-3116, 1987 A;Title: Cloning and DNA sequence of the mercuric- and organomercurial-resistance deter A;Reference number: A94150; MUID:87204087; PMID:3033633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-145 cKAW>
A;Cross-references: GB:AJ248287; GB:AL096836; NID:G5458657; PIDN:CAB50148.1; PID:G54586
A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: G75031
R; anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome sta
A; Reference number: A75001
                                                                                                                                                                      hypothetical protein MTH109 - Methanobacterium thermoautotrophicum (strain Delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: Methanobacterium thermoautotrophicum hypothetical protein MTH109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                  C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein PAB0821 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Ler
. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.8%; Score 6; DB 2; Ler
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.8%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 3.2
Matches 6; Conservative 0; Mismatches
           ||||||
125 IVEILL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 DIASDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIASDA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIVKIL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 EIVKIL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: G75031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: PAB0821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: MTH109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: B82878
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-145 cGLA>
A,Residues: 1-145 cGLA>
A,Cross-references: GB.AE002153; GB.AF222894; NID:g6899544; PIDN:AAF30964.1; GSPDB:GN001
A,Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ribosomal protein L9 UU551 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: B82878
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, Pebruary 2000
A; Molecule type: DNA
A; Molecule type: 1-144 < MOR>
A; Cross-references: EMBL:D67086; NID:g1009362; PIDN:BAA11089.1; PID:g1009363
C; Genetics: 44/1; 67/1; 102/3
A; Introns: 44/1; 67/1; 102/3
C; Superfamily: giycine-rich RNA-binding protein; ribonucleoprotein repeat homology
C; Keywords: RNA binding
                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:ALS90842; PIDN:CAC88931.1; PID:g15978178; GSPDB:GN00175
C;Genetics:
A;Gene: YPO0065
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 6; DB 2; Length 13.7., Pred. No. 3.2e+02;
                                                                                                                                                                                                                    1.8%; Score 6; DB 2; Length 144;
100.0%; Pred. No. 3.2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 2; Length 145; 100.0%; Pred. No. 3.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Genetic code: SGC3
C;Superfamily: Bscherichia coli ribosomal protein L9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.8%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 3.2.
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.00
The 6; Conservative
                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: glpE protein
                                                                                                                                                                                                                                                                                                                                 182 DAFATF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              285 HKTQPI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 IVEILL 295
                                                                                                                                                                                                                                                                                                                                                                                       56 DAFATF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 HKTQPI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Gene: rpL9; UU551
                                                                                                                                                                                                                         Query Match
```

RESULT 160

à DP

ö

```
Cydrages, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke R.; Glasser, P.; Frangeul, L.; Buchrieser, C.; Amend, L.; Dussurget, O.; Entian, K.D.; Feihi, H.D.; Jones, L.M.; Karst, U.

Science 244, 849-8852, 200.

Science 244, 849-8852, 200.

A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M. Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland A; Title: Comparative genomics of Listeria species.

A; Reference number: AB1077; MUID:21537279; PMID:11679669

A; Reference number: AB1077; MUID:21537279; PMID:11679669

A; Residues: 1-147 < GLA>

A; Residues: 1-147 < GLA>

A; Residues: Litty collab

A; Experimental source: strain Clip11262

C; Genetics:

A; Gene: lin2433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein PH0862 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C;Accession. B71137
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein Z1467 [imported] - Escherichia coli (strain O157:H7, substrain EDL C'Species: Escherichia coli (c'Species: Escherichia coli (c'Accession: B85641 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C'Accession: B85641 #s.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe iller, L.; Grothesck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca Nature 409, S29-533, Z001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-148 «KAW» A;Residues: 1-148 «KAW» A;Cross-references: GB-AP000003; NID:g3236130; PIDN:BAA29956.1; PID:g3257273 A;Experimental source: strain OT3 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
                                                                                                                conserved hypothetical protein lin2433 [imported] - Listeria innocua (strain Clip11262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                    C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AD1736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 2; Length 148;
100.0%; Pred. No. 3.3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.8%; Score 6; DB 2; Len
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 NPAEIV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 EIVKIL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 NPAEIV 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B85641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T10511

hypothetical protein - Rhodobacter capsulatus
c;Species: Rhodobacter capsulatus
C;Species: Rhodobacter capsulatus
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C;Accession: T10511
R;Larimer, F.W.
Submitted to the EMBL Data Library, November 1995
A;Description: Sequence and expression of the pentose-5-phosphate 3-epimerase (cbbE) Cal
A;Reference number: 217063
A;Accession: T10511
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T10511
A;Residues: 1-146 <LAR>
A;Residues: 1-146 <LAR>
A;Residues: 1-146 <LAR>
A;Coss-references: BMBL:U23145; NID:g2564972; PID:g2564977
A;Experimental source: strain ATCC 11166
C;Superfamily: Neisseria conserved hypothetical protein NMB1727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40S ribosomal protein S13 [imported] - Guillardia theta nucleomorph Guillardia theta
A; Species nucleomorph Guillardia theta
A; Note: a nucleomorph Guillardia theta
A; Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
B; Date: 10-May-2001 #text_change 15-Jun-2001
B; Douglas, S:; Zauner, S:; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Mu, X.; Rei
Nature 410, 1091-1096, 2001
A; Reference number: A99082; MUD:11323671; PMID:11323671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Genome: nucleomorph
C;Superfamily: rat ribosomal protein S13; eubacterial ribosomal protein S15 homology
C;Keywords: nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: AJ010592; NID: 912580664; PIDN: CAC26981.1; GSPDB: GN00151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
A;Accession: E29010
A;Molecule type: DNA
A;Residues: 1-145 <GRI>
A;Cross-references: GB:M15049; NID:g150627; PIDN:AAA88372.1; PID:g1196707
C;Genetics:
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.8%; Score 6; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                            1.8%; Score 6; DB 2; Length 145;
100.0%; Pred. No. 3.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Ler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.8%; Score 6; DB 2,
Best Local Similarity 100.0%; Pred. No. 3.28
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                        Query Match 1.8°
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 APQIAL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 APQIAL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-147 <DOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 IVKILK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 IVKILK 73
                                                                                                                                                                                                                                                                                                                                                                                     66 VAQLAQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 VAÇLAÇ 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

```
Cispecies: Nostoc sp. PCC 7120
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. Strain PCC 7120
A;Note: Nostoc sp. Strain PCC 7120
A;Note: Nostoc sp. Strain PCC 7120
C;Accession: A12048
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, DNA Res. S. 205-213, 2001
A;Pitle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An A;Reference number: AB1807; MUD:21595285; PMID:11759840
A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-149 <KUR>A;Residues: 1-149 <KUR>A;Residues: 1-149 <KUR
                                                                                                                                                                                                                                                                                                                                              Rishe, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Char Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001 A; Description: Sulfolobus solfataricus complete genome.

A; Reference number: A99139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE006641; NID:g13813169; PIDN:AAK40403.1; GSPDB:GN00155 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN:BAB73642.1; PID:g17131033; GSPDB:GN00179
                                                                                                                                                                                                                                  conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: vaccinia virus
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 24-Sep-1999
C;Accession: C23768; A26351; Ā40246
K;Weinrich, S.L.; Hruby, D.E.
Nucleic Acids Res. 14, 3003-3016, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein all1943 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 2; Length 149;
.00.0%; Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 2; Lei
Local Similarity 100.0%; Pred. No. 3.3e+02;
Nes 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Prec. M. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: GB:BA000019; PIDN:I
A,Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.8%
Best Local Similarity 100.(
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17K protein - vaccinia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 VAÇLAÇ 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 SLKLLG 233
                                       73
                                                                                          34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-148 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 SLKLLG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 VAQLAQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                       OLAOEL
                                                                                       29 OLAQEL
                                                                                                                                                                                                                                                                                                                            C; Accession: D90143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: D90143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: SS00038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: all1943
                                    89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 173
                                                                                                                                                                                                             D90143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WMVZR2
                                       à
                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable phage tail protein STY3686 [imported] - Salmonella enterica subsp. enterica ser C;Species: Salmonella enterica subsp. enterica serovar Typhi A,Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AE0928 R;Parkhill. 7. hower
                                                                                                            A;Regidues: 1-148 <STO>
A;Reosidues: 1-148 <STO>
A;Cross-references: GB:AE005174; NID:g12514319; PIDN:AAG55590.1; GSPDB:GN00145; UWGP:Z14
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cispecies: Escherichia coli

Cibate: 18-Uul-2001 #sequence_revision 18-Uul-2001 #text_change 18-Uul-2001

Cibate: 18-Uul-2001 #sequence_revision 18-Uul-2001 #text_change 18-Uul-2001

Cibate: 18-Uul-2001

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

B;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

BNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gency

A;Acefeston: C90780

A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C90780
hypothetical protein EC81211 [imported] - Escherichia coli (strain 0157:H7, substrain RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Aitle: Complete genome sequence of a multiple drug resistant Salmonella enterica serow A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA A;Residues: 1-148 <PAR>
A;Residues: 1-148 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD09447.1; PID:g16504564; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-148 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB34634.1; PID:g13360671; GSPDB:GN00154
A;Experimental source: strain O157:H7; substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 148; 3.3e+02; ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
1.8%; Score 6; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                        DB 2; Length 148;
                                                                                                                                                                                                                                                                                                                                                    0; Indels
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85641
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 2
100.0%; Pred. No. 3.3
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 2
100.0%; Pred. No. 3.3
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 EPPTEA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPPTEA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              60 EPPTEA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPPTEA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: STY3686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: ECs1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       임
```

ó,

```
June 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 NLLRDK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NLLRDK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 NLLRDK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 NLLRDK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 NLLRDK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NLLRDK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-150 < MAS>
                  R;Johnson, G.P.
submitted to GenBank,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 176
B36848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C;Accession. F72163
R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopan submitted to GenBank, March 1998
A;Pescription: Analysis of the complete coding sequence of DNA of alastrim variola minor A;Reference number: A72150
A;Accession: F72163
                                                                                                                                              A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-150 < WELD.
A, Residues: 1-150 < WELD.
A, Experimental source: strain WR
A, Experimental source: strain WR
A, Experimental source: strain WR
A, Experimental source: strain WR
A, Eabldick Or., C.1; Moss, B.
A, Title: Resistance of vaccinia virus to rifampicin conferred by a single nucleotide sub A, Accession: A26351
A, Molecule type: DNA
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Residues: 1-150 <BAL>
A)Cross-references: GB:M16556; NID:g335729; PIDN:AAA48304.1; PID:g335730
B;Carpenter, M.S.; DeLange, A.M.
Virology 188, 233-244, 1992
A;Title: Identification of a temperature-sensitive mutant of vaccinia virus defective in
A;Title: A tandemly-oriented late gene cluster within the vaccinia virus genome.
A;Reference number: A93617; MUID:86176781; PMID:3008103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      All protein - vaccinia virus (strain Copenhagen)
C;Species: vaccinia virus
A;Note: host Homo sapiens (man)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 16-Feb-1997
C;Accession: C42517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Cross-references: GB:M86531; NID:g335303; PIDN:AAB59802.1; PID:g335304 A.Experimental source: strain WR, mutant tsC63 C.Comment: This protein is probably synthesized after viral DNA replication. C.Superfamily: vaccinia virus 17K protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosafidues: 1-150 - SHC>
A;Cross-references: GB:Y16780; NID:g5830555; PIDN:CAB54704.1; PID:g5830665
A;Experimental source: strain Garcia-1966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.8%; Score 6; DB 1; Length 150; Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 2; Length 150;
[00.0%; Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A40246; MUID: 92230221; PMID: 1566576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlL protein - variola minor virus (strain Garcia-1966)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Comment: This process are 17K protein C; Superfamily: vaccinia virus 17K protein C; Keywords: late protein; transcription regulation C; Keywords: late protein; transcription regulation C; Keywords: late protein; transcription regulation C; Keywords: late protein; transcription regulation C; Keywords: late protein; transcription regulation C; Keywords: late protein; transcription regulation C; Keywords: late protein; transcription regulation control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Preq. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: AlL
C;Superfamily: vaccinia virus 17K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A40246
A; Molecule type: genomic RNA
A; Residues: 1-150 < CAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 NLLRDK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 NLLRDK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 NLLRDK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NLLRDK 126
                                                                                                              A; Accession: C23768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
hypothetical protein AlL - variola major virus (Species: variola major virus Cispecies: variola major virus Cispecies: variola major virus Cispecies: variola major virus Cispecies: variola major virus Rimasura; 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000 Ciscession: T28842 Rimasura; R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubi Nature 366, 748-751, 1993 A.Fitle: Potential virulence determinants in terminal regions of variola smallpox virus A.Reference number: 220488; MUID:94088747; PMID:8264798 A.Reference number: T28542 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      All protein - variola virus (strain India-1967)
C;Species: variola virus
C;Species: variola virus
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
C;Accession: B36848
B;Blinov, V.M.
Submitted to GenBank, November 1992
A;Reference number: A36859
A;Accession: B36848
A;Status: preliminary
A;Nolecule type: Dn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60852.1; PID:g439022
A,Experimental source: strain Bangladesh-1975
C,Superfamily: vaccinia virus 17K protein
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Residues: 1-150 <BLI>A, Cross-references: GB:X69198; NID:g456758; PIDN:CAA49045.1; PID:g297284 C, Superfamily: vaccinia virus 17K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 2; Length 150; 100.0%; Pred. No. 3.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                              Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 2; Length 150;
100.0%; Pred. No. 3.3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                          1.8%; Score 6; DB 2; Ler 100.0%; Pred. No. 3.3e+02; tive 0; Mismatches 0;
A, Reference number: A33172
A, Accession: 042517
A, Status: pre-liminary
A, Molecule type: DNA
A, Residues: 1.150 < AORA
C, Superfamily: vaccinia virus 17K protein
C, Keywords: transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: transcription regulation
```

```
A; Experimental source: clone M01B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ਨੇ
                  VLTF-2, late gene transactivator - vaccinia virus (strain Ankara)
C.Species: vaccinia virus
C.Species: vaccinia virus
C.Species: vaccinia virus
C.Species: vaccinia virus
C.Species: vaccinia virus
C.Species: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C.Spacession: T37387
R.Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.
R.Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.
R.Antoine, G.; Scheiflinger, F.; Falkner, P.G.; Dorner, F.
R.Antoine: T3787
A.Speciescon: T37387
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 220877
A.Stelerence number: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein MOIB2.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Saccession: T23641
R;Lloyd, C.
R;Lloyd, C.
R;Lloyd, C.
A;Reference number: Z19776
A;Reference number: Z19776
A;Reference number: Z19776
A;Reference type: DNA
A;Reference number: L15078
A;Residues: 1-150 eWIL>
A;Residues: 1-150 eWIL>
A;Coss-references: EMBL:Z83116; PIDN:CAB05566.1; GSPDB:GN00023; CESP:MOIB2.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:Z93383; PIDN:CAB07622.1; GSPDB:GN00023; CESP:F54B8.1
A;Experimental source: clone F54B8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F54B8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Adze: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: T22617
R;Barlow, K.
Submitted to the EMBL Data Library, March 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 5
A;Introns: 33/1; 84/2
C;Superfamily: Caenorhabditis elegans hypothetical protein T13C5.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.8%; Score 6; DB 2; Length 150; Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

1.8%; Score 6; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Reference number: 219590
A,Accession: T22617
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-150 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
A;Note: MVAlll
C;Superfamily: vaccinia virus 17K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 NLLRDK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 NLLRDK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 EPPTEA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 EPPTEA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP: F54B8.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ДD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
C)Accession: D97188

KNO11ing, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
J. Bacteriol. 183, 4823-4838, 2001
J. Bacteriol. 183, 4823-4838, 2001
A)Fittle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: D97188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: A55209
R;Whelan, K.F.; Maher, D.; Colleran, E.; Taylor, D.E.
R;Whelan, K.F.; Maher, D.; Colleran, E.; Taylor, D.E.
A;Title: Genetic and nucleotide sequence analysis of the gene htdA, which regulates cor. A;Reference number: A55209; MUID:94209223; PMID:7908903
A;Accession: A55209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uncharacterized protein, YBBK B. subtilis ortholog [imported] - Clostridium acetobutyli C;Species: Clostridium acetobutylicum
C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE001437; PIDN:AAK80295.1; PID:g15025348; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H. transfer determinant A - plasmid R478
C;Species: plasmid R478
C;Date: 05-May_1995 #sequence_revision 05-May-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-150 <WHS>
A,Cross-references: GB:L20341, NID:g442357; PIDN:AAB05912.1; PID:g1326033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                           .
0
C;Genetics:
A;Gene (SEP:MOIB2.8
A;Map position:
A;Introns: 33/1; 84/2
C;Superfamily: Caenorhabditis elegans hypothetical protein T13C5.3
                                                                                                                                                                          1.8%; Score 6; DB 2; Length 150;
100.0%; Pred. No. 3.3e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 2; Length 150;
100.0%; Pred. No. 3.3e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 2; Length 150;
100.0%; Pred. No. 3.3e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.(
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 LKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 LKLLGE 144
                                                                                                                                                                                                                                                                                                  60 EPPTEA 65
                                                                                                                                                                                                                                                                                                                                                          EPPTEA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 NPAEIV 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 NPAEIV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-150 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CAC2339
```

```
1.8%; Score 6; DB 2; Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                             A,Gene: jhp1337
C,Superfamily: small protein smpB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 KROSLK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 KRÓSLK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 KRQSLK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 KROSLK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-152 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: AI3529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    position: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: BMEII0163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G71820
hypothetical protein jhp1337 - Helicobacter pylori (strain J99)
hypothetical protein jhp1337 - Helicobacter pylori
C,Specieses Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 29-Sep-1999
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G71820
C;Accession: G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein alr3100 [imported] - Nostoc sp. (strain PCC 7120)
hypothetical protein alr3100 [imported] - Nostoc sp. (strain PCC 7120)
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AE2193
R;Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Reterence number: AB1807; MUID:21595285; PMID:11759840
A;Reterence number: AB1807; MID:21595285; PMID:11759840
                                                                                                                                                                                        Rightson, Transcoll L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. B.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. Science 294, 894-9822, 2001
A.Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Mieference number: AB1077; MUID:21537279; PMID:11679669
A.; Motatilis preliminary
AC1758

AC1758

Protein gp15 from Bacteriophage A118 homolog lin2608 [imported] - Listeria innocua (stra proteins: Listeria innocua (stra C.Space: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C.Spacession: AC1758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-151 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB74799.1; PID:g17132194; GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule,type: DNA,
A,Residues: 1-150 <GLA>
A,Residues: 1-150 <GLA>
A,Cross-references: GB:AL592022; PIDN:CAC97835.1; PID:g16415145; GSPDB:GN00178
A,Experimental source: strain Clip11262
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Experimental source: strain PCC 7120
C, Genetics:
A, Gene: alr3100
C, Superfamily: Haemophilus influenzae conserved hypothetical protein HI0305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 2; Length 151;
100.0%; Pred. No. 3.3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 2; Ler 100.0%; Pred. No. 3.3e+02; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 MTKYIS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 VADFLE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 VADFLE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MTKYIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Gene: lin2608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

```
Swall protein - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: Helicobacter pylori
C;Species: D64700

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D
Feterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn
Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID:97394467; PMID:9252185
A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric patil A; Reference number: A71800; MUID:99120557; PMID:9923682 A; Accession: G71820 A; Accession: G71820 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues: 1-152 <ARN> A; Residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Delvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P. Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A.Title: The genome sequence of the facultative intracellular pathogen Brucella meliten A; Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-152 <TOM>
A;Cross-references: GB:AE000644; GB:AE000511; NID:g2314609; PIDN:AAD08482.1; PID:g23146
C;Superfamily: small protein smpB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Superfamily: post-transcriptional regulator of flagellin biosynthesis, FlbT type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: AE008918; PIDN: AAL53404.1; PID: 917984299; GSPDB: GN00191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: D64700
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 28-Jul-2003
C;Accession: Al3529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 2; Length 152; 100.0%; Pred. No. 3.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 2; Length 152;
100.0%; Pred. No. 3.4e+02;
ive 0; Mismatches 0; IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       flbT protein [imported] - Brucella melitensis (strain 16M)
```

ò

```
interleukin-2 precursor - bovine
Cispecies: Bos primigenius taurus (cattle)
Cispecies: Bos primigenius taurus (cattle)
Cipate: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
Cipacession: 145913, $21470; $20761
Cipacession: 145913, $21470; $20761
Ficerretti, D.P.; McKereghan, K.; Larsen, A.; Cantrell, M.A.; Anderson, D.; Gillis, S.; Proc. Natl. Acad. Sci. US.A. 83, 3223-3227, 1986
A;Title: Cloning, sequence, and expression of bovine interleukin 2.
A;Reference number: 145913; MUID:86205869; PMID:3517854
A;Accession: 145913
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 145913
A;Accession: 145913
                                                                                                                                                                                                                    A,Cross-references: EMBL:X53934; NID:g1281; PIDN:CAA37881.1; PID:g1282
R,Seow, H.P.; Rothel, J.S.; Radford, A.J.; Wood, P.R.
Nucleic Acids Res. 18, 7175, 1996
A,Title: The molecular cloning of ovine interleukin 2 gene by the polymerase chain reac
A,Reference number: S13102; MUID:91088336; PMID:2263496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Superfamily: interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-155 <CER>
A;Cross-references: GB:M12791; NID:g163204; PIDN:AAA30586.1; PID:g163205
A;Cross-references: GB:M12791; NID:g163204; PIDN:AAA30586.1; PID:g163205
B;Anixeeva, N.N.; Vinogradova, T.V.; Votoshin, O.N.
submitted to the BMBL Data Library, December 1989
A;Reference number: S21470
A;Accession: S21470
A;Molecule type: DNA
A;Residues: 1-22 <AN2>
A;Cross-references: EMBL:X17201; NID:g452; PIDN:CAA35062.1; PID:g453
                                                                                                                                                                                                                                                                                                                                                                                                         A.Status: preliminary
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-5, 'L', 7-155 <SEO>
A.Cross-references: EMBL:X55641; NID:g1810; PIDN:CAA39165.1; PID:g1811
ENGINED ON R.; Williammon, M.L.; Sargan, D.R.; Hein, W.H.; McConnell, I.
Submitted to the EMBL Data Library, April 1991
A.Reference number: 815517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.8%; Score 6; DB 2; Length 155; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 2; Length 155; 100.0%; Pred. No. 3.4e+02; tive 0; Mismatches 0; Indele
                             A;Title: cDNA cloning of ovine interleukin 2 by PCR. A;Reference number: $11488; MUID:91016933; PMID:2216781 A;Accession: $11488
         Nucleic Acids Res. 18, 5883, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 21-153 <BUJ>
A;Cross-references: EMBL:X60148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 PENLKL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 PENLKL 257
                                                                                                                            A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-155 <GOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 PENLKL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 PENLKL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S15517
                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S13102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: IL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Isnard, M.; Granier, M.; Frutos, R.; Reynaud, B.; Peterschmitt, M.
J. Gen. Virol. 79, 3091-3099, 1998
A;Title: Quasispecies nature of three related maize streak virus isolates obtained throu
A;Reference number: 216955; MUID:99094636; PMID:9880027
A;Accession: T10115
                                                                                                                                                                                                                                                                                                   Cisperved hypothetical protein YPO3607 [imported] - Yersinia pestis (strain C092)
C;Species: Yersinia pestis
C;Species: Versinia pestis
C;Species: O2-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession. AH0438
R;Parkhill, J: Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
                                    ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: AH0438
A; Statutus: preliminary
A; Molecule type: DNA
A; Residues: 1-152 cKUR>
A; CROSS - references: GB: AL590842; PIDN: CAC93076.1; PID: g15981528; GSPDB: GN00175
A; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-153 <ISN>
A;Cross-references: EMBL:AJ225008; NID:g2980718; PIDN:CAA12319.1; PID:g2980724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interleukin-2 precursor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C;Accession: S11488; S13102; S15517
R;Goodall, J.C.; Emery, D.C.; Perry, A.C.F.; English, L.S.; Hall, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Species: maize streak virus
C.Species: maize streak virus
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 17-Nov-2000
C.Accession: T10115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replication-associated protein B - maize streak virus (isolate SP2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 2; Length 153;
100.0%; Pred. No. 3.4e+02;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 152;
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
100.0%; Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 6; DB 2; Ler 100.0%; Pred. No. 3.4e+02; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: repB
C,Superfamily: tomato golden mosaic virus AL1 protein
C,Keywords: DNA replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
Best Local Similarity 100.08 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                           184 FATFKD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 PPTEAV 148
                                                                                                                                                      90 FATFKD 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PPTEAV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 ILKDNL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 ILKDNL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 190
S11488
                                                                                                                                                                                                                                               RESULT 188
```

à g ð

A; Gene: YPO3835

RESULT 193 T24304

à

ö

```
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: D90045
R;Kuroda, M.; Obta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Iancet 357, 1255-1240, 201
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. Accession: AG1112
R. Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke:
f. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mc
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: GB:NC 003210; PIDN: CAC99981.1; PID:g16411356; GSPDB: GN00177
                                   A; Cross-references: GB: AE005673; NID: 913423588; PIDN: AAK24074.1; GSPDB: GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:BA000018; PID:g13702384; PIDN:BAB43525.1; GSPDB:GN00149
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thioredoxin homolog lmo1903 [imported] - Listeria monocytogenes (strain EGD-e) C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SA2223 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 2; Length 157;
100.0%; Pred. No. 3.5e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.8%; Score 6; DB 2; Length 157; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                    Length 157
                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                Query Match
1.8%; Score 6; DB 2; Les
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                     178 DIASDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-157 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 IADLOL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43 IADLOL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 TDKASE 40
A; Residues: 1-157 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-157 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                            3 DIASDA 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: D90045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: AG1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: 1mo1903
                                                                                                          A; Gene: CC2103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: SA2223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 196
                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conserved hypothetical protein CC2103 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: F87509
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Accession: F87509
A;Accession: F87509
A;Status: preliminary
A;Molecule type: DNA
               Conserved hypothetical protein YPO3835 [imported] - Yersinia pestis (strain C092)
C.Species: Yersinia pestis
C.Species: Yersinia pestis
C.Species: Yersinia pestis
C.Species: Yersinia pestis
C.Species: Yersinia pestis
C.Species: Yersinia pestis
C.Species: Yersinia pestis
C.Species: Yersinia pestis
C.Species: Yersinia Coll #sequence revision 02-Nov-2001 #text_change 02-Nov-2001
R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
A.Partaraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Nature 413, 523-527, 2001
A.Reference number: AB0001; MUID:21470413; PMID:11586360
A.Reference number: AB0001; MUID:21470413; PMID:11586360
A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AL590842; PIDN:CAC93303.1; PID:g15981750; GSPDB:GN00175 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z92811; PIDN:CAB07272.1; GSPDB:GN00022; CESP:T01G1.2
A;Experimental source: clone T01G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein T01G1.2 - Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cibate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
CiAccession: T24304
Ricershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
Airershaw, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 4
A;Introns: 51/3; 107/2; 145/3
C;Superfamily: Caenorhabditis elegans hypothetical protein T01G1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 2; Length 157;
100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.8%; Score 6; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 IRHEPL 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 ILFMLL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule_type: DNA_
A;Residues: 1-156 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 IRHEPL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 ILFMLL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Gene: CESP: T01G1.2
```

Query Match

ð

C;Genetics:

ô

g

```
A;Variety: ATCC 29342
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
C;Accession: 873630
R;Himmelreich, R; Hilbert, H; Plagens, H; Pirkl, E; Li, B.C.; Herrmann, R.
Rwholeic Res 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumonian A;Reference number: 873327; MUID:97105885; PMID:8948633
A;Accession: 873630
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: C65113
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-159 < BLATA
A; Residues: 1-159 < BLATA
A; Residues: 1-159 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 < BLATA
A; Residues: 1-150 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule_type: DNA
A;Residues: 1-160 <ARN>
A;Cross-references: GB:AE001808; GB:AE000512; NID:g4982233; PIDN:AAD36745.1; PID:g49822:
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Residues: 1-161 <HIM>
A, Cross-references: EMBL:AE000028, GB:U00089, NID:g1673972; PIDN:AAB95552.1; PID:g16739
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A,Reference number: A72200; MUID:99287316; PMID:10360571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: D72226
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein - Thermotoga maritima (strain MSB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ribosomal protein L10 - Mycoplasma pneumoniae (strain ATCC 29342)
N;Alternate names: hypothetical protein G12_orf161
C;Species: Mycoplasma pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 6; DB 2; Length 160;
100.0%; Pred. No. 3.5e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 6; DB 2; Les
Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: Escherichia coli ribosomal protein L10
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.8%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 3.5.
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 IASDAF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 MKKMPL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 IASDAF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKMPL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: D72226
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: yhcE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: rplJ
A;Genetic cod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                    AGI684
thioredoxin homolog lin2017 [imported] - Listeria innocua (strain Clip11262)
(c.Species: Listeria innocua
(c.Species: Listeria innocua
(c.Species: Listeria innocua
(c.Species: Listeria innocua
(c.Species: Listeria innocua
(c.Species: Listeria innocua
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Species: Listeria)
(c.Spe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE000747; NID:g2983944; PIDN:AAC07504.1; PID:g2983956; GB:AE00065
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 198
D70438
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b70404
b7040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yncB protein - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date 12-Sep1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: C65113
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: D70438
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:ALS92022; PIDN:CAC97247.1; PID:g16414518; GSPDB:GN00178
A;Experimental source: strain Clip11262
C;Genetics: A;Genetics:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Lens
No. 3.5e+02;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 2; Length 158; 100.0%; Pred. No. 3.5e+02; tive 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 6; DB 2
100.0%; Pred. No. 3.5
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDKASE 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 KPENLK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 KPENLK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35 TDKASE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-158 < AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
A;Gene: aq_1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 199
C65113
                                                                                                                                                                                                RESULT 197
```

d

ò

ē

ó

Gaps

; 0

ö

Gaps

.; 0

```
A;Gene: AGR C_898
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100. Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 AKIILF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 VTLIAD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 AKIILF 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 VTLIAD 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-165 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: PAB1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C'Accession: Al2638
Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I. Riwood, D.W.; Setubal, J.C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 203

164239

164239

164239

165239

165239

165239

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

165230

16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: Ab2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Residues: 1-162 <TIGR>
A, Cross-references: GB:U39720, GB:L43967, NID:g1046063; PID:g1046069; TIGR:MG361
                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-161 -KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41527.1; PID:g17738857; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                         phaE protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C;Accession: A12638
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.8%; Score 6; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 161;
    Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Genetics:
A,Genetic code: SGC3
C;Superfamily: Escherichia coli ribosomal protein L10
1.8%; Score 6; DB 2; Ler 100.0%; Pred. No. 3.5e+02; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.8%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 3.5
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: phaE
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain G-37
                                                                               6; Conservative
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 AKIILF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 NNILRR 107
                                                                                                                                                               102 NNILRR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 AKIILF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 NNILRR 62
                                                                                                                                                                                                                               56 NNILRR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: AI2638
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tur A;Reference number: A97359; WUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: E75100
R;anorymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stri
A;Reference number: A75001
A;Accession: E75100
A;Accession: E75100
A;Accession: Lorence apysions preliminary
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions abysions archaeal chromosome stri
A;Accession: Lorence abysions archaeal chromosome accessions archaeal chromosome accessions archaeal chromosome accessions archaeal chromosome accessions archaeal chromosome accessions archaeal chromosome accessions archaeal chromosome accessions archaeal chromosome accessions archaeal chromosome accessions archaeal chromosome accessions archaeal chromosome accessions archaeal chromosome accessions archaea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Acropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: G72486
B;Kawarabayasi, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takal
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; J
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy:
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB50106.1; PID:g54586:
A;Experimental source: strain Orsay
probable poly(3-hydroxyalkanoate) polymerase [imported] - Agrobacterium tumefaciens (str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: B97421
A;Status: preliminarry
A;Molecule type: DNA
A;Residues: 1-162 -KUUR>
A;Cross-references: GB:AE007869; PIDN:AAK86323.1; PID:g15155441; GSPDB:GN00169
                                                                      C,Species: Agrobacterium tumefaciens
C,Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C,Accession: B97421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein PAB1584 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 2; Length 162;
100.0%; Pred. No. 3.6e+02;
tive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 2; Length 164; 100.0%; Pred. No. 3.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein APE2535 - Aeropyrum pernix (strain K1)
```

```
C. Accession: B96916
R. Nolling, U.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
R. Dacky, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A; Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RiLecanidou, R.; Rodakis, G.C.
J. Mol. Evol. 34, 304-314, 1992
A;Title: Three copies of the early gene 6F6 are interspersed in and around the late chc
A;Reference number: S23060; MUID:92235869; PMID:1569584
                                                                                                                                                                                                                                                                                               early chorion protein - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C;Accession: S42070
Silkarvariti, L.; Lecanidou, R.; Rodakis, G.C.
Submitted to the EMBL Data Library, February 1994
A;Description: Sequence analysis of a small early chorion gene subfamily interspersed naner: S42070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE001437; PIDN:AAK78117.1; PID:g15022959; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ArCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 early chorion protein - silkworm
C;Species: Bombyx mori (silkworm)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL:X77747; NID:9456246; PIDN:CAA54795.1; PID:9456247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein CAC0133 [imported] - Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.8%; Score 6; DB 2; Length 168; Best Local Similarity 100.0%; Pred. No. 3.7e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.8%; Score 6; DB 2; Length 168;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 17/3
C;Superfamily: chorion class A protein pc292
                                                                                                                               120 MNLLRD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 AKIILF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Accession: S42070
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-168 < KRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-168 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 VKILKD 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 AKIILF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Status: preliminary A, Molecule type: DNA
                                                             259 MNLLRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: S23060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CAC0133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                         RESULT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       823060
                                                                 ò
                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AD2596
biopolymer transport protein exbD [imported] - Agrobacterium tumefaciens (strain C58, Du C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Becies: Agrobacterium tumefaciens
C;Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Artitle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                      ó
A;Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BAAG1551.1; PID:g5106240
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE2535
C;Superfamily: Pyrococcus abyssi hypothetical protein PAB0162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Cross-references: GB: AE008688; PIDN: AAL41186.1; PID: 917738486; GSPDB: GN00186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB:AE007869; PIDN:AAK85983.1; PID:g15155044; GSPDB:GN00169
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                   ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                               Query Match
1.8%; Score 6; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 2; Length 167;
100.0%; Pred. No. 3.7e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 2; Length 167; 100.0%; Pred. No. 3.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Gene: exbD
A, Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: AGR C 265
A,Map position: circular chromosome
C,Superfamily: tolR protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: tolk protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 MNLLRD 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 MNLLRD 125
                                                                                                                                                                                                                                                                                                                                                         77 GLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                35 GLLVTL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA A; Residues: 1-167 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-167 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C, Genetica:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 207
                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                       du
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

ð

ö

RESULT 212 S42071

à

```
Transcription regulator, Lrp/AsnC family - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Accession: B75548
B;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.
S; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
                                                                                                                                                                                                                                                                                                                                                                                                                     A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-170 <WHI>
A,Cross-references: GB:AE001882; GB:AE000513; NID:g6457865; PIDN:AAF09787.1; PID:g64578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C)Accession: D81278
R)Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilli C.*.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable periplasmic protein Cj1343c [imported] - Campylobacter jejuni (strain NCTC 111 C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73770.1; PID:g69687
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fibroblast growth factor receptor - Japanese medaka (fragment)
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Oryzias latipes (Japanese medaka)
C;Species: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 20-Jun-2000
C;Accession: S27022
R;Emori, Y.; Yasuoka, A.; Saigo, K.
FEBS Lett. 314, 176-178, 1992
A;Title: Identification of four FGF receptor genes in Medaka fish (Oryzias latipes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 2; Length 170;
100.0%; Pred. No. 3.7e+02;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.8%; Score 6; DB 2; Ler
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 1
C;Superfamily: regulatory protein asnC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.8
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 LLGELI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 LLGELI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-171 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 EVSKSL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 EVSKSL 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: B75548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: D81278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: Cj1343c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: DR0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 213
C90175
MDN dehydrogenase subunit C (NuoC) NuoC [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: C90175
R;She, Q.; Singh, R.K.; Confalonieri, F; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Effries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Bescription: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: C90175
                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-169 <KUR>
A;Cross references: GB:AE006641; NID:g13813468; PIDN:AAK40658.1; GSPDB:GN00155 C;Genetics:
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
A,Accession: S23060
A,Status: preliminary
A,Molecule type: DNA
A,Rolsdues: 1-169 <LEC>
A,Cross-references: EMBL:X66164; NID:g5737; PIDN:CAA46946.1; PID:g5738
C,Genetics:
A,Introns: 17/3
C,Superfamily: chorion class A protein pc292
                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                           Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 169;
                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 2; Length 169;
100.0%; Pred. No. 3.7e+02;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                             Query Match
1.8%; Score 6; DB 2; Ler
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.8%; Score 6; DB 2; Ler
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 17/3
C;Superfamily: chorion class A protein pc292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                         156 AKIILF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 AKIILF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 LAKIIL 160
                                                                                                                                                                                                                                                                                                                                                                                                          3 AKIILF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 LAKIIL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 AKILLE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
```

ð g

ö

٥:

A; Gene: Nuoc

δ

```
1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity luv.v.
                           Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                   317 QFADEK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 ILKDNL 151
                                                                                                                                                                                                           51 QPADEK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 ILKDNL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: F70112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Gene: CC1579
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C, Genetics
                                                                                                                                                                                                                                                                                                                                F70112
                                                                                                                                                   à
                                                                                                                                                                                                        엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        엄
A;Reference number: S27019; MUID:93093167; PMID:1459248
A;Accession: S27022
A;Status: not compared with conceptual translation
A;Rocicule type: mRNA
A;Rosidues: 1-172 <EMO->
A;Cross-references: GB:D13553; NID:9222938; PIDN:BAA02752.1; PID:9222939
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote F;1-172/Domain: protein kinase homology (fragment) <KIN>F;2.40,132/Active site: Lys, Glu, Asp #status predicted F;137,150/Binding site: magnesium (Asn, Asp) #sratus predicted F;137,150/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Natures 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: G64555
A;Accession: G64555
A;Accession: G64555
A;Accession: G64555
A;Accession: G64552
A;Accession: G64552
A;Accession: G64552
A;Accession: G64552
A;Accession: G64552
A;Accession: G64552
A;Accession: G64552
A;Accession: G64552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pallola 218

Hypothetical protein NMB1084 [imported] - Neisseria meningitidis (strain MC58 serogroup P81122

Hypothetical protein NMB1084 [imported] - Neisseria meningitidis (strain MC58 serogroup C;5pecies: Neisseria meningitidis

C;5pecies: Nai-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001

C;Accession: F81122

Hypotheticalin, H; Saunders, Naj; Heidelberg, J; Jeffries, A.C; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Hatt, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H; Qin, H; Vamathevan, J; Gill, J; Scarlato, V; Masignani, V; Pizza, M. A;Authors: Grandl, G; Sun, L; Smith, H.O.; Frasser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Accession: P81122

A;Accession: P81122

A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE000547; GB:AE000511; NID:g2313377; PIDN:AAD07359.1; PID:g231338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE002459; GB:AE002098; NID:g7226320; PIDN:AAF41476.1; PID:g722632
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1084
C;Superfamily: Neisseria meningitidis hypothetical protein NMB1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: G6455; White, 0.: Kerlavade, A R : Clavton P A : Sutton C C : Eaclavade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 217
G64555
hypothetical protein HP0287 - Helicobacter pylori (strain 26695)
                                                                                                                                                                                                                                                                                                                                                                              ; DB 2; Lens.
No. 3.86+02;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 172; 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       y Match
1.8%; Score 6; DB 2
Local Similarity 100.0%; Pred. No. 3.8
nes 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 2
100.0%; Pred. No. 3.8
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 TFKDLL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 TFKDLL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 LSSFOK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 LSSFOK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-173 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
Approxide dismutase (EC 1.15.1.1) (Cu-Zn) precursor - Caulobacter crescentus c'species: Caulobacter crescentus c'species: Caulobacter crescentus c'species: Caulobacter crescentus c'species: Caulobacter crescentus C'species: Caulobacter crescentus C'species: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 18-Jul-2001 C'species: 112, 2901-2910, 1990 #text_change 18-Jul-2001 R.Steinman, H.M.; Ely, B. J. Title: Copper-zinc superoxide dismutase of Caulobacter crescentus: cloning, sequencing A;Reference number: A55383 MUID:90264275; PMID:2345128 A;Accession: A35383 A;Eques: preliminary A;Actacter: preliminary A;Residues: 1-174 cSTE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:MS5259; NID:g144282; PIDN:AAA23054.1; PID:g144283; GB:M37908
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Ludw, M.T.; DeBoy, R.T.; DoBoon, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: B87445
A;Accession: breliminary
A;Residues: 1-174 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Residues: 1-173 <KLB>
A,Residues: 1-173 <KLB>
A,Cross-references: GB:AE001123; GB:AE000783; NID:g2687987; PIDN:AAC66505.1; PID:g26880
A,Experimental source: strain B31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: F70112
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Haure 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Aitle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; MUID: 98065943; PMID: 9403685
                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Status: preliminary, nucleic acid sequence not shown, translation not shown A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: AE005673; NID: 913422970; PIDN: AAK23558.1; GSPDB: GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                          C'Species: Borrelia burgdorferi (Lyme disease spirochete)
C'Date: 13-Feb_1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
DB 2; Lt.,
No. 3.88+02;
O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 2; Length 173; 100.0%; Pred. No. 3.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein BB0102 - Lyme disease spirochete
                   1.8%; Score 6; DB 2
100.0%; Pred. No. 3.8
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: superoxide dismutase (Cu-Zn) C; Keywords: metalloprotein; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;167/Active site: Arg #status predicted
```

Length 174;

DB 2;

Pred. No. 3.8e+02; Mismatches 0;

1 '0 1 '0 001

6; Conservative

Best Local Similarity

Matches

ò g hypothetical protein - Deinococcus radiodurans (strain R1)

```
Cispecies: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: A40523
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) [imported] - Yersinia pestis (strair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: AB0414
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypoxanthine phosphoribosyltransferase [imported] - Salmonella enterica subsp. enterica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-176 <LEI>
A;Cross-references: EMBL;AF032691; NID:92792225; PIDN:AAB96988.1; PID:92792226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: AL590842; PIDN: CAC92638.1; PID: 915981335; GSPDB: GN00175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species: Yersinia pestis
C.Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 2; Length 176;
100.0%; Pred. No. 3.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 6; DB 2; Length 178;
Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: subsp. Japonica, cultivar. Nipponbare
C;Gentics:
A;Gene: Y4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: hypoxanthine phosphoribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Keywords: glycosyltransferase; pentosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.8%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 3.9
Matches 6; Conservative 0; Mismatches
C;Species: Oryza sativa (rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 EILLKN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 EILLKN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-178 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 VKILKD 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: AB0414
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: AH0523
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB0414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AH0523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                          Cipate: 03-Decocas radiodurans (Strain KI)
Cipate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
Cipate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
Cipates sion: F75606
RiMite, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma.; Saich, M.O.; Venter, J.D.; Dodson, R.J.;
A.; Saith, M.; Venter, J.D.; Praser, C.M.
Science 286, 1571-1577, 1999
A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: F75606
A;Accession: F75606
A;Accession: F75606
A;Accession: F75606
A;Accession: Bredimnary
A;Molcule type: DNA
A;Accession: Commandation of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresistand of the radioresist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 222
E90006
hypothetical protein rpoE [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 27-Oct-2003
C;Accession: E90006
R;Auroda, M; Ohta, T; Uchiyama, I; Baba, T; Yuzawa, H; Kobayashi, I; Cui, L; Oguc ma, A.; Mizutani-Ui, Y; Kobayashi, N:; Sawano, T; Inoue, R; Kaito, C; Sekimizu, K; C; Shiba, T; Hattori, M; Ogasawara, N; Hayashi, H; Hiramatsu, K.
Lance, 557, 1225-1240, 2001
                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:BA000018; PID:g13701922; PIDN:BAB43214.1; GSPDB:GN00149
A;Bxperimental source: strain N315
C;Genetics:
A;Gene: rpoE
C;Superfamily: DNA-directed RNA polymerase delta subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 2; Length 176;
100.0%; Pred. No. 3.9e+02;
Live 0; Mismatches 0; Indels
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
```

1.8%; Score 6; DB 2 100.0%; Pred. No. 3.8 ative 0; Mismatches

6; Conservative

à d

Best Local Similarity

Matches

A; Map position: 2 Query Match T02217 NBS-LRR type resistance protein - rice (fragment)

RESULT 223

셤

6; Conservative

Best Local Similarity Matches 6; Conserv

Ouery Match

A; Molecule type: DNA A; Residues: 1-176 < KUR> A;Accession: E90006 A;Status: preliminary

229 LKLLGE 234 LKLLGE 116

A; Residues: 1-178 <PAR>

ö g

```
Approtein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CTIE Cispecies: Salmonella enterica subsp. enterica serovar Typhi A.Note: this species has also been called Salmonella typhi Cjbate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 RyParkhilly J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher K.; Tonnerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farran Nature 413, 848-852, 2001
A; Aththors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A; Tile: Complete genome sequence of a multiple drug resistant Salmonella enterica serrant A; Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Cross-references: EMBL.AF018174; NID:g2921093; PIDN:AAC04671.1; PID:g2921094
A,Experimental source: 30-day old green leaves
A,Genetics:
A,Gene: TRXF
A,Genome: nuclear
C,Function:
A,Description: activates fructose 1,6-bisphosphatase during photosynthesis
C,Superfamily: thioredoxin; thioredoxin homology
C,Keywords: chloroplast; redox-active disulfide
F,79-163/Domain: thioredoxin homology <TXN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB: AL513382; PIDN: CAD06080.1; PID: g16504046; GSPDB: GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thioredoxin f precursor - rape
C;Species: Brassica napus (rape)
C;Species: Brassica napus (rape)
C;Accession: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jan-2000
C;Accession: T07837
R;Mora-Garcia, S.E.F.; Rodriguez-Suarez, R.J.; Wolosiuk, R.A.
B;Nora-Garcia, S.E.F.; Rodriguez-Suarez, R.J.; Wolosiuk, R.A.
A;Reference number: 216164
A;Reference number: 216164
A;Accession: T07837
A;Attus: preliminary; translated from GB/EMBL/DDBJ
A;Reference mRNA
A;Residues: 1-182 <MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thioredoxin f precursor - garden pea
Cispecies: Pisum sativum (garden pea)
Cibate: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 11-Jun-1999
CiAccession: S20929
RiLepiniec, L.; Hodges, M.; Gadal, P.; Cretin, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 2; Length 181; 100.0%; Pred. No. 4e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 2; Length 182;
100.0%; Pred. No. 4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: Escherichia coli syd protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317 QFADEK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 KİLKDN 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-181 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 OFADEK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 KILKDN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: AI0861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: STY3106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 230
S20929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Aquifex aeolicus
C.Species: Aquifex aeolicus
C.Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 28-Jul-2003
C.Accession: E70358
R.Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-180 <AQP>
A;Cross-references: GB:AE000701; NID:g2983260; PIDN:AAC06859.1; PID:g2983265; GB:AE00065
A;Experimental source: strain VP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 392, 353-358, 1998
Affille: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: E70358
                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
A Cross-references: GB:AL513382; PIDN:CAD01328.1; PID:g16501456; GSPDB:GN00176 C;Genetics: A;Gene: STY0192 C;Superfamily: hypoxanthine phosphoribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Typecies: Caenorhaboditis elegans
C; Decies: Loct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T23601
R; Kershaw, J
submitted to the EMBL Data Library, November 1996
A; Reference number: Z19768
A; Reference number: Z19768
A; Reterence number: Z19768
A; Reterence number: Z19768
A; Reterence number: Z19768
A; Reterence number: Z19768
A; Residues: T-178
A; Molecule Lype: DNA
A; Residues: L-178
A; Residues: L-178
A; Residues: L-178
A; Residues: L-178
A; Residues: L-178
A; Residues: L-178
A; Residues: L-178
A; Residues: L-178
A; Residues: L-178
A; Residues: L-178
A; Residues: L-178
A; Residues: MBL: Z83115; PIDN: CAB05555.1; GSPDB: GN00019; CESP: KI1D2.1
A; Conservations: Mainer Conservations A; Respectives: C; Genetics: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respectives: C; Conservations A; Respe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Gene: hupE
C;Superfamily: [NiFe]-hydrogenase/urease accessory protein HupE/UreJ
                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                      Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match
Local Similarity 100.0%; Pred. No. 3.9e+02;
Les 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 2; Length 178; 100.0%; Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                              DB 2; Lenç
5. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T23601
hypothetical protein K11D2.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HupE hydrogenase related function - Aquifex aeolicus
                                                                                                                                                                                      Query Match
1.8%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 3.9
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ilarity 100.0%; Pred. No. 3.9
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 GYEAPQ 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 GYEAPO 132
                                                                                                                                                                                                                                                                                                                                                18 VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                        80 VKILKD 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 EIVKIL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 EIVKIL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP:K11D2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 1
A; Introns: 109/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
```

Matches

셤

ö

Matches

à g

ö

Gaps

0

```
R; Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch DNA Res. 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:D26562; NID:9473770; PIDN:BAA05581.1; PID:9473792
A;Cross-references: Extain K-12, substrain W3110
A;Experimental source: strain K-12, substrain W3110
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Experimental source: strain OT3
A, Note: this accession replaces an interim accession for a sequence replaced by GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Residues: 1-182 <BLAT>
A;Residues: 1-182 <BLAT>
A;Cross-references: GB:AE000122; GB:U00096; NID:g1786315; PIDN:AAC73236.1; PID:g1786317
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                           hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - Escherichia coli (strain K-12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Status: preliminary; nucleic acid sequence not shown; translation not shown A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-182 <KAW>
A;Cross-references: GB:AP000005; NID:g3236132; PIDN:BAA30376.1; PID:g3257693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein PH1273 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: P71072
                                                                                                                                                                                                                                                                                                                                                           C;Species: Escherichia coli
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 01-Mar-2002
C;Accession: S45202; E64735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Keywords: glycósyltransferase; pentosyltransferase; salvage pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: E64735
A,Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 2; Length 182;
100.0%; Pred. No. 4e+02;
tive 0; Mismatches 0; Indels
      Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: hypoxanthine phosphoribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.8%; Score 6; DB 2; L
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0
                                           4e+02;
1.8%; buc. 100.0%; Pred. No. ...
         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R:Fujita, N. submitted to the EMBL Data Library, January 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Reference number: S45181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 VKILKD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S45202
A; Molecule type: DNA
A; Residues: 1-182 <FUJ>
                                           Best Local Similarity
Matches 6; Conserv
                                                                                                                                      23
                                                                                                                                                                                                 84 VKILKD 89
                                                                                                                                         18 VKILKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: PH1273
                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetics;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: hpt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                  à
                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE005174; NID:g12512840; PIDN:AAG54429.1; GSPDB:GN00145; UMGP:201
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apples by the phosphoribosyltransferase [imported] - Escherichia coli (strain O157:H7, gu bypoxanthine phosphoribosyltransferase [imported] - Escherichia coli (species: Escherichia coli (species: Escherichia coli (species: Escherichia coli (species: Bacherichia coli (species: Bacherichia coli (species: Bacherichia coli) (species: Bayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Hattori, M.; Shinagawa, H. Byasashi, T.22, 2001

A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench appleanned number: A99629; MUID:21156231; PMID:11258796

A; Reference number: A99629; MUID:21156231; PMID:11258796

A; Residues: preliminary

A; Molecule type: DNA

A; Residues: 1-182 cHAX>

A; Residues: 1-182 cHAX>
A; Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D.J.; Mayhew
K.; Apodaca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypoxanthine phosphoribosyltransferase [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
Plant Mol. Biol. 18, 1023-1025, 1992
A;Title: Isolation, characterization and nucleotide sequence of a full-length pea cDNA
A;Reference number: S20929; MUID:92256804; PMID:1581563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: A85496
C;Accession: A85496
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Roge, iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                      A; Molecule type: mRNA
A;Residues: 1-182 <LEP>
A;Residues: 1-182 <LEP>
A;Croser-references: EMBL:X63537; NID:g20906; PIDN:CAA45098.1; PID:g20907
C;Superfamily: thioredoxin; thioredoxin homology
C;Superfamily: thioredoxin; thioredoxin disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                      F;1-74/Domain: transit peptide (chloroplast) #status predicted <TNP>F;1-74/Domain: transit peptide (chloroplast) #status predicted <MAT>F;75-182/Product: thioredoxin f #status predicted <MAT>F;83-167/Domain: thioredoxin homology <THR>F;83-167/Domain: thioredoxin homology <THR>F;106-109/Disulfide bonds: redox-active #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.8%; Score 6; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: hpt
C;Superfamily: hypoxanthine phosphoribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: hypoxanthine phosphoribosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 6; DB 2; L
Local Similarity 100.0%; Pred. No. 4e+02;
hes 6; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-182 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 KILKDN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKILKD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KILKDN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A85496
                                                                                                          A; Accession: S20929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene: ECs0129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: ECs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

ö

Gaps

ö

ö

Gaps

g

```
Nature 389. S. Joftus, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388. 539-547, 1997

A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A.; Rieference number: A64520; MUID:97394467; PMID:9252185

A.; Reference number: A64520; MUID:97394467; PMID:9252185

A.; Status: preliminary; nucleic acid sequence not shown; translation not shown
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spri Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUD:20083488; PMID:10617198
A;Accession: C85439
A;Accession: C85439
A;Residus: preliminary
A;Molecule type: DNA
A;Residues: 1-183 <270>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Residues: 1-184 <TOM>
A,Cross-references: GB:AE000571; GB:AE000511; NID:g2313686; PIDN:AAD07645.1; PID:g23136
A,Cross-references: GB:AE000571; GB:AE000511; NID:g2313686; PIDN:AAD07645.1; PID:g23136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: S27936
R;Boublida, M.; Lockhart, B.; Olszewski, N.E.
Rsbmitted to the BBL Data Library, May 1992
A;Description: The complete sequence of an infective sugarcane mosaic virus genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                               A;Cross references: GB:NC_001268; NID:g7270667; PIDN:CAB80384.1; GSPDB:GN00140 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein HP0579 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein 1 - sugarcane bacilliform virus
C;Species: sugarcane bacilliform virus
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: M89923; NID: G294836; PIDN: AAA47452.1; PID: G294837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 2; Length 184;
100.0%; Pred. No. 4e+02;
tive 0; Mismatches 0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 2; Length 183;
100.0%; Pred. No. 4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 1.8%; Score 6; DB 2; Lenk Local Similarity 100.0%; Pred. No. 4e+02; les 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S27936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 QPKLIE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 EFLSSF 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 QPKLIE 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 KQIRDL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 EFLSSF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-185 <BOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 KQIRDL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S27936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: C64592
                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: AT4g37180
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C64592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-183 <ARN>
A;Coss-references: GB:AE001485; GB:AE001439; NID:g4155057; PIDN:AAD06107.1; PID:g415507
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0526
                                                                                                                                                                                                                                                                                                                   hypothetical protein Rv0513 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Unl-1998 #sequence_revision 17-Unl-1998 #text_change 22-Oct-1999
C;Accession: F70509
C;Accession: F70509
C;Accession: F70509
C;Accession: F70509
C;Accession: F70509
C;Accession: F70509
C;Accession: F70509
C;Accession: F70509
A;Authors: Sqares, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Mature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: DNA
A;Accession: DNA
A;Accession: DNA
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;Accession: F70509
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Helicobacter pylori
A;Variety: strain J99
A;Variety: strain J99
C;Date: 1.2-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Date: 1.2-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: G71221
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Inves, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A1800; MUID:99120557; PMID:9923682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:Z97831; GB:AL123456; NID:g3261825; PIDN:CAB10750.1; PID:e329664; A;Experimental source: strain H37Rv C;Genetics: A;Gene: Rv0513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable cytoskeletal protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C;Accession: C85439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 236
G71921
hypothetical protein jhp0526 - Helicobacter pylori (strain J99)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.8%; Score 6; DB 2; Length 182; Best Local Similarity 100.0%; Pred. No. 4e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 2; I
100.0%; Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 EFLSSF 308
                                                                                                                                              125 VTLIAD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFLSSF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-182 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 AEIVKI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 AEIVKI 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary A; Molecule type: DNA
                                                                              80 VTLIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: G71921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

A;Gene: 22K

RESULT 241

à

ö

```
protein C18A11.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
C;Accession: G89581
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo A;Reference number: A75000; MUID: 99659613; PMID: 9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_el A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an A;Accession: G89561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: GB:chr_X; PIDN:AAC69008.1; PID:g1049416; GSPDB:GN00028; CESP:C18A11 C;Genetics: A;Gene: C18A11.4 A;Map position: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: AG3395
R;DelYecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes. Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten. A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NADRIZ dehydrogenase (ubiquinone) (BC 1.6.5.3) [imported] - Brucella melitensis (strain C,Species: Brucella melitensis
C,Species: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: AG3395
A;Status: preliminary
A;Nolecule type: DNA
A;Molecule type: DNA
A;Residues: 1-189 <KUR>
A;Residues: 1-189 <KUR>
A;Residues: 4-189 <KUR>
A;Residues: 1-189 <KUR>
C;Genetics: GB:AE008917; PIDN:AAL52330.1; PID:g17983124; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.8%; Score 6; DB 2; Length 190; Best Local Similarity 100.0%; Pred. No. 4.1e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 2; Length 189; 100.0%; Pred. No. 4.1e+02; trive 0; Mismatches 0; Indels
                                                                                                                                  Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: I
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 6
C;Keywords: oxidoreductase
                                                                                                                              Query Match
1.8%; Score 6; DB 2; Le:
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0;
                                  A; Gene: comEB
C; Superfamily: phage T4 dCMP deaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 ISKPEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 ISKPEN 147
                                                                                                                                                                                                                                                                                                                                                                 145 ILDRHN 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 LLGELI 236
                                                                                                                                                                                                                                                                                        236 ILDRHN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 LLGELI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-190 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: BMEI1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 244
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ठ
                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         late competence operon required for DNA binding and uptake comEB [imported] - Bacillus h C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #text_change 15-Jun-2001 C;Date: 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: F83816 Equence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: F83816 Equence Explain Equence C; Basaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 A;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Accession: F83816 A;Accession: F83816 A;Accession: F83816 A;Accession: Eyge: DNA A;Residues: 11-188 < FTO> A;Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB05053.1; GSPDB:GNOG A;Experimental source: strain C-125
                                                                                                                                                                                                                                                      C;Accession: JQ1623
R;Ling, R.; Easton, A.J.; Pringle, C.R.
Gen. Virol. 73, 1709-1715, 1922
A;Title: A;Title: P00405; MUID:92333255; PMID:1629697
A;Reference number: PQ0405; MUID:92333255; PMID:1629697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R,Yu, Q.; Davis, P.J.; Brown, T.D.K.; Cavanagh, D.
Gen. Virol. 73, 1335-1363, 1992
A;Title: Sequence and in viro expression of the M2 gene of turkey rhinotracheitis pneum
A;Reference number: JQ1987; MJID:92300329; PMID:1607858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JQ1987

hypothetical 21.0K protein - turkey rhinotracheitis virus (strain UK/3BV/85)

N/Alternate names: ORF 1 protein

C;Species: turkey rhinotracheitis virus

C;Species: turkey rhinotracheitis virus

C;Species: turkey rhinotracheitis virus

C;Species: 101983 #sequence_revision 20-Aug-1994 #text_change 28-May-1999

C;Accession: JQ1987

R;Yu, Q;Davis, P.J.; Brown, T.D.K.; Cavanagh, D.
                                                                                                                                          envelope-associated 22K protein - turkey rhinotracheitis virus
C;Species: turkey rhinotracheitis virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: mRNA
A,Residues: 1-186 < YUQ>
A,Cross-references: GBX.63408; NID:g297846; PIDN:CAA45004.1; PID:g297847
C,Superfamily: respiratory syncytial virus envelope-associated 22K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: respiratory syncytial virus envelope-associated 22K protein C; Keywords: glycoprotein F;86/Binding site: carbohvdrate (Asn) (Annalone) Annalone Site: carbohvdrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: mRNA
A,Residues: 1-186 <LIN>
A,Cross-references: GB:S40185; NID:g251600; PIDN:AAB22544.1; PID:g251602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :Keywords: glycoprotein
:86/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 1.8%; Score 6; DB 2; Length 186; Best Local Similarity 100.0%; Pred. No. 4.1e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 186; .. 4.1e+02; ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.8%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No. 4.1.
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 LAKIIL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 LAKİİL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 LAKIIL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 LAKIIL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: JQ1987
```

RESULT 242

Db ð

ö

```
A, Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.8
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             231 LLGELI 236
                                                                                     A, Accession: 876506
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-192 < KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 LLGELI 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule_type: DNA
A;Residues: 1-192 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 EIVKIL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Gene: all7084
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 249
                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C'Species: Synechocystis sp.

Variety: PCC 6803

C;Date: 25-Apr-1997 #text_change 20-Jun-2000

C;Accession: 876506

C;Accession: 876506

C;Accession: Sizero, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                       Gordon, s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C,Accession: C81279
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyph:Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73777.1; PID:g696878
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: mobA; Cj1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-191 <COL>
A;Cross-references: GB:AL021899; GB:AL123456; NID:g3242282; PIDN:CAA17230.1; PID:g289675
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                     R;Cole S.T., Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - Carr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable molybdopterin-guanine dinucleotide biosynthesis protein Cj1350 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Campylobacter jejuni
C.Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                     C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                         hypothetical protein Rv2016 - Mycobacterium tuberculosis (strain H37RV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.8%; Score 6; DB 2; Length 191; Best Local Similarity 100.0%; Pred. No. 4.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 2; Length 191; llarity 100.0%; Pred. No. 4.2e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            876506 hypothetical protein - Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 FLEONY 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 FLEONY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-191 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 LVTLIA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 LVTLIA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: C81279
A;Status: prelimina
                                                                                                                                                                                                                  C; Accession: G70940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: Rv2016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 07-Jul-2003
C;Accession: A84191
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, E; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T.
Jung, K.H.; Alam, M.; Freitas, T.
Ayuthors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A, Title: Genome sequence of Halobacterium species NRC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch: Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ank A;Reference number: AB1807; MUID:21595285; PMID:11799840
                                                                                                                                                                       A;Cross-references: EMBL:D64002; GB:AB001339; NID:g1001612; PIDN:BAA10352.1; PID:g10016; A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Superfamily: conserved hypothetical protein s1r2127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein all7084 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120a] C,Species: Nostoc sp. PCC 7120
C,Species: Nostoc sp. PCC 7120
A)Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C,Accession: AD2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: aroD
C,Superfamily: 3-dehydroquinate dehydratase; 3-dehydroquinate dehydratase homology
                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: A84191
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-195 <STO>
A;Cross-references: GB:AE004437; NID:g10579943; PIDN:AAG18893.1; GSPDB:GN00138
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:BA000020; PIDN:BAD78168.1; PID:g17135622; GSPDB:GN00180
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3-dehydroquinate dehydratase [imported] - Halobacterium sp. NRC-1
                                                                                                                                                                                                                                                                                                                            Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 6; DB 2; Length 192;
Pred. No. 4.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indele
A; Reference number: S74322; MUID: 97061201; PMID: 8905231
                                                                                                                                                                                                                                                                                                                    Match
Local Similarity 100.0%; Pred. No. 4.2e+02;
les 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Scot.
100.0%; Pred. No. 2...
0; Mismatches
```

```
RESULT 250
JC7106
Gravelopment related unidentified 25K protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: U77106
C;Accession: U77106
C;Axcuma-Takagi, M.; Tohyama, Y.; Kasama-Yoshida, H.; Sakagami, H.; Kondo, H.; Kurihara, Biochem. Biophys. Res. Commun. 263, 737-742, 1999
A;Title: Novel related cDNAs (C1841, C184M, and C184S) from developing mouse brain encod A;Accession: U77106; MUID: 99443733; PMID:10512749
A;Accession: U77106
A;Molecule type: mRNA
A;Residues: 1-199 <SAK>A;Cross-references: DDBJ:AB012727
A;Experimental source: brain, C184S
C;Keywords: brain; zinc finger
                                                                                0; Gaps
Query Match
1.8%; Score 6; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                       190 LIADLO 195
                                                                                                                               82 LIADLO 87
                                                                                                                                                                                        qq
```

0; Gaps

Query Match
1.8%; Score 6; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels

60 EPPTEA 65 |||||| 14 EPPTEA 19

<u>ک</u> ۾

Search completed: April 12, 2004, 10:37:19 Job time : 30 secs

500 502 504 535 762	923 1237	123.9 1489 2869 3433	3788 15 38 40	55 72 82	83 87	101	101	110 113 124	128	133	134 135 135	140	1 1 4 4 1 1 4 2 0 1 4 3 3	145 150	151	122	153	155	161	161 162	162	165	170	176 176	178	178	179	181	182	182	185 186	
44444																																
rrrrr																																
4 N O C O	9 4 9	T 4 4 4	44 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	449 50 51	522	54	56 57	5 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	61	643	9 9 9 N	696	7 7 7 7 8 7 8 7 8 7 8 8 8 8 8 8 8 8 8 8	47.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.7.	77	67.	81	883	8 8 8 5 4	98	88		92	93	100	97.	86	1000	101	103	105	-
Ltd.		e 18 Seconds 1ignments) llion cell updates/sec	. PADEKNYLIKQIRDLKKTAP 337				141681				y chance to have a me result being printed, distribution.		Description	Q9h9s4 homo sapien Q9db16 mus musculu Q9y376 homo sapien	mus n	Q9p7q8 schizosacch P91891 drosophila	O18211 caenorhabdi	O60032 emericeita P18475 drosophila	Q8xrml ralstonia s O60313 methanococc	051875 buchnera ap	OBrf15 fusobacteri	P77044 escherichia P21359 candida gla	P17576 polyporus t O9m0m4 arabidoosis	Offgk3 arabidopsis	Q59175 brucella ab	Q8ycyl brucella me P47459 mycoplasma			P53663 mycoplasma 09sfh9 arabidopsis	rhodobacte	P38358 saccharomyc O70624 mus musculu	
93 c	ein search, using sw model	April 12, 2004, 10:29:13; Search time 18 Second (without alignments) 974.869 Million cell	US-10-025-730-1 337 1 MKKMPLFSKSHKNPAEIVKIFADEKG	OLIGO Gapop 60.0 , Gapext 60.0	1416Bl seqs, 52070155 residues	0	hits satisfying chosen parameters:	length: 0 length: 2000000000	: Listing first 300 summaries	SwissProt_42:*	is the number of results predicted becr than or equal to the score of the ived by analysis of the total score	SUMMARIES	* Query Match Length DB ID	69.1 334 1 MOZI 35.9 334 1 MOZI 6.8 341 1 MOZ5	6.8 341 1 MO25 4.7 321 1 DE76	4.7 329 1	4.2 338 1 MO2M	2.7 384 I 2.4 923 1	2.1 139 1	2.1 177 1	2.1 232 1 RADC	2.1 293 1 2.1 339 1	2.1 340	2.1	2.1 359 1	2.1 359 1 2.1 372 1	2.1 373 1	2.1 399 1 2.1 421 1	2.1 423	2.1 438 1	2.1 474	2.1 492 I
	OM protein - prot	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Word size :	Total number of	Minimum DB seg ] Maximum DB seg ]	Post-processing	Database :	Pred. No. : score great and is der:		Result No. Score	1 233 2 121 3 23	121		1 1-1															

droconhila	attus no	omo sapi	rosop	chizosacc	i g	10 10 10 10 10 10 10 10 10 10 10 10 10 1	ch:	lasmod	omo sa	mus musculu	nas pl	ŏ	ÖĞ	3 5	ravia pse	ynechocy	ethanococ	gallus gall	mus musculu	canine ente	maize strea	chlorella p	apiysia car	archaeogrou	halobacteri	chlamydia p	pyrobotrys	euglena gra	methanobact	bacillus su	oenothera h	pyrococcus	pyrococcus	pyrococcus	marek's die	caenornama	vaccinia vi	vaccinia vi	variola vir	anabaena st	helicobacte	helicobacte	hos taurus	huhalus buk	ovis aries	mycoplasma	mycoplasma	cervus elai	mycopiasma	caemorinabu		caulobacter	nycticeius	staphyloco	escherichia	arabidopsis	vibrio para	salmonell	salmon		pisum	bacter	arabidop	turkey rum
0.0000	09v2u2 09r1i4	099972	09va27	010415	P25360	Q00000	014188	000798	P46939	P97412	P12801	P46166	P46165	043227	010314	P73882	P54009	P12264	Q80vv3	004703	P14988	P05720	P29233	029357	09hm15	09ZZ60	002984	P32060	027797	034959	Q9mtj0	O9uyre	Q8u315	058312	005104	PUESEL	D20082	P07610	P33814	Q8ysi5	09zjh2	025985	P14978	04560	P19114	Q8evj0	P75240	P51747	P36263	009243	O9rib4	P20379	Q36572	09860	P36766	094678	087r29	P60085	P60084	P45421	P29450	P70889	O9xfb9	P33494
í	RASP DROME			PMIP_SCHPO			NMES MOUSE	RBP1_PLAVB	TRO HUMAN	LYST MOUSE	'IBA_ANAPL	DOS BOVIN	DOOT BOVIN	NIVOS BOVIN	TOSE NEVOD	746S SYNY3	L31 METUA	11 CHICK	BP3 MOUSE	NS7_CVCAE	718K MSVK	CX1 CHLPY	SENA APLCA	7905_ARCFU	C35 CIAFA	CHI.DN	TST PYRST	RED EUGGR	IF2B METTH	YJAV BACSU	RRB OENHO	IF2B_PYRAB	IF2B_PYRFU	IF2B_PYRHO	U426_HSVMG	HS16 CAEEL	KLY OKEPA	TAA1 VACCU	TAA1 VARV	RUVX ANASP	SSRP_HELPJ	SSRP_HELPY	Y18K MSVN	TLZ BOVIN	TI.2 SHEED	RL10 MYCPE	RL10 MYCPN	IL2_CEREL	RL10 MYCGE	YP92 CAREL	KSI6 COKGL	SODO CATICR	CYB NYCHU	RPOE STAAM	HPRT ECOLI	HPKT SALTY	V969 VIRPA	SYDP SALTI	SYDP_SALTY	YHCE ECOLI	THIF BRAINA		THFZ ARATH	
												ш	., .,	4 H	4 2				7	_	_		~, ~,	_,,						l m	-	т.	7	ਜ	_	Н :		- ا	-		7	_	٦,	٠.	٠.	4	· ~	н	д.	Η,	<b>-</b> -	٦.		н	, i	٦,	٦,		_	٦,	٦.	1		н
					923	237		698	433	788																																																					182	
		7 7	2.1	2.1	2.1	2.1	7.	1.0	7 7	2.1	1.8	1.8	9.5		æ. c	α	ο α • -	00	1.8	1.8	1.8	1.8	8.4	8.		, ,	0 a		000	α.	8.	1.8	1.8	1.8	₩. 1	1.8	ч. 6	. a		1.8	1.8	1.8	1.8	B . 1	90.0	9 60		1.8	1.8	1.8				1.8	1.8	60.0	, r	. 4.	1.8	1.8		ο α	. 60	1.8
	١ - ١	- 1-	7	7	7	7		- [		7	9	9	9 (	φ.	ø	ט ע	o ve	o ve	ω (	9	9	9	9	9	۰ م	י פ	שם	o ve	·	י ע	œ	9	· vo	9	9	9	9 (	ρų	o ve	· vo	φ	9	9	ا ه	o u	o vo	o	9	9	יטי	<b>о</b> (	שם	o vo	9	9	φι	י ס	9	9	9	9 4	ט ע	φ	φ
	34	0.00	37	38	39	40	4.	4 4	4 4	4.5	46	47	48	4. 0.1	200	51	7 6	) r.	. 10	26	57	28	59	09	61	200	5 4	# L	9 9	20	80	69	70	11	72	73	74	7.5	0 7	7.8	79	80	81	82	600	0 0 4 L	9 60	87	88	83	90	y 0	26 66	0.00	95	96	7.60	0 0	100	101	102	104	105	106

Q87te0 vibrio para Q8ddg7 vibrio vuln Q9uil8 homo sapien Q97dj3 streptococc Q8cwr2 streptococc Q8cwr2 streptococc P52845 rattus norv P52845 rattus norv P49890 rattus norv P49890 rattus norv P49890 rattus norv P49890 rattus norv P49890 rattus norv P49890 rattus norv P49890 rattus norv P49890 rattus norv P49890 rattus norv P49890 rattus norv P49890 rattus norv P49591 ragental Q8rfp5 fusobacteri Q8rfp5 fusobacteri Q84469 dictyosteli P59453 buchnera ap Q8ddq1 syncohococc Q8tx60 methanopyru P24859 kluyveromyc P24859 kluyveromyc P36184 apis mellif P3614 schizosacch Q8gb99 heliobacill Q25411 heliobacill	Q801/12 homo sapien Q801/12 sulfolobus Q97124 sulfolobus P54128 caenorhabdi Q805/7 homo sapien Q805/7 homo sapien Q805/7 homo sapien Q805/7 homo sapien Q955a2 listeria mo Q955a2 listeria mo Q9724 homo sapien Q955a2 listeria mo Q955a2 homo sapien Q957/7 macaca fasc Q47823 enterococcus Q81920 bacillus su P3203 mus musculu P3203 mus musculu P3203 mus musculu P3203 saccharomyc P22135 saccharomyc P22135 saccharomyc P22135 saccharomyc P26593 lactococcus Q9403 streptococc Q94048 equine rota Q96049 wiggleswort Q96049 ureaplasma Q91077 kulyveromyc Q81080 treponema p Q90408 ureaplasma Q91077 kulyveromyc Q9408 musculu Q9408 methanococc P52950 mus musculu Q9408 rattus norv Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus Q94187 pyrococcus
HSLO VIBPA HSLO VIBPA HSLO VIBVU PHEB HUMAN TRUB STRPN SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT SUOZ RAT HRAN FUSNN HTSZ AGABI HRAN FUSNN KTOZ ACRA SCHO ZYNEL HSLO ZYNEL FTRL METKA SCHO TRUB HELMO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HELPO MRAW HE	OGAGE HUMAN DHYS SULTO NADA SULTO NADA SULTO NADA SULTO NADA SULTO NADA SULTO NADA SULTO NADA SULTO NADA SULTO NADA SULTO NASA SULTO DHRY CAREL HUMAN PRNAT LISMO DHRY CAREL MYTTC HUMAN WCJR LEDIN WCJR LACI LACLA LACI LACLA LACI LACLA LACI STRPU RAPE MSVJ 6 ATPT YRAJ LACI STRPU RROJ STRPU RROJ STRPU RROJ STRPU RROJ STRPU RROJ STRPU RROJ STRPU RROJ STRPU RROJ STRPU RROJ STRPU RROJ STRPU RROJ STRPU RROJ STRPU RROJ STRPU RROJ WUGBR GILK BACHD GJJP TREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW UREPA SYW STRSU HRCA STRSU HRCA STRSU HRCA STRSU
	339 1 0405 F 3311 1 0405 F 3311 1 0405 F 3311 1 0405 F 3312 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 3314 1 0405 F 331
	00000000000000000000000000000000000000
Ogpmug campylobact Og6129 methanosarc O60132 home sapien P56873 methanopyru O9pms6 campylobact O81702 saccharromyc O81996 bacillus ce O41477 escherrichia P40080 saccharromyc O81197 home sapien O81996 thermoanaer P22654 bovine coro O81996 thermoanaer P22654 bovine coro O81996 thermoanaer P22654 methanococc P3325 bufo bufo ( O55503 sprechocyst O9jiy3 mus musculu P22915 bacteriopha P3846 haemophilus P3846 methanococc P38467 methanococc P38467 methanococc P38487 methanococc P38487 methanococc P38487 methanococc P38487 methanococc P38487 methanococc P38487 methanococc P38487 methanococc P38487 methanococc P38487 methanococc P38487 methanococc P38487 methanococc P38487 methanococc P38487 methanococc P38487 methanococc P38487 methanococc P38487 methanococc P384871 haemophilus O99krn0 vibrio chol O89kry6 arabidopsis	Q37906 bacteriopha Q37906 bacteriopha P04095 mus musculu P04095 mus musculu P18918 mus musculu P18918 mus musculu Q9hsb4 halobacteri Q86714 staphylococ P31402 mus musculu Q86714 staphylococ P31402 mus musculu Q87304 drosophila Q267316 methanobact P75428 mycoplasma Q87368 vibrio para P5228 mycoplasma Q87368 vibrio para P52318 mycoplasma Q87368 vibrio para P52318 mycoplasma Q87368 vibrio para P52318 mycoplasma Q87368 vibrio para P52318 mycoplasma Q87368 vibrio para P52318 mycoplasma Q87368 mycoplasma Q87368 reponema p Q8736 mycopacteri Q1344 methanobact Q1344 orgyia pseu Q26137 methanococc Q25911 halicobacte Q96038 rattus norv Q01036 herpesvirus P76513 escherichia P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 decherichia P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76513 mycoplasma P76514 mycoplasma P76514 mycoplasma P76514 mycoplasma P76514 mycoplasma P76514 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614 mycoplasma P76614
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	1.8 222 1 GLIS_AAATH 1.8 224 1 PLP1 MOUSE 1.8 224 1 PLP2 MOUSE 1.8 226 1 AROD_HAIN1 1.8 226 1 AROD_HAIN1 1.8 226 1 AROD_HAIN1 1.8 226 1 AROD_HAIN1 1.8 226 1 AROD_HAIN1 1.8 227 1 GLI3_ARATH 1.8 232 1 VATE_MANSE 1.8 236 1 VATE_MANSE 1.8 236 1 VATE_MANSE 1.8 236 1 VATE_MANSE 1.8 236 1 VATE_MANSE 1.8 236 1 VATE_MACPN 1.8 250 1 VATE_MACPN 1.8 250 1 VATE_MACPN 1.8 250 1 VATE_MACPN 1.8 250 1 VATE_MACPN 1.8 250 1 VATE_MACPN 1.8 250 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1 VATE_MACPN 1.8 260 1
	133 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

253	v	a	220		•	COLLOR ACTIV	9		
254	o vo		, 4 , 4			. ່ ຕ	<u> </u>	P9/369	mus musculu
255	9		34.			YM69 VIBVU	12	O8dad7	; i
256			34				3	Q9uk28	homo sa
257			34.			RTCA_PYRAB	e)	920460	pyroc
258			34			NAGZ YERPE	ñ	Q8zfB3	versini
259	v v	1.8	345	10			ŭ	Q8tmk1	methanosar
760			34			MELA_SHECO	ဥ	P23996	shewanella
797			ω (			FTSY MYCPN	X.	P75362	mycoplasma
707			£. (				<b>H</b> 1	09zq77	arabido
263			יית מינ				Η.	P36547	
#07 201			ה נ י			PANE SCHPO	၌ ရု	09hdu6	schizos
200			n c			KITH HSVMD	9 !	P17653	marek's
267			200			YPBB_BACSU	Đ.	P50728	
900			ח ני			DHAS METO	4	057658	methanococc
0 0			יי ה ה			EZB XYLFA	! ــ	Q9pag5	xylella fas
600			ה ה ה			WN11 BRAR	<u>H</u>	073864	brachydanio
2 10			n (			CCIO CANAL	-3	P39827	candida alb
1/7						FIBP_CERAE	EJ :	046431	cercopithec
272			io m			FIBP MOUSE	EQ.	Q9ji19	mus musculu
273			328			DDL_ENTHR		047827	
274			328			RF1_CORGL		Q8nr57	corynel
275			361			AROC VIBAN	7	P39198	vibrio
0 17 0			361			AROC VIBPA	K I	087mm9	
7 7 7			36			AROC VIBVO	Þ	08db42	vibr
B (7)			36			IDIZ AERPE	<u>ш</u> ;	09yb30	aeropyrum p
א כי מי כי			361			V227 FOWPV	; ج	09,1508	fowl
200			700			HUMA TELEFICION	<b>4</b> 1	043427	homod
287			200			YOU ECOLL	<b>⊒</b> ₽	P32066	esch
283			י			0 4 4 4 C C K C	9 5	P4 /2 / 0	mycopiasma
284			200			VECO CONV	E C	UVGZEQ	arabidopsis
285			200				n E	F/3003	synechocys
286						TAK BOVIN	4 12	Cocky	mycopiasma
287						MNCP OXYTE	4 <u>P</u>	C2111129	
288			377			B2X HAET	<b>4</b> 2	086233	basmonhiling t
289			372			3BH1 MESAU		060555	
290			372			BH2 MESA	: E	064421	11 5 Det
291			372			3BH3 MESAII	: =	702570	100
292			372			BH3 MOIISE	i tri	02520	E
293			373			3 RH6 MOTISE	i fa	035450	1 3 Del
294			372			PEX3 MOTSE	1 62	00100	
295			372					0 44 t t t 0 0	rattio
296			373			PEX3 CRITO	c	447.000	ָלְיָלָ מְלָלָ
297			373				· 2	54.5.2.2 54.5.3.9	
298			374			SYW AERPE		094924	aeronym n
299			375					0821115	nvrobaculum
300			379			AMBC		078928	amblonyx ci
						ALIGNMENT	ENTS		
RESULT 1									
21.									
	MAN		STANDARD			PRT;	334 AA.		
	2001	, e e ( o e )		0	4	-			
DT 16-0CT-2001 (R	2001	(Rel.	40,1	Lreated) Last sec	מ מ מ	ed) segmence undate)	יתשדה)		

```
RESULT 1

MO2L HUMAN

DM STANDARD; PRT; 334 AA.

COSH554; OSB233;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE MO25-like protein.
OS Homo saptens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX MCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 4-334 FROM N.A.
RA Nishikawa T., Otsuki T., Suzuki Y., RA Nishikawa T., Otsuki T., Suzuki Y., RA Nishikawa T., Otsuki T., Suzuki Y., RA Nishikawa T., Ushida S., Murakawa K., Ono Y., Takiguchi S., Rakanashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Ramamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 EAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYISAHP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 HILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIASDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 FATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHNFA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 IMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPKLIE 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 IMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPKLIE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEVISAHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 MPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKEPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 FATFKOLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHNFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 69.1%; Score 233; DB 1; Length 334; Local Similarity 99.7%; Pred. No. 5.5e-237; Les 333; Conservative 0; Mismatches 1; Indels
Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                  Pearce A., Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF03204; Mo25; 1.
SEQUENCE 334 AA; 38728 MW; 97702273D8548432 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 FLSSFQKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 FLSSFQKERTDDEQFADEKNYLIKQIRDLKKTAP 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Cerebellum, Eye, Pituitary, and Testis;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MO2L_MOUSE STANDARD, PRT; 334 AA. Q9DB16, Q8BG22; Q91WB8; Q91YLO; 16-OCT-2001 (Rel. 40, created) 10-OCT-2003 (Rel. 42, Last sequence update) 110-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                        -!- SIMILARITY: Belongs to the Mo25 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1] SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                        EMBL; AK022639; BAB14147.1; ALT_INIT.
EMBL; AL138875; CAC28084.1; -.
InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
                                                                             SEQUENCE OF 276-334 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MO25-like protein.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
  ਨੋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

us-10-025-730-1.oligo.rsp

```
STRAIN=FVB/N; TISSUE=Manmary gland, and Salivary gland;
MEDINE=22388257; PubMed=12477932;
MEDINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uddin T.B., Toshiyui S., Carninol F., Milahy S.J.,
Bosak S.A., McEwan P.J., McKernen K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villaion D.K., Muzny D.W., Sodergen B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Youdhan J.W., Green B.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Meneration and initial analysis of more than 15,000 full-length human
          A Schriml L.M., Kanapin A., Matenda H., Gatchenbush J.,

Bard C., Corbani L.E., Cousins S.,

Barke J.A., Bradt D., Brusto V., Chothia C., Corbani L.E., Cousins S.,

Barke J.A., Bradt D., Brusto V., Chothia C., Corbani L.E., Cousins S.,

A Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

Basterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Ronagaya A., Kurochkin I.V., Lee Y., Lemhard B.L., Miki H.,

Ragott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Rayashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Ravasi T., Reed J.C., Reed DJ., Reid J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setcu M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Walls.

A Wilming L.G., Wynshaw Boris A., Yanagisawa M., Yang I., Yang L.,

Kawai T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

Ravashi A., Yoshino M., Materston R., Innagawa A.,

Yasunishi A., Yoshino M., Materston R., Iander E.S., Rogers J.,

Ranalysis G. the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=09DB16-2; Sequence=VSP 007417, VSP 007418;
Note=No experimental confirmation available;
-!- SIMILARITY: Belongs to the Mo25 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9DB16-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AK005323; BAB23953.2; ALT_INIT.
EMBL; AK030474; BAC26978.1; ALT_INIT.
EMBL, AK053642; BAC35457.1; ALT_INIT.
EMBL, AK076788; BAC36470.1; ALT_INIT.
EMBL, AK076867; BAC3643.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC016128; AAH16128.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
EMBL;
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                 179 DAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLIGELILDRHN 238
                                                                                                                                                                                                                                                                                                                                        HPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIAS 181
                                                                                                                                                                                                                                                                                                                                                                        119 HPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDIAS 178
                                                                                                                                                                                                                                                                                                                                                                                                               182 DAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22388257; PubMed=12477932; Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Robuler G.D., Straubberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Maruslina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., McGunlan N.A., Peters G.J., Abrameon R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                        VFVASPHKTQPIVEILLK -> NSVFITNRIHGLKRWLSS
                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jin W., Shi J., Ren S., Gu J., Fu S., Huang Q., Dong H., Yu Y., Fu Wang Y., Chen Z., Han Z.;
"A novel gene expressed in the human hypothalamus.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=20272150; PubMed=10810093;
Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
Identification of novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics.";
Genome Res. 10:703-713 (2000).
                                                                                                                      (in isoform 2).
|FILACHORP 007417.
|Missing (in isoform 2).
|FILACHORP 007418.
|FILACHORP 007418.
|S -> R (IN REF. 1; BAB23953).
|L -> R (IN REF. 2; AA416546).
|W; 822F04487FB4EB6F CRC64;
                                                                                                                                                                                                                                                                    Length 334;
                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                35.9%; Score 121; DB 1; Le
100.0%; Pred. No. 3.8e-119;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
MO25 protein (CGI-66).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
              MGD; MGI:1916258; 1500031K13Rik.
InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
Pfam; PF03204; Mo25, 1.
Alternative splicing.
VARSPLIC 276 293 VFVJ
                                                                                                                                                                                                              229 L
38718 MW;
 BC016546; AAH16546.1;
                                                                                                                                                                                                                                                                                 Best_Local Similarity 100.
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                               42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                             42
229
334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Duodenum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 F 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                             CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                        122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239
                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3
HUMAN
75
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SET TET TET S
                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schlerd Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schain J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences: "16899-16903(2002).

-I. SIMILARITY: Belongs to the Mo25 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BEGGE MOUSE EMBYOS.";
Mol. REPROG. Dev. 34:1-7(1933).
-!-FUNCTION: ONE OF THE FIRST GENES TO BE TRANSCRIBED DURING MOUSE
DEVELOPMENT, MAY FLAY SOME GENERAL FUNCTION.
-!-SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!-DEVELOPMENTAL STAGE: TRANSCRIBED DURING BARLY MOUSE DEVELOPMENT.
DETECTED AT ALL DEVELOPMENTAL STAGES FROM THE EGG THROUGH THE
BLASTOCYT, MOST ABUNDANT AT THE 2-CELL STAGE.
-!- SIMILARITY: Belongs to the Mo25 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93119656; PubMed=8418809;
Miyamoto H., Matsushiro A., Nozaki M.;
"Molecular cloning of a novel mRNA sequence expressed in cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8%; Score 23; DB 1; Length 341;
100.0%; Pred. No. 4.9e-16;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 AA; 39869 MW; EC710A528B6F9811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 IMTKYISKPENLKLMMNLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 IMTKYISKPENLKLMMNLLRDKS 267
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF151824; AAD34061.1; -.
EMBL; AF113536; AAF14873.1; -.
EMBL; BC020570; AAH20570.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR004892; Mo25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR008938; ARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF03204; Mo25;
SEQUENCE 341 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MO25 protein.
MO25 OR CAB39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MO25 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
MO25 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlorella protothecoides.
Eukaryota, Viridiplantae, Chlorophyta, Trebouxiophyceae, Chlorellales,
Chlorellaceae, Auxenochlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hortensteiner S., Chinner J., Matile P., Thomas H., Donnison I.S., "Chlorophyll breakdown in Chlorella protothecoides: characterization of degreening and cloning of degreening-related genes."; Plant Mol. Biol. 42:439-450(2000).
-1- SIMILARITY: Belongs to the Mo25 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                 6.8%; Score 23; DB 1; Length 341;
100.0%; Pred. No. 4.9e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.7%; Score 16; DB 1; Length 321
100.0%; Pred. No. 1.1e-08;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                  Pfam; PF03204; Mo25; 1.
SEQUENCE 341 AA; 39842 MW; E7F668529D6FE811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF03204; Mo25, 1.
SEQUENCE 321 AA, 37262 MW, 918FD02964B09071 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
SPACCHRICAL protein C1834.06c in chromosome:
SPACC1834.06C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-EFB-2003 (Rel. 41, Last annotation update)
Degreening related gene dee76 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 AA
                                                                                                                                                                                                                              100.08; Preu. ...
                                                                                                                                                                                                                                                                                                                                          244 IMTKYISKPENLKLMMNLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                           245 IMTKYISKPENLKLMMNLLRDKS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20256472; PubMed=10798614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ238632; CAB42595.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 ASDAFATFKDLLTRHK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 ASDAFATFKDLLTRHK 183
                          MGD; MGI:107438; Cab39.
InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
EMBL; S51858; AAB24801.1;
                                                                                                                                                                                                                                 Best Local Similario,
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
'-heq 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YFV6 SCHPO
Q9P7Q8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE76 CHLPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOXFY6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB76_CHIPR

AC OSKEVE

DD COSTED

DT 16-OCT

DT 16-OCT

DT 16-OCT

DT 16-OCT

DT 16-OCT

DT 16-OCT

DT 16-OCT

DT 16-OCT

DT 16-OCT

DT 16-OCT

DT 16-OCT

DT 16-OCT

DT 16-OCT

DT 16-OCT

DC CHIPR

RM HOTH

RM HOTH

RM HOTH

RM HOTH

RM HOTH

RM HOTH

RM HOTH

RM HOTH

RM HOTH

CC This S

CC This S

CC This S

CC This S

CC This S

CC This S

CC This S

CC This S

CC This S

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

CC COT SED

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YFV6_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
8 8 8 8 8 8 8 8 8
                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OSCIPLIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

```
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MO25 protein (dMo25).
MO25 OR CG4083.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                       Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                1 protein.
329 AA; 38521 MW; 073DD0607A64C952 CRC64;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                      Score 16; DB 1; Le
Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P91891; O9VV85;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.1e
Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the Mo25 family.
                                           MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                  GeneDB SPombe; SPAC1834.06c; -. InterPro; IPR008938; ARM.
InterPro; IPR008892; Mo25.
Pfam; PF03204; Mo25; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                      EMBL; AL157734; CAB75774.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   219 SENYVTKRQSLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                 216 SENYVTKROSLKLIGE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
       Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                              T50117; T50117
                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MO25 DROME
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
g
```

```
RA MEDINELS 195006; PubMed=10731132;
RA MADINELS 195006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Gacoge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Gacoge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Champe M., Pfeiffer B.D.,
RA Barndon R.C., Ragers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Apdayani A., Barman B.P., Bhandrai D., Beagley E.M.,
Rabeson K.Y., Bence P.V., Berman B.P., Bhandrai D., Bolshakov S.,
RA Beris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Beson K.Y., Bence P.W., Berman B.P., Bhandrai D., Botchar P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Davenport L.B., Ly Harris M.,
RA Fosler C. Gabrielian A.E., Garra C., Ferriaz S., Ferlisch M.,
RA Fosler C., Gabrielian A.E., Garra J.H., Harris M.,
RA Hostin D., Houston K.A., Heiman T.J., Hermide S., Richischman W.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li S., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li S., Liang Y., Lin X.,
RA Lasko P., Lei Y., Marthy B., Murphy D., Murphy D.M., Noslson D.L.,
RA Rainel B.E., McIntosh T.C., McLeod M.P., Pacleb J.M.,
Rablazzolo W., Pitirman G.S., Pan S., Pollard J., Purit V., Resse M.G.,
Rablazzolo W., Pitirman G.S., Pan S., Pollard J., Purit V., Resse M.G.,
Rablazzolo W., Pitirman G.S., Pan S., Pollard J., Purit V.,
Rablazzolo W., Pitirman G.S., Pan S., Pollard J., Purit Y.,
Rabler E.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Raiter R., Spardling A.C., Stapleton M., Skupski M.P., Smith T.,
Raiter R., Rober R. M., Raiter R., Variers R. Wang A. H., Wang X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sylickas R., Tectors C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Noodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.G Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.; Schore Sequence of Drosophila melanogaster.";
                                                                                                               MEDLINE=96268479; PubMed=8672247;
Nozaki M., Onishi Y., Togashi S., Miyamoto H.;
Nolecular characterization of the Drosophila Mo25 gene, which is conserved among Drosophila, mouse, and yeast.";
DNA Cell Biol. 15:505-509(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 Y -> H (IN REF. 1).
102 V -> L (IN REF. 1).
39385 MW; 5790BD91754ClC74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the Mo25 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE003526; AAF49432.1; -. FlyBase; FBgn0017572; Mo25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB000402; BAA19098.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
Pfam; PF03204; Mo25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                           SEQUENCE FROM N.A.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
```

DB 1; Length 339; 1.3e-07;

4.5%; Score 15; 100.0%; Pred. No.

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
        Gaps
                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99126010; PubMed=9928930; Acros M., Fischer R.; Farors M., Fischer R.; Molecular characterization of HymA, an evolutionarily highly conserved and highly expressed protein of Aspergillus nidulans."; Mol. Gen. Genet. 260:510-521(1999).
        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Burotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical MO25-like protein Y53Cl2A.4 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14; DB 1; Length 338;
Pred. No. 1.4e-06;
      Indels
                                                                                                                                                                                                                                                                                                                                                           Kershaw J., Lennard N., Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 protein.
338 AA; 39431 MW; 1D0C34A35D9116F5 CRC64;
        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.2%; SCUL.
100.0%; Pred. No. 1...
                                                                                                                                              338 AA
                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the Mo25 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384 AA.
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conidiophore development protein hymA.
                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last seqn
16-0CT-2001 (Rel. 40, Last ann
                               105 LRRQIGTRSPTVEYI 119
                                                      103 LRRQIGTRSPTVEYI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z99277; CAB16486.1; -.
PIR; T27129; T27129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WormPep; Y53C12A.4; CE14890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 LRRQIGTRSPTVEY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 LRRQIGTRSPTVEY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
15; Conservative
                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03204; Mo25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                              STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                            SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
                                                                                                                                         CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYMA EMENI
                                                                                                                                                                                                                               Y53C12A.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       060032;
                                                                                                                         MOZM_CAEEL
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IYMA EMENI
                               ò
                                                                                                                                                                                                                   ≿
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sprenger F., Torsoclair M.M., Morrison D.K.,
"Biochemical analysis of torso and D-raf during Drosophila
"Biochemical implications for terminal signal transduction.",
Mol. Cell. Biol. 13:1163-1172(1993)
-!- FUNCTION: Probable receptor with tyrosine-protein kinase activity.
Required for determination of anterior and posterior terminal
structures in the Drosophila embryo. The ligand of torso seems to
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sprenger F., Stevens L.M., Nuesslein-Volhard C., "The Drosophila gene torso encodes a putative receptor tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [yrosine-protein kinase receptor torso precursor (BC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- TISSUE SPECIFICITY: Expressed throughout the embryo but is activated specifically at the poles.
-1- SIMILARITY: Belongs to the Tyr family of protein kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endobterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                         2.7%; Score 9; DB 1; Length 384;
100.0%; Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                              384 AA; 44392 MW; 2E203D0D110C5FD6 CRC64;
-!- FUNCTION: Required for conidiophore development.
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the Mo25 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                923 AA.
                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=89181943; PubMed=2927509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93140754; PubMed=8423783;
                                                                                                                                                                                                                                      EMBL; AJ001157; CAA04556.1; -.
                                                                                                                                                                                                                                                     InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 338:478-483(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                    274 FHVFKVFVA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 FHVFKVFVA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine phosphate.
                                                                                                                                                                                                                                                                                            Pfam; PF03204; Mo25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOR DROME
                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
TOR DROME
  $$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
.
0
                                  R HSSP; P11652. IFGK.
R HSSP; P11652. IFGK.
R HSSP; P11652. IFGK.
R HSSP; P11652. IFGK.
R GO, GO:005886; C:plasma membrane; NAS.
R GO, GO:0005881; P:eggshell pattern formation imP.
R GO, GO:0007362; P:terminal region determination; IMP.
R GO, GO:0007362; P:terminal region determination; IMP.
R GO, GO:0007362; P:terminal region determination; IMP.
R GO, GO:0007362; Prof. Kinase.
R InterPro; IPR001045; Prof. Kinase.
R InterPro; IPR001045; Tyr pkinase.
R Fram; PP00060; Prof. Kinase.
R Fram; RP00060; Prof. Kinase; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP synthase epsilon chain 2 (EC 3.6.3.14) (ATP synthase F1 sector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYROSINE-PROTEIN KINASE RECEPTOR TORSO. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                      SMART; SM00060; FN3; 1.
SMART; SM000219; TYrKc; 1.
PROSITE; PS00107; PROTEIN KINASE APP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Prosine-protein; Receptor; Glycoprotein;
Tyrosine-protein kinase; ATP-binding; Transferase; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales;
Burkholderiaceae, Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.4%; Score 8; DB 1; Length 923; 100.0%; Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105163 MW; FB25881F5757CF41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epsilon subunit 2).
ATPC2 OR RSP0810 OR RS01897.
Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLCNAC. . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Pred. No. 7.2
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (BY SIMII
BY SIMILARIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=GMI1000;
MEDLINE=21681879; PubMed=11823852;
           EMBL; X15150; CAA33247.1; -. PIR; S03900; S03900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.4
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37
63
107
142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                923
420
923
874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          489
502
741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 SSGLLVTL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 SSGLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ransmembrane; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid megaplasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           923 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
21
400
421
475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
DOMAIN
DOMAIN
NP BIND
BINDING
ACT SITE
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATE2 RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATE2 RALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC DE DE DE DE DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA DE LA SECULIA D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensealsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-JAL-1 / DSW 2661 / ATCC 43067;

XI BDLINE-96337999; PubMed=8688087;

XI BDLINE-96337999; PubMed=8688087;

XI BDLINE-96337999; PubMed=8688087;

XI BDLINE-96337999; PubMed=6.5... Zhou L., Fleischmann R.D.,

XI BULC J.C., White O., Olash G. J.C., Norrick J.M., Glayton R.A., Gocayne J.D.,

XI Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

XI Kerlavage A.R., Kirkness B.F., Weinfams M.D., Reich A., Marmann J.E., Nguyen D.,

XI Coctt J.L., Geoghagen N.S.M., Weinfams J.F., Fuhrmann J.E., Nguyen D.,

XI Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

XI Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

XI KIERK H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

XI Jannaschii.",
                                                                                                                                                                                                                                                                                                                                                                                                                     -:- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), peta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c. similarity: Belongs to the ATPase epsilon chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                            wacture along the produced ATP from ADP in the presence of a proton produced are membrane.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00401; ATP-Synt DE 1.

Pfam; PF00401; ATP-Synt DE N; 1.

ProDom; PP0080944; ATPSynt DE; 1.

TIGRFAMG; TIGR01216; ATP_Synt epsi; 1.

Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport; Plasmid;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Walen M., Wincker P., Levy M., Weissenbach J., Boucher C.A., "Genome sequence of the plant pathogen Ralstonia solanacearum."; "Atture 415.497-502 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 2.1%; Score 7; DB 1; Length 139; Local Similarity 100.0%; Pred. No. 15; or Indels or 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 AA; 15304 MW; A506B25345D28C1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AL646081; CAD17961.1; --
HAMAP; MF 00530; -; 1.
InterPro; IPR001469; AIPSYNC_DE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein MJ0003.
MJ0003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 EAVAQLA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 EAVAQLA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome
SEQUENCE 139 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y003 METUA
Q60313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YOO3 METUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE S
                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

```
CHICK
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTA3 CF
P26697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus
                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTA3_
        셤
                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(1), beta(3), pamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c. -! SIMILARITY: Belongs to the ATPase delta chain family.
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=22084549; PubMed=12089438;
Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
Tamas I., Klasson L., Canbaeck B., Moran N.A., Anderson S.G.E.;
"So million years of genomic stasis in endosymbiotic bacteria.";
Schence 296:2376-2379(2002).
-I-FUNCTION: This protein seems to be part of the stalk that links
CF(0) to CF(1). It either transmits conformational changes from
CF(0) inco CF(1) or is implicated in proton conduction.
-I- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence analysis of a 34.7-kb DNA segment from the genome of the profile of a sphidicola (endosymbiont of aphids) containing groEL, dnaA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clark M.A., Baumann P.;
"The (FIFO) ATP synthase of Buchnera aphidicola (endosymbiont of
                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 1; Length 156;
100.0%; Pred. No. 16;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aphids): genetic analysis of the putative ATP operon.";
Curr. Microbiol. 35:84-89(1997).
                                                                                                                                                                                                                   Hypothetical protein; Complete proteome.
SEQUENCE 156 AA; 18428 MW; 364797DB0EE38AB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            segment from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) ATP synthase delta chain (EC 3.6.3.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark M.A., Baumann L., Baumann P.,
"Sequence analysis of a 34.7-kb DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the atp operon, gidA, and rho.";
Curr. Microbiol. 36:158-163(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97361981; PubMed=9216881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98184963; PubMed=9516544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998 (Rel. 37, Created)
   Science 273:1058-1073(1996).
                                                                                                                                                                     EMBL; U67459; AAB97990.1; -.
                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                     PIR; C64300; C64300.
TIGR; MJ0003; -
                                                                                                                                                                                                                                                                                                                                         291 VEILLKN 297
                                                                                                                                                                                                                                                                                                                                                                            34 VEILLKIN 40
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=98794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATPH OR BUSG005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H(+)(Out)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BUCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATPD_BUC
051875;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
g
```

```
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
Glutathione S-transferase 3 (BC 2.5.1.18) (GST-CL3) (GST class-alpha).
Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Avee; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

STRAIN=White leghorn, TISSUE=Liver;

MEDLINE=92143826; PubMed=1339283;

Chang L.-H., Fan J.-Y., Liu L.-F., Taxi S.-P., Tam M.F.;

Cloning and expression of a chick liver glutathione S-transferase CL

Subbunit with the use of a baculovirus expression system.";

Biochem. J. 281:545-551(1992).

-!-FUNCTION: CATALYZES THE CONUGATION OF GSH TO A WIDE VARIETY OF

ELECTROPHILIC ALKYLATING AGENTS. ALSO INVOLVED IN THE METABOLISM
OF LIPID HUNDOPEROXIDES, PROSTAGIANDING AND LEUKOTRIENE A4 AND IN

NUMBER OF DRUGS AND THYROLD HORMONES. THIS GST DOES NOT EXHIBIT

PERCYLLARS ACTIVITY.

PRENCIPAGE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- MISCELLANEOUS: THE VARIATIONS WERE FOUND FROM AA SEQUENCING AND IMPLY THERE ARE MULTIPLE FORMS OF CL-3.
-!- SIMILARITY: Belongs to the GST superfamily. Alpha family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione. SUBUNIT: HOMODIMER OR HETERODIMER (WITH A SUBUNIT FROM GROUP
                                                                                                                                                                                                                                                                 PRINTS, PRO0125, ATPASEDBLTA.
TIGREAMS, TIGR01145, ATP synt delta; 1.
PROSITE; PS00389; ATPASE_DELTĀ; FALSE NEG.
Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                             177 AA; 20671 MW; E1BD82A7529C01B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 7; DB 1;
100.0%; Pred. No. 18;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                   InterPro; IPR000711; ATPsynt_OSCP. Pfam; PF00213; OSCP; 1.
                                                                                                                                           EMBL; AF008210; AAC38113.1; -. EMBL; AE014076; AAM67577.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M38219; AAA62731.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 IFNNILR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S19734; S19734.
                                                                                                                                                                                              HSSP; P00831; 1ABV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 IFNNILR 94
                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 177 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P24472; 1GUK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation she European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=1886394, PubMed=11889109,
Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
Vasieva O., Chu L., Kogur Y., Chaga O., Goltsman E., Bernal A.,
Larsen N., D'Souza M., Walumas T., Pusch G., Haselkorn R.,
Fonstein M., Kyrpides N., Overbeck R.;
"Genome sequence and analysis of the oral bacterium Fusobacterium
J. Bacteriol. 184:2005-2018(2002).
                                                                                                                                                                                                                                                                                                                .
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                     Length 228;
                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAWAP; MF 00018; -; 1...,
InterPro; IPR001405; RadC.
Pfam; PF04002; Madc; 1...
Probom; P0000415; RadC; 1...
TIGREAMS; TIGR00608; radc; 1...
PROSITE; PS01302; RADC; 1...
DNA repair; Complete protecome—
SEQUENCE :232 AA; 26730 MW; 0FD3D4CE84E5A93 CRC64;
                                                                                                                                                                                                                                                         C7450E146F41E787 CRC64;
                                                                                                                                                                                                                                                                                   DB 1;
5. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA repair protein radC homolog.
                                                                                                                                                                                                                                                                          2.1%; Scc...
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                      232 AA.
                                                                                                           S -> A.

I -> F.

F -> R.

TS -> R.

AY -> VF.

W -> R.

IH -> VV.
                                                                                                                                                                                                                 A -> H
E -> A.
InterPro; IPR004046; GST_Cterm.
InterPro; IPR004045; GST_Nterm.
Pfam; PF00043; GST_C; 1.
Pfam; PF02798; GST_N; 1.
                                                      Transferase; Multigene family.
                                                                                                                                                                                                                                                         26194 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE010599; AAL95105.1; -.
                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                        213 YEKLLQS 219
                                                                                                                                                                                                                                                                                                                                                               YEKLLOS 46
                                                                                                                                                                                                                                                         228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ATCC 25586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fusobacterium.
NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FN0909.
                                                                                                                                                                                                                                                                                                                                                                                                                                  RADC FUSNN
Q8RF15;
                                                                INIT MET
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                 40
                                                                                                                                                            VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                  VARIANT
VARIANT
                                                                                           VARIANT
                                                                                                         VARIANT
                                                                                                                       VARIANT
                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
RADC_FUSNN
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lew H., Lin D.,
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [3]
SEQUENCE FROM N.A.
STRAIN=KIZ / MG1655,
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Man B., Shao Y.,
"The Complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lii Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                 Table 2011 293 AA.
P77044; P71204; P77205;
01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
2-hydroxy-6-ketonona-2,4-dienedioic acid hydrolase (RC 3.7.1.-).
                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: 3-hydroxyphenylpropionate degradation.
-!- SIMILARITY: STRONG, TO B.CEPACIA AND PSEUDOMONAS BPHD.
                 Length 232;
                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Kawamukai M.,
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ferrandez A., Garcia J.L., Diaz E.,
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                 2.1%; Score 7; DB 1;
100.0%; Pred. No. 24;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000142; AAC73452.1; ALT INIT.
EMBL; U73857; AAB18073.1; ALT_INIT.
MEROPS; S33.UNW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ecodene, EG20275, mhpC.
InterPro, IPR000073; A/b hydrolase.
InterPro, IPR003089, AB hydrolase.
InterPro, IPR000639; Epox hydrolase.
InterPro, IPR000379; Ser_estrs.
                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00561; abhydrolage; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00111; ABHYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D86239; BAA13054.1; -. EMBL; Y09555; CAA70749.1; -.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                    229 LKLLGEL 235
                                                                                                                    83 LKLLGEL 89
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=K12 / W3110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=K12 / CS520;
                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                             MHPC OR B0349.
                                                                                                                                                                                                        MHPC ECOLI
                                                                                                                                                                                      MHPC_ECOLI
                                                                                                                                                                    RESULT 16
                                                                                    ð
```

```
Polyporus tulipiferae (Irpex lacteus).
                                                                                       Murakami K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MO2M ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 19
MO2M ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
SUBCELLULAR LOCATION: Mitochondrial.
SIMILARITY: BELONGS TO THE VARI FAMILY OF RIBOSOWAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-86011564; PubMed-3900417;
Ainley W.M., Macreadie I.G., Butow R.A.;
Ainley W.M. He mitochondrial genome of Torulopsis glabrata.";
"VAR1 Gene on the mitochondrial genome of Torulopsis glabrata.";
"MOL. Biol. 184:565-576(1985).
-!- FUNCTION: Essential for mitochondrial protein synthesis and required for the maturation of small ribosomal subunits (By
                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
       Aromatic hydrocarbons catabolism, Hydrolase, Complete proteome. ACT SITE 90 80 BY SIMILARITY.

CONFLICT 158 158 E -> G (IN REF. 1 AND 2).

SEQUENCE 293 AA; 32585 MW; 4407DF7B90EA0E80 CRC64;
                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                       DB 1; Length 293;
                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40828 MW; 354820A9C1FE9E50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Polyporopepsin (EC 3.4.23.29) (Aspartic proteinase).
                                                                                                                                                                                                                                                                                         Candida glabrata (Yeast) (Torulopsis glabrata).
                                                                                                                                                                                                                            01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Mitochondrial ribosomal protein VAR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
5. 33;
                                                                     2.1%; Score 7; DB 1;
100.0%; Pred. No. 29;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 1
100.0%; Pred. No. 33;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S04682; S04682.
InterPro; IPR007980; Yeast VAR1.
Pfam; PF05316; Yeast VAR1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosomal protein; Mitochondrion. SEQUENCE 339 AA.
PRINTS; PR00412; EPOXHYDRLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMRL; X02893; CAA26652.1; -.
                                                       Query Match
Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                     253 ENLKLMM 259
                                                                                                                                             173 ENLKLMM 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 IMTKYIS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMTKYIS 186
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARP POLTU
                                                                                                                                                                                                       CANGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P17576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 18
CARP POLTU
ID CARP POL
AC P17576;
DT 01-AUG-
DT 28-FEB-
DE POLYDOX
                                                                                                                                                                               RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                          a
                                                                                                                                                                                                        DR KW
FT
SO
                                                                                                                     à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                    proceinase.";
Agric. Biol. Chem. 53:1927-1933(1989).
-!- CATALYTIC ACTIVITY: Milk clotting activity, broad specificity, but
- Eails to cleave 15-Leu-|-Tyr-16 or 16-Tyr-|-Leu-17 of insulin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. Columbia;
MEDLINE=98121113; PubMed=9461215;
MEDLINE=98121113; PubMed=9461215;
MEDVAND M., Bant E., Love K., Goodman H.M., Dean C.,
Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,
Ridley P., Hudson S.-A., Patel K., Murphy G., Piffanelli P.,
Wedler H., Wedler E., Wambutt R., Weitzenegger T., Pohl T., Terryn N.,
Gielen J., Villarroel R., De Clercq R., van Montagu M., Lecharny A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledóns, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
Eukaryota, Fungi, Basidiomycota, Hymenomycetes, Homobasidiomycetes,
Aphyllophorales, Polyporaceae, Polyporus.
NCBI_TaxID=29885;
                                                                                                                                                                                                                                               "Cloning and sequence analysis of cDNA for Irpex lacteus aspartic
                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 1-24.
Kobayashi H., Sekibata S., Shibuya H., Yoshida S., Kusakabe I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 238 N-LINKED (GLCNAC. . .) (PC 340 AA; 35050 MW; 9BAF837264D42FEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to peptidase family Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09M0M4; 023570;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hypothetical MO25-like protein At4g17270.
AT4G17270 OR DL4670W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 1;
100.0%; Pred. No. 33;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase, Aspartyl protease, Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001969; Aspprotease AS.
InterPro; IPR009007; Pept A acid.
InterPro; IPR001461; Peptidase Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00026; asp; 1.
PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP_PROTEASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D00589; BAA00467.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212
192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 IASDAFA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 IASDAFA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; JU0057; PEIKL.
HSSP; P32329; 1YPS.
MEROPS; A01.019; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
```

```
RA Malourg S., Oy I. Kirger M., Lao N., Kavensey H., Funke B. S., Monitor L. A., Ponk A., Males E. A., Bark A., Bark A., Males E., Britan K.-D., Rieger M., Schaefer M., Punk B., Malles-Aner S. Silvey W., James M., Monitor D., Matorge M., Punkeller A., Punk A., Punkeller M., Males E., Monitor L., Marcheller M., Monitor B., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Males E., Ma
```

```
the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-mib.ch/announce/or send an email to license@isb-mib.ch).
                                                                                                               Science 302:842-846(2003).
-!- SMILARITY: Belongs to the Mo25 family.
-!- CAUTION: Ref.1 sequence differs from that shown due to erroneous
gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J., Kamiya A., Mayers C., Nakajima M., Narusaka M., Seki M., Sakurai T. Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R., "Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structural analysis of Arabidopsis thaliana chromosome 5. XI."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 7; DB 1; Length 343; 100.0%; Pred. No. 33; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l protein.
343 AA; 39650 MW; D340B49A4924B7D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical MO25-like protein At5g47540.
AT5G47540 OR MNJ7.13.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 343 AA.
                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z97343; CAB10508.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL161546; CAB78730.1; -. EMBL; AF380659; AAK55740.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB025628; BAB09080.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
Pfam; PF03204; Mo25; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
Pfam; PF03204; Mo25; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 EAFHVFK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 EAFHVEK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MO2N_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPFGK3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MO2N ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 20
    ð
```

Matches

Š

RESULT 21

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN=16M / ATCC 23456 / Biotype 1;

MEDLINE=20020109; PubMed=11756688;

MEDLINE=20020109; PubMed=11756688;

Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Rezzik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.;

"The genome sequence of the facultative intracellular pathogen Brucella melitensis.";

Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).

-!- CATALYTIC ACTIVITY: L-ornithine = L-proline + NH(3).
                                                                                                                                                                                                                       Kim J., Mayfield J.B.;
"Brucella abortus arginase and ornithine cyclodeaminase genes a
similar to Ti plasmid arginase and ornithine cyclodeaminase.";
Biochim. Biophys. Acra 1334:55-57(1997).
-! - CATALYTIC ACTIVITY: L-ornithine = L-proline + NH(3).
                                                                                                                                                                                                                                                                                                                                                        -1- PATHWAY: Arginine degradation, second step.
-1- SIMILARITY: Belongs to the ornithine cyclodeaminase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- PATHWAY: Arginine degradation; second step.
                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBL_TaxID=235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 7; DB 1; Length 359;
100.0%; Pred. No. 35;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003462; ODC_Mu_crystall.
Pfam; PF02423; ODC_Mu_crystall; 1.
Lyase; NAD; Arginine metabolism.
SEQUENCE 359 AA; 39420 MW; 94CFD9C69CB785F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ocnithine cyclodeaminase (BC 4.3.1.12) (OCD).
ARCB OR BMEII0397.
      Ornithine cyclodeaminase (EC 4.3.1.12) (OCD)
                                                                                                                                                                                                       MEDLINE=98041640; PubMed=9375792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U57319; AAC05589.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 EKLLQSE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 EKLLQSE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brucella melitensis.
                                                                                                                                                         SEQUENCE FROM N.A.
                                                Brucella abortus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BRUME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCD_BRUME
ID OCD 1
      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-22247741; PubMed=12271122;
MEDLINE-22247741; PubMed=12271122;
Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J., Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E. Riedmuller S., Terlerin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.; "The Brucella suis genome reveals fundamental similarities between
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: Arginine degradation; second step.
                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBI_TaxID=29461;
                                       2.1%; Score 7; DB 1; Length 343; 100.0%; Pred. No. 33; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 7; DB 1; Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     animal and plant pathogens and symbionts.", Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003462; ODC_Mu_crystall.
Pfam; PF02423; ODC_Mu_crystall; 1.
Lyase; NAD; Arginine metabolism; Complete proteome.
SEQUENCE 358 AA; 39299 MW; DA2F02B1171B4C81 CRC64;
343 AA; 39457 MW; 46950D6A9A82FBB5 CRC64;
                                                                                                                                                                                                                                                                                                                     15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Anchthine cyclodeaminase (BC 4.3.1.12) (OCD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                        358 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Prea. w.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE014583; AAN34071.1; -
                                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                              272 EAFHVFK 278
                                                                                                                                                                     278 EAFHVFK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 EKLLQSE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 EKLLQSE 352
                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COFACTOR: NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Brucella suis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; BRA0899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OCD_BRUAB
QS9175;
                                                                                                                                                                                                                                                                                 OCD BRUSU
QBFVE4;
SEQUENCE
                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
```

RESULT 22 OCD_BRUAB

DA LL

Matches

ð

ö

; 0

REPEAT

```
between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN-ATCC 33530 / G-37;

MEDLINE-96026346; Pubmed=756993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fleischmann R.L., Weidmann J.F., Small K.V., Sanducky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
"The minimal gene complement of Mycoplasma genitalium.";
science 270:397-403(1995).
-!- SIMILARITY: TO M.PNEUMONIAE PROTEIN P65.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 359; .35;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                   InterPro; IPR003462; ODC_Mu_crystall.
Pfam; PF02423; ODC_Mu_crystall; 1.
Lyase; NAD; Arginine metabolism; Complete proteome.
SEQUENCE 359 AA; 39460 MW; F29E90021EF950B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X DPNQQ(Q) FNQ REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Proline-rich P65 protein homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 AA.
                                                                                                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 1
100.0%; Pred. No. 35;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE009677; AAL53639.1; -.
PIR; AD3559; AD3559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U39701; AAC71436.1; -.
PIR; 164223; 164223.
TIGR; MG217; -.
                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity luc...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
100
100
111
131
1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma genitalium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 EKLLQSE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347 EKLLÖSE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
29
41
41
61
73
81
93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P65H MYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P65H MYCGE
5555555584448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIDDELLING COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD COORD C
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                   Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 392/353-358(1998).
-!- CATALYTIC ACTIVITY: 6-carboxyhexanoyl-CoA + L-alanine = 8-amino-7-oxononanoate + CoA + CO(2).
-!- COPACTOR: Pyridoxal phosphate (By similarity).
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
8-amino-7-oxonomanoate synthase (EC 2.3.1.47) (AONS) (8-amino-7-ketopelargonate synthase) (7-keto-8-amino-pelargonic acid synthetase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- PATHWAY: Biotin biosynthesis; first step.
-i- SIMILARITY: Belongs to class-II of pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                 Length 372;
                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 373; . 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
139 150 1-7.
151 162 1-8.
372 AA; 44664 MW; 4C29701D213CE19E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biotin biosynthesis; Transferase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 AA; 42532 MW; 536B34A5D5F84401 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           7-KAP synthetase (L-alanine--pimelyl CoA ligase).
                                                                 2.1%; Score 7; DB 1;
100.0%; Pred. No. 36;
                                                                                                                                                                                                                                                       373 AA.
                                                                          100.0%; Prec. Mc. tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
2.1%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02490; ALA synthase; 1.
Pfam; PF00155; aminotran 1 2; 1.
TIGRFAMS; TIGR00858; bioF; 1.
PROSITE; PS00599; AA_TRANSFER_CLASS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004839; Aminotrans I/II.
InterPro; IPR001917; Aminotrans II.
InterPro; IPR004723; BioF.
                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003408; Ala_synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000699; AAC06836.1; -.
                                                                                                   Conservative
                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aminotransferases.
                                                                                                                                 257 LMMNLLR 263
                                                                                                                                                                  324 LMMNLLR 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR, G70355; G70355.
HSSP; P12998; 1BS0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 PKLIEFL 305
                                                                            Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                         BIOF OR AQ 626.
Aquifex aeolicus.
                                                                                                                                                                                                                                                    BIOF AQUAE
066875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aeolicus.
                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
                 REPEAT
                                                                                                                                                                                                                                      BIOF AQUAE
                                                                                     Best Loc
Matches
                                                                                                                                                                                                                    RESULT 25
                                                                                                                                                                                                                                                                      FT
                                                                                                                                                                  g
                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

100.0%; Pred. No. 38;

```
Best Local Similarity
                  Matches
                                                                  ò
                                                                                                          셤
                                                                                                                                                                                                                                 HERE THE SECOND COURSE SEE THE SEE THE SECOND COURSE SEE THE SECOND COURSE SEE THE SECOND COURSE SEE THE SECOND COURSE SEE THE SECOND COURSE SEE THE SECOND COURSE SEE THE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE SECOND COURSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dorland S., Deegenaars M.L., Stillman D.J.; "Roles for the Saccharomyces cerevisiae SDS3, CBK1 and HYM1 genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Banrevi A., Ansorge W.;
"Sequencing and analysis of 51.6 kilobases on the left arm of chromosome XI from Saccharomyces cerevisiae reveals 23 open reading frames including the FAS1 gene.";
Yeast 9:1343-1348(1993).
                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maia e Silva A., Bossier P., Vilela C., Fernandes L., Soares H., Guerreiro P., Rodrigues-Pousada C.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cheret G., Mattheakis L.C., Sor F., "DNA sequence analysis of the YCN2 region of chromosome XI in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005622; C:intracellular; IDA.
GO; GO:0016564; F:transcriptional repressor activity; IMP.
GO; GO:0007109; P:cytokinesis, completion of separation; IMP.
GO; GO:0008360; P:regulation of cell shape; IGI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94205264; PubMed=8154185; Wiemann S., Voss H., Schwager C., Rupp T., Stegemann J., Zimmermann J., Grothues D., Sensen C., Erfle H., Hewitt N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45853 MW; F48860754C892BA9 CRC64;
                                                                                                                                                                                         01-OCT-1993 (Rel. 27, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics 154:573-586(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcriptional repression by SIN3.";
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAINEGREBB; PubMed=8394042; MEDLINE=93348778; PubMed=8394042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20157038; PubMed=10655212;
                                                                                                                                                                      01-0CT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, X69765, CAA49422.1; -.
EMBL, X74151, CAA52249.1; -.
EMBL, Z28189, CAA82032.1; -.
EMBL, S34681, S34681.
GermOnline, 139944, -.
SGD, S0001672, HYM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae.";
Yeast 9:661-667(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR004892; Mo25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR008938; ARM.
                                                                                                                           STANDARD;
         274 PKLIEFL 280
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            399 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      HYM1 protein.
HYM1 OR YKL189W.
                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                        YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENE NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro
                                                                                                                                           P32464;
         a
```

2.1%; Score 7; DB 1; Length 399;

Query Match

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I- PATHWAY: Exopolysaccharide biosynthesis.
-I- SUBCELLULAR LOCATION: Periplaemic (Probable).

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bainformatics and the EMBL outstation. the European Bioinformatics Institute.

The European Bioinformatics Institute.

We by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIR=RCRSO11 / SU47;
MEDLINE=93177026, PubMed=8439670;
Medlir P., Keller M., Weng W.M., Quandt J., Arnold W., Puehler A.;
"Genetic analysis of the Rhizobium meliloti exoYFQ operon: ExoY is
homologous to sugar transferases and ExoQ represents a transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE-21396508; PubMed-11481431;
Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
Golding B., Puchler A.,
"The complete sequence of the 1,683-kb psymB megaplasmid from the N2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fixing endosymbiont Sinorhizobium meliloti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
-!- FUNCTION: INVOLVED IN SUCCINOGLYCAN (EPS I) SYNTHESIS. NEEDED THE ADDITION OF THE FIRST SUGAR (GALACTOSE) TO THE ISOPRENOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXOPOLYSACCHARIDE PRODUCTION PROTEIN
     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02563; Poly export; 1.
Exopolygaccharide synthesis; Plasmid; Periplasmic; Signal;
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 AA; 45871 MW; 55D8EC55B3A469EF CRC64;
                                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Exopolysaccharide production protein exoF precursor.
EXOF OR RB1068 OR SMB20945.
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 1;
100.0%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                   (Sinorhizobium meliloti).
                                                                                                                                                                                                                                               421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein.";
Mol. Plant Microbe Interact. 6:55-65(1993).
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; D95975; D95975.
InterPro; IPR003715; Poly_export.
     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL603645; CAC49468.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pSymB (megaplasmid 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L05588; AAA26265.1;
     Conservative
                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31
                                                     222 YVTKRQS 228
                                                                                                        244 YVTKRQS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Rest Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobium meliloti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 AQLAQEL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=382;
                                                                                                                                                                                                                                            RHIME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                               EXOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pneumoniae cytoskeletal protein HMW2 and cytadherence.";
J. Bacteriol. 179:2668-2677(1997).
-!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED, WITH EPITOPES EXPOSED
AT THE CELL SURFACE (FROBABLE).
-!- DOMAIN: THE PENTA/HEXAPEPTIDES REPEATS FORM A PROLINE-RICH ACIDIC
DOWAIN: IN ADDITION, A PART OF THIS REGION CONTAINS A PERFECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proft T., Hilbert H., Layh-Schmitt G., Herrmann R.; "The proline-rich P65 protein of Mycoplasma pneumoniae is a component of the Triton X-100-insoluble fraction and exhibits size polymorphism in the strains M129 and HF."; J. Bacteriol. 177:3370-3378 (1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: The N-terminus is blocked (Probable).
POLYMORPHISM: Duplication in FH strain leads to a proline-rich domain composed of 15 repeats, instead of the 12 repeats found in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Transposon mutagenesis reinforces the correlation between Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: THE SEQUENCE SHOWN HERE IS THAT OF STRAIN FH.
                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krause D.C., Proft T., Hedreyda C.T., Hilbert H., Plagens H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X DPN (Q) AY REPEATS.
                                                                                                                                                                       P53663; P53664;
01-007-1996 (Rel. 34, Created)
10-007-1996 (Rel. 34, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
                                                                                                                                                       423 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 24:4420-4449(1996).
                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=FH, and ATCC 29342 / M129;
MEDLINE=95286529; PubMed=7768845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97252497; PubMed=9098066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.7.2.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z34978; CAA64430.1; -.
EMBL; Z34977; CAA84429.1; -.
EMBL; AE000051; AAB95175.1; -.
EMBL; U59886; AAB52526.1; -.
PIR; S73853; S73853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; Complete proteome.
DOMAIN 40 190
                                                                                                                                                                                                                                                                                                    Proline-rich P65 protein.
P65 OR MPN309 OR MP527.
                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
80
93
93
336 AQLAQEL 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIRECT REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pneumoniae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herrmann R.;
                                                                                                                                                   MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
```

REPEAT REPEAT

```
MEDINE-21016719; PubMed-11130712;

MEDINE-21016719; PubMed-11130712;

MEDINE-21016719; PubMed-11130712;

MEDINE-21016719; PubMed-11130712;

MEDINE-21016719; PubMed-11130712;

MINITEO CO., Alloafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Chenk R.F., Chin C.W.,

MINITEO C. M., Comn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fuli, C.Y.,

A hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lanz C.A., Li J.H., Li Y.-P.,

Miltscher J., Miranda M., Nguyen M., Nicram W.C., Osborne B.I.,

Miltscher J., Miranda M., Nguyen M., Nooney T., Rowley D.,

Mal G., Peterson J., Plam P.K., Rizzo M., Rooney T., Rowley D.,

Sun H., Fallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EC 4.2.1.24) (Porphobilinogen synthase) (ALADH).
AT1G69740 OR TGC23.6.
ATabidopsis thaliama (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LE 408:818-820(2000).
CATALYTIC ACTIVITY: 2 5-aminolevulinate = porphobilinogen + 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Delta-aminolevulinic acid dehydratase, chloroplast precursor
6.

7.

8.

9.

11.

12.

13.

14.

15. K (IN STRAIN M129).

B. > K (IN STRAIN M129).

MISSING (IN STRAIN M129).
                                                                                                                                                                                                                                                                                                                                                                                                           Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: Porphyrin biosynthesis; second step.
-!- SUBUNIT: Homooctamer (By similarity).
-!- SUBCELLULAR LOCATION: Chloroplast (By similarity).
-!- SIMILARITY: Belongs to the ALADH family.
                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 7; DB 1; ; Pred. No. 40; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - COFACTOR: Magnesium (By Bimilarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                    49051 MW;
                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 408:816-820(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 LMMNLLR 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    372 LMMNLLR 378
                                                                                                                                                                                                                                                                                                                                                    423 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
                              1107
1107
1108
1108
1108
1108
1108
1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEM2 ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thaliana,
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                           VARIANT
                                                                                                                                                REPEAT
                                                                                                                                                                           REPEAT
                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                   REPEAT
                                                                  REPEAT
                                                                                                                     REPEAT
                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 29
         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAHLADA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA BABARA B
```

```
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YB8G YE2
P383<u>5</u>8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YB8G_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STITES SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER SEPTEMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Suinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95562690; PubMed=7635841;
Borghese R., Wall J.D.;
"Requlation of the glnBA operon of Rhodobacter capsulatus.";
J. Bacteriol. 177:4549-4552(1995).
-!- CATALXTIC ACTIVITY: ATP + L-glutamate + NH(3) = ADP + phosphate
                                                                                                                                            PIR; D96719; D96719.
HSSP; P15002; 1B4E.
InterPro; 1PR001731; AlaD_dehydratase.
Pfam; PR0049; ALAD; 1.
PRINTS; PR00144; DALDHYDRTASE.
PRODOM; PD0002304; AlaD_dehydratase; 1.
PROSTIE; PS00169; D ALA DEHYDRAYEE; 1.
PROSTIE; PS00169; D ALA DEHYDRAYEE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- ENZYME REGULATION: The activity of this enzyme is controlled by
                                                                                                                                                                                                                                                                                                                                                                                                                             CHLOROPLAST (BY SIMILARITY).
DELTA-AMINOLEVULINIC ACID DEHYDRATASE.
MAGNESIUM-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90094270; PubMed=2152916;
Kranz R.G., Pace V.M., Caldicott I.M.;
"Inactivation, sequence, and lacz fusion analysis of a regulatory
locus required for repression of nitrogen fixation genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adenylation. The fully adenylated enzyme complex is inactive. SUBUNIT: Oligomer of 12 subunits arranged in the form of two hexagons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
Rhodobacteraceae; Rhodobacter.
NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN'1990 (Rel. 13, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase)
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the glutamine synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7; DB 1; Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44B0984247FC6147 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhodobacter capsulatus (Rhodopseudomonas capsulata)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score /; ____
100.0%; Pred. No. 41;
+ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhodobacter capsulatus.";
J. Bacteriol. 172:53-62(1990).
                                                                                                                     EMBL; AC013289; AAG52549.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast; Transit peptide.
TRANSIT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46690 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 31-438 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-130 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Overy Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLRDKSP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 LLRDKSP 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 2
351 3
430 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=B100:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RHOCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLNA_RHOCA
      HID BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BELLE BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fritz C., Hollenberg C.P., Kirchrath L., Rad M.R.;
Submitted (ANG-1994) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCCATION: Integral membrane protein (Probable).
---- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                AMP (UNDER CONDITIONS OF ABUNDANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CJ-1997 (Rel. 35, Last amotation update)
Hypothetical 51.7 kDa protein in CTP1-SUL2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 7; DB 1; Length 438; 100.0%; Pred. No. 42; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              GLUTAMINE) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48391 MW; 07B81EBF6534991F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transport; Transmembrane. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, 236162; CAA85258.1; -.
PIR, S46175; S46175.
GermOnline; 138836; -.
SGD, S0000497; YBR293M.
InterPro; IPR007114; MFS.
InterPro; IPR00714; MFS.
FRAM; PF00083; Sugar It; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
EMBL; U35953; AAA87025.1; -...
EMBL; M28244; AAA26123.1; -...
HSSP; P06201; 1LGR.
INTERPO: IRR008147; Gln synt beta.
INTERPO: IPR008146; Gln synt C.
INTERPO: IPR008146; Gln synt C.
INTERPO: IPR04809; Gln - synt; 1.
Pfam; PP00120; gln - synt; 1.
ProDom; PD001057; gln - synt C; 1.
IIGRAMS; TIGR00653; Gln Synt C; 1.
PROSITE; PS00180; GLNA 1; 1.
PROSITE; PS00181; GLNA AIP; 1.
                                                                                                                                                                                                                                                                                                                                                                       Nitrogen fixation; Ligase.
BINDING 397 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity lvv...
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50850; MFS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 VTLIADL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 VTLIADL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZBR293W OR YBR2109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=S288c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aypothetical
```

·;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fingert J.H., Ying L., Swiderski R.E., Nystuen A.M., Arbour N.C., Alward W.L.M., Sheffield V.C., Stone E.M.; "Characterization and comparison of the human and mouse GLC1A glaucoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98340858; PubMed=9675094;
Takahashi H., Noda S., Imamura Y., Nagasawa A., Kubota R., Mashima Y.,
Kudoh J., Oguchi Y., Shimizu N.;
"Mouse myocilin (Myoc) gene expression in ocular tissues.";
Biochem. Biophys. Res. Commun. 248:104-109(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Húm. Mol. Genet. 11:1291-1301(2002).
-!- FUNCTION: May participate in the obstruction of fluid outflow in
the trabecular meshwork.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Torrado M., Trivedi R., Zinovieva R., Karavanova I., Tomarev S.I.; "Optimedin: a novel olfactomedin-related protein that interacts with
                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BALB/CJ, C3H/HeJ, and C57BL/CJ; TISSUE=Brain, and Muscle; MEDLINE=98249809; PubMed=9588210; Tomarev S.I., Tamm E.R., Chang B. Moo/Tigr gene."; Characterization of the mouse Myoc/Tigr gene."; Biochem. Biophys. Res. Commun. 245:887-893(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: Homodimer. Interacts with OLFM3.
                                                                                                                                                                                                                                                                                MYOC_MOUSE STANDARD; PRT; 490 AA.
070654; 070289;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 42, Last annotation update)
MYOCILIN precursor (Trabecular meshwork-induced glucocorticoid response protein).
MYOC OR TIGR.
                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND VARIANT ALA-164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abderrahim H., Jaramillo-Babb V.L., Zhou Z., Vollrath D.; "Characterization of the murine TIGR/myocilin gene."; Mamm. Genome 9:673-675(1998):
                                                                                                                           Length 474;
                                                                                                                                                       0; Indels
                                                                                               1F3FDC877795ACFA CRC64;
                                                                                                                           DB 1;
                                                                                                                 2.1%; Scc.
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND TISSUE SPECIFICITY. STRAIN=BALB/c; TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                    POTENTIAL. POTENTIAL.
              POTENTIAL. POTENTIAL.
                                         POTENTIAL
 POTENTIAL
                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22013900; PubMed=12019210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=98217378; PubMed=9548973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98345432; PubMed=9680392;
                                                                                                51677 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 8:377-384(1998).
                                                                                                              Query Match
Best Local Similarity luv...
T, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERACTION WITH OLFM3.
 2217
2294
3324
468
                                                                                                                                                                                                              462 ILKDNLA 468
197
239
274
304
332
376
4448
474 PA;
                                                                                                                                                                                 20 ILKDNLA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=129/Sv
                                        TRANSMEM
                                                                    TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                  SEQUENCE
                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes.
                                                                                                                                                                                                                                                      RESULT 32
                                                                                                                                                                                                                                                                                      FT
FT
FT
FT
FT
SQ
                                                                                                                                                                                    ð
                                                                                                                                                                                                           g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                 POLYMORPHISM: Variant Ala-164 is found in strain BALB/cJ which has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rootlet and basal body of the connecting cilium of photoreceptor cells, and in the rough endoplasmic reticulum. Also secreted. TISSUE SPECIFICITY: Expressed in ciliary body, iris, retina, trabecular network and sclera but not in lens or cornea. Also expressed strongly in skeletal muscle and weakly in heart, brain, testis, liver, kidney, thyroid and epididymis. No expression detected in embryo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                           a low intraocular pressure. Variant Thr-164 is found in strains C3H/HeJ and C57BL/6J, two strains which have a relatively high intraocular pressure.

-!- SIMILARITY: Belongs to the olfactomedin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
T -> A (IN STRAIN BALB/CJ).
2F090571E97B0425 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLLED COIL (POTENTIAL). OLFACTOMEDIN-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005615; C:extracellular space; IDA.
GO; GO:0005515; F:protein binding; IPI.
InterPro; IPR003112; Olfac_like.
Ffan; PF02191; OLF; 1.
SWART; SM00284; OLF; 1.
Coiled coil; Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7; DB 1;
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                      entities requires a license agreement (St
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                       AF041333; AAC32805.1; JOINED. AF041334; AAC32805.1; JOINED. AF049796; AAC14265.1; --
                                                                                                                                                                                                                                                                                                                                                  JOINED.
                                                                                                                                                                                                                                                                                                                                                                JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=97094702; PubMed=8939936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1%; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55314 MW;
                                                                                                                                                                                                                                                                                                                                                  EMBL, AF049795; AAC14265.1;
EMBL, AF049794; AAC14265.1;
EMBL, AF0439869; AAC40112.1;
EMBL, AB013592; BAA32031.1;
                                                                                                                                                                                                                                                                                           EMBL; AF041335; AAC32805.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
490
170
490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419
                                                                                                                                                                                                                                                                                                                                                                                                    PIR; JE0096; JE0096.
MGD; MGI:1202864; Myoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 NLLRDKS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 1
490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CP26 BRARE
P79739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CP26_BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 33
          g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438 438 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
492 AA; 56281 MW; FD471435B2F30509 CRC64;
                                                     acid 4-hydroxylase.";
J. Biol. Chem. 271:29922-29927(1996).

-!-FUNCTION: Plays a key role in retinoic acid metabolism. Acts on retinoids, including all-trans-retinoic acid (RA) and its stereoisomer 9-cis.RA. Capable of 4-hydroxylation, hydroxylation. Responsible for generation of several hydroxylated forms of RA, including 4-OH.RA and 4-oxo-RA.

-!-SUBCELLUIAR LOCATION: Membrane-bound. Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chamoun Z., Mann R.K., Nellen D., von Kessler D.P., Bellotto M., Beachy P.A., Basler K.; "Skinny hedgehog, an acyltransferase required for palmitoylation and sctivity of the hedgehog signal."; Science 293:2080-2084(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09VZÜZ; 095VYO;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Protein-Cysteine N-palmitoyltransferase (EC. 2.3.1.-) (Rasp protein)
White J.A., Guo Y.-D., Baetz K., Beckett-Jones B., Bonasoro J., Hsu K.E., Dilworth F.J., Jones G., Petkovich M.; "Identification of the retinoic acid-inducible all-trans-retinoic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee J.D., Treisman J.E.; "Sightless has homology to transmembrane acyltransferases and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00086; CYTOCHROME P450; 1.
Oxidoreductase; Monooxygenase; Membrane; Heme; Microsome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                -!- INDUCTION: By retinoic acid.
-!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., FUNCTION, AND DEVELOPMENTAL STAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              required to generate active Hedgehog protein.";
Curr. Biol. 11:1147-1152(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Skinny hedgehog protein) (Sightless protein). RASP OR SKI OR SIT OR CG11495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          500 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 1;
100.0%; Pred. No. 46;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZFIN; ZDB-GENE-990415-44; cyp26al.
InterPro; IFRO01128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21442023; PubMed=11486055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21400488; PubMed=11509241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U68234; AAC60045.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 SLOAMKE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 SLQAMKE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 34
    à
```

```
RR SEQUENCE FROM N.A.

REAL STATISTICATION OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE OF THE CASE
```

```
-!- SIMILARITY: Belongs to the olfactomedin family.
                                                                                                                                                                                                                                                                      BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                  2.1%; Sco...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVISIONS, AND SEQUENCE OF 1-6 AND 33-37.
                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                      MYOCILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 273:6341-6350(1998)
                                                                                                                                                               EMBL; AB019393; BAA34199.1; -.
InterPro; IPR003112; Olfac_like.
Pfam; PF02191; OLF; 1.
SMART; SM00284; OLF; 1.
Coiled coil; Glycoprotein; Signa
                                                                                                                                                      EMBL; AF093567; AAD46401.1; -.
EMBL; AB019393; BAA34199.1; -.
                                                                                                                                                                                                                                                                                                                     56442 MW;
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                    502
183
502
431
229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            response protein).
MYOC OR TIGR OR GLCIA.
                                                                                                                                                                                                                                                                                                                                                                                       260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                            143 NLLRDKS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Human)
                                                                                                                                                                                                                                                                                             6
329 3
502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYOC HUMAN
                          glands
                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 36
MYOC HUMAN
                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                      ö
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAINE-Sprague-Dawley, TISSUE-Bye,
MEDLINE-20295350; PubMed=10833334;
MEDLINE-20295350; PubMed=10833334;
MOLOCULAR CLORING AN, Kubota R., Miwa S., Shishiba Y., Ozawa Y.;
"Molecular cloning and expression profile of rat myocilin.";
Mol. Genet. Metab. 70:75-80(2000).
-!-FUNCTION: May participate in the obstruction of fluid outflow in the trabecular meshwork (By similarity).
-!-SUBUNIT: Homodimer. Interacts with MYOC (By similarity).
-!-SUBCELULAR LOCATION: Located preferentially in the ciliary rootlet and basal body of the connecting cilium of photoreceptor cells, and in the rough endoplasmic reticulum. Also secreted (By
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: Highly expressed in sK+eletal muscle and
                                                                                                                                                                                                                                                                                                                                                     .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSRIJ4; Q9Z2Y4;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 40, Last annotation update)
Myocilin precursor (Trabecular meshwork-induced glucocorticoid response protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Wistar Kyoto; TISSUE=Eye;
Yaoeda K., Yamamoto T., Funaki H., Koyama Y., Nihei K., Tani
Yaoita E., Kawagaki K., Abe H., Kihara I.;
"Molecular cloning of myocilin gene from rat eye.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                           EMBL; AF393157; AAK73748.1; -.
EMBL; AF38410; AAK97480.1; -.
EMBL; AF38410; AAK97480.1; -.
EMBL; AX119202; AAM51062.1; -.
FlyBase; FBGN0024194; rasp.
C), GO:007225; P:patched receptor ligand processing; IMP.
InterPro; IPR004299; MBOAT, I.
Pfam; PF03062; MBOAT; 1.
                                                                                                                                                                                                                                                                                                                              Length 500;
                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                       4498DC306976F2A2 CRC64;
                                                                                                                                                                                                                                                                                            G -> V (IN REF. 1 AND 4)
                                                                                                                                        Transferase; Acyltransferase; Developmental protein;
                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                       2.1%; bcc.
100.0%; Pred. No. -..
0; Mismatches
                                                                                                                                                      protein; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                          502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                       POTENTIAL. POTENTIAL.
                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                        58105 MW;
                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                    Segmentation polarity
TRANSMEM 15 35
                                                                                                                                                                                                                                                                                                                                                                                                LLVTLIA 130
                                                                                                                                                                                  10,5
1134
1134
1243
2293
372
372
442
461
91
91
381
                                                                                                                                                                                                                                                                                                                                                                          78 LLVTLIA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYOC OR TIGR
                                                                                                                                                                                                TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                 ACT SITE
CONFLICT
                                                                                                                                                                                                                                  TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                 124
                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYOC RAT
                                                                                                                                                                          LRANSMEM
                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
retina. Also detected at lower levels in thyroid gland but not in other endocrine glands such as the adrenal or pituitary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98165818; PubMed=9497363; Nguyen T.D., Chen B., Johnson D., Polansky J.R.; Nguyen T.D., Chen P., Huang W.D., Chen H., an olfactomedin-related Gene Structure and properties of TIGR, an olfactomedin-related glycoprotein cloned from glucocorticoid-induced trabecular meshwork
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANTS JOAG VAL-364 AND HIS-437.
MEDINE=97158493; PubMed=9005883;
Stone E.M., Fingert J.H., Alward W.L.M., Nguyen T.D., Polansky J.R.,
Sunden S.L.F., Nishimura D., Clark A.F., Nystuen A., Nichols B.E.,
Mackey D.A., Ritch R., Kalenak J.W., Craven E.R., Sheffield V.C.;
"Identification of a gene that causes primary open angle glaucoma.";
Science 275:668-670(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      099972; 000620;
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 34). Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Myocilin precursor (Trabecular meshwork-induced glucocorticoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=9742189; PubMed=9280311;
Ortego J., Estribano J., Coca-Prados M.;
Cloning and characterization of subtracted cDNAs from a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 7; DB 1; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y -> R (IN REF. 2).
S -> A (IN REF. 2).
2FE8FBE53CF48BBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COILED COIL (POTENTIAL). OLFACTOMEDIN-LIKE.
```

2

RETITAR BARKER RETITAR BARKER RETITAR BARKER RETITAR BARKER RETITAR KERKER RETITAR BARKER RETITAR BARKER RETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BETITAR BARKER BARKER BETITAR BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARKER BARK Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Mang J., Heich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Broax S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachas S., Modan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Radiquez A.C., Garimwood J., Schmutz J., Myers R.M.,

Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

T. "Generation and initial analysis of more than 15,000 full-length SEQUENCE FROM N.A.
MEDLINE=98217378; PubMed=9548973;
Fingert J.H., Ying L., Swiderski R.E., Nystuen A.M., Arbour N.C.,
Alward W.L.M., Sheffield V.C., Stone E.M.;
"Characterization and comparison of the human and mouse GLCIA glaucoma MEDLINE=22501919; PubMed=12615070; Nagy I., Trexler M., Patthy L.; "Expression and characterization of the olfactomedin domain of human Kubota R., Noda S., Wang Y., Minoshima S., Asakawa S., Kudoh J., Mashima Y., Oguchi Y., Shimizu N., Marahima Y., Oguchi Y., Shimizu N., Marahima Y., Oguchi P., Shimizu N., A novel myosin-like protein (myocilin) expressed in the connecting cillum of the photoreceptor: molecular cloning, tissue expression, MEDLINE=98113364; PubMed=9446806; Kubota R., Kudoh J., Mashima Y., Asakawa S., Minoshima S., Hejtmancik J.F., Oguchi Y., Shimiau N.; "Genomic organization of the human myocilin gene (MYOC) responsible for primary open angle glaucoma (GLC1A)."; Biochem. Biophys. Res. Commun. 242:396-400(1998). MEDLINE=22013900; PubMed=12019210; Torrado M., Trivedi R., Zinovieva R., Karavanova I., Tomarev S.I.; ciliary body library encoding TIGR, a protein involved in juvenile open angle glaucoma with homology to myosin and olfactomedin."; FEBS Lett. 413:349-353(1997). Garchon H.-J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases. Deadman R., Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). Biochem. Biophys. Res. Commun. 302:554-561(2003). OLFACTOMEDIN DOMAIN DISULFIDE BOND. MEDLINE=22388257; PubMed=12477932; TISSUE=Retina; MEDLINE=97312692; PubMed=9169133; human and mouse cDNA sequences Genome Res. 8:377-384(1998). and chromosomal mapping."; Genomics 41:360-369(1997). INTERACTION WITH OLFM3. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE=Leukocyte; TISSUE=Brain; myocilin. genes."; 

MEDLINE=98027214; PubMed=9361308; Stoilova D., Child A., Brice G., Crick R.P., Fleck B.W., Sarfarazi M.; "Identification of a new 'TIGR' mutation in a family with juvenile-Adam M.F., Belmouden A., Binisti P., Brezin A.P., Valtot F., Bechetoille A., Dascotte J.-C., Copin B., Gomez L., Chaventre A., Bach J.-F., Garchon H.-J.; Bach J.-F., Garchon H.-J.; Bach J.-E., Garchon H.-J.; Single exon encoding the evolutionarily conserved olfactomedin-homology domain of TIGR in familial open-angle Suzuki Y., Shirato S., Taniguchi F., Ohara K., Niehimaki K., Ohta S., "Mutations in the TIGR gene in familial primary open-angle glaucoma Wiggs J.L., Allingham R.R., Vollrath D., Jones K.H., De La Paz M., Kern J., Patterson K., Babb V.L., Del Bono E.A., Broomer B.W., Pericak-Vance M.A., Haines J.L.; "Prevalence of mutations in TIGR/Myocilin in patients with adult and "Optimedin: a novel olfactomedin-related protein that interacts with Novel mutations in the TIGR gene in early and late onset open angle MEDLINE-99079298; PubMed=9863594; Stoilova D., Child A., Brice G., Desai T., Barsoum-Homsy M., Ozdemir N., Chevrette L., Adam M.F., Garchon H.-J., Pitts Crick R., "Novel TIGR/MYOC mutations in families with juvenile onset primary MEDLINE=98361153; PubMed=9697688; Morissette J., Clepet C., Moisan S., Dubois S., Winstall E., Worissette J., Clepet C., Polansky J.R., Cote G., Anctil J.-L., Amyot M., Plante M., Falardeau P., Raymond V.; "Homozygotes carrying an autosomal dominant TIGR mutation do not VARIANTS COAG LYS-352 AND MET-377, AND VARIANTS JOAG LEU-370 AND Polansky J., Nguyen T., Timmerman V., van Broeckhoven C., Naumann G.O.H., Pfeiffer R.A., Rautenstrauss B.W.; "Juvenile open angle glaucoma: fine mapping of the TIGR gene to 1q243-q25.2 and mutation analysis."; Hum. Genet. 102:103-106(1998). Mansergh F.C., Kenna P.F., Ayuso C., Kiang A.-S., Humphries P., VARIANTS JOAG LEU-370; ALA-380 AND PRO-502, AND VARIANT LYS-76. MEDLINE=98141135; PubMed=9490287; Michels-Rautenstrauss K.G., Mardin C.Y., Budde W.M., Liehr T., POAG AKG-246; LEU-370; SER-477; LYS-480 AND PHE-499. 37472461; PubMed=9328473; VARIANT COAG ARG-367, AND VARIANT JOAG PHE-426. juvenile primary open-angle glaucoma."; Am. J. Hum. Genet. 63:1549-1552(1998). ... udpan."; Am. J. Hum. Genet. 61:1202-1204(1997) [13] onset primary open angle glaucoma."; Ophthalmic Genet. 18:109-118(1997). myocilin.", Hum. Mol. Genet. 11:1291-1301(2002) Hum. Mol. Genet. 6:2091-2097(1997). VARIANTS JOAG ARG-367 AND LEU-370. VARIANTS JOAG ARG-367 AND LEU-370. MEDLINE=99008006; PubMed=9345106; MEDLINE=98180724; PubMed=9521427; MEDLINE=99011274; PubMed=9792882; Med. Genet, 35:989-992(1998). Mutat. 11:244-251(1998). manifest glaucoma."; Nat. Genet. 19:319-321(1998). [20] angle glaucoma." VARIANT POAG GLU-423. VARIANT JOAG ARG-337. VARIANTS POAG ARG MEDLINE=97472461; Sarfarazi M.; glaucoma." glaucoma.' open

```
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Ananatides P.G., Scherer S.E., Li P.W., Hoskins K.A., Galle R.F.,
Ananatides P.G., Scherer S.E., Li P.W., Hoskins K.A., Galle R.F.,
As bandatides P.G., Scherer S.E., Holt W., Hoskins K., Headerson S.N.,
B. Bardon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
A Baria W. B.W., Barter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.W., Baros P.V., Berman B.P., Bhandari D., Bolshakov S.,
Abril J.F., Agbayani A., Butler H., Cadieu E., Genter A., Chandra I.,
RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P.,
RA Borkova D., Botchan W.R., Dauler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Perrara C., Ferriera S., Fleischmann W.,
RA Dodson K., Doup L. E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabrielian A.B., Garrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Hehman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Liasko P., Lei Y., Lei Y., Liang Y., Lin X.,
RA Liasko P., Lei Y., Mattei B., McInrosh T.C., Morris J., Morberson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Morperson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                         MEDLINE=99214031; PubMed=10196380;
Fingert J.H., Heon E., Liebmann J.M., Yamamoto T., Craig J.E.,
Rait J., Kawase K., Hoh S.-T., Buys Y.M., Dickinson J., Hockey R.R.,
Williams-Lyn D., Trope G., Kitazawa Y., Ritch R., Mackey D.A.,
              MEDLINE=98181799; PubMed=9535666;
Alward W.L.M., Fingert J.H., Coote M.A., Johnson A.T., Lerner S.F.,
Junqua D., Durcan F.J., McCartney P.J., Mackey D.A., Sheffield V.C.,
                                                                                                                                                                                        MEDLINE=99264259; PubMed=10330365;
Yoon S.-J.K., Kim H.-S., Moon J.-I., Lim J.M., Joo C.-K.;
"Mutations of the TIGR/MYOC gene in primary open-angle glaucoma in
                                                                                            features associated with mutations in the chromosome 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              535 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Prea. ....
                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 7; I
.00.0%; Pred. No.
                                                                                                              open-angle glaucoma gene.";
New Engl. J. Med. 338:1022-1027(1998).
                                                                                                                                                                                                                                                                  J. Hum. Genet. 64:1775-1778(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                             VARIANTS POAG, AND VARIANTS.
VARIANTS POAG, AND VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 NLLRDKS 150
                                                                                                                                                                     VARIANT JOAG ILE-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYP4C3 OR CG1438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Berkeley;
                                                                         Stone E.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DROME
                                                                                              'Clinical
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                     Korea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 37
C4C3_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C4C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch):
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Remington K., Sanders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Xhen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.W., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 481 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
535 AA; 60757 MW; 0C78200AC2D35979 CRC64;
                                                                                                                                                                                                                                                                                     STRAIN=Berkeley; TISSUB=Head;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.W.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R.A., Gonzalez M., Glarin H., Kronmiller B., Li P.W., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J.M., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase, Monooxygenase, Membrane, Heme, Microsome,
Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the cytochrome P450 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 1;
100.0%; Pred. No. 50;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   762 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR001128, Cytochrome_P450.
Pfam, PF00067, p450, 1.
PRINTS, PR00385, P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Haag-79;
MEDLINE=96262181; PubMed=8676871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE003775; AAF57098.1; -. EMBL; BT010108; AAQ2557.1; -. EMBL; U34323; AAA80657.1; -. FlyBase; FBgn0015032; Cyp4c3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 347-472 FROM N.A.
                                                                                                                                                                                                                                       Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity luv...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 LIGELIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLGELIL 521
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                     S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 38
PMIP_SCHPO
ID PMIP_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               515
                                                                                                                                                                                                                                                                                                                                                                                                   Celniker
           a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
```

```
THE HEAVE BEARED BY A REAL FOR SOLUTION AND A REAL FROM THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FOR THE FO
FT
SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAY

WOOD V., GWilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RADINE=2184801; PubMed=11859360;

WOOD V., GWilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RODINES G., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RADOWS K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RADOWS K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RADORS E., Hornsby T., Howarth S., Hudgel T., Feltwell T., Fraser A.,

Gentles S., Goble A., Hamilin N., Harris D., Hidalo J., Nodesn G.,

RADOROWS E., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,

Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,

RADOROWS P., Moule S., Mungall K., Mulchel B.J., Milten J.,

RADOROWS P., Moule S., Mungall K., Milter B., Nodell C.,

Skelton J., Simmondan B., Squares R., Squares R., Sharp S.,

Alor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RADOWARI J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RADOR K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RADOROWAR M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RADOROWAR G., Walsh W., Fritzc C., Holzer E., Moestl D., Mottier S.,

RADOROWAR G., Walsh W., Fillardin C., Moore K., Hurst S.M.,

Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

Galibert R., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

BORTOWN R., Condet M., Galillardin C., Tallada V.A., Galzon A., Thode G.,

RADOROWAR M., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RADOROWAR M., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

Rhadres M., Rochelt W., Ballsen I., Potashkin J.,

Shpakovski G.V. Ussery D., Barrell B.G., Nurse P.;

RINGHINGEL P. B. Rinker M. P. Moreno S., Munter P., Benito J.,

RINGHINGEL P. B. Rinker M. M. Reinhard M. M. Reinhard M. M. Reinhard M. M. Reinhard M. M. Reinhard M. M. Reinhard M. M. Reinhard M. M. Reinhard M. M. Reinhard M. M. Reinhard M. M. Reinhard M. M. Reinhard M. M. Reinhard M. M. Reinhard M. M. Reinhard M. M. Reinhard M. M. Reinhard M. M. Reinhard M. M. M. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Cleaves proteins, imported into the mitochondrion, to their mature size (By similarity).
-!- CATALYTIC ACTIVITY: Release of an N-terminal octapeptide as second stage of processing of some proteins imported in the
                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-203 (Rel. 41, Last annotation update)
Probable mitochondrial intermediate peptidase, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolage; Metalloprotease; Zinc; Transit peptide; Mitochondrion.
TRANSIT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROBABLE MITOCHONDRIAL INTERMEDIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZINC (CATALYTIC) (BY SIMILARITY)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COFACTOR: Binds 1 zinc ion (By similarity). SUBCELLULAR LOCATION: Mitochondrial matrix. SIMILARITY: Belongs to peptidase family M3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEPTIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenebB SPombe, SPACIF3.10c, -.
InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001657; Peptidase_M3.
Pfam; PF01422; Peptidase M3; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z70690; CAA94628.1; -. PIR; T38081; T38081.
MEROPS; M03.006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     544
545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                762
                                                                                                                                                                                                                   (EC 3.4.24.59) (MIP).
SPAC1F3.10C.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
ACT_SITE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
16-DEC-1998 (Rel. 37, Last annotation update)
16-DEC-1998 (Rel. 37, Last sequence)
16-DEC-1998 (Rel. 37, Last sequence)
16-DEC-1998 (Rel. 37, Last sequence)
17-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 38-DEC-1998)
18-DEC-1998 (Rel. 38-DEC-1998)
18-DEC-1998 (Rel. 38-DEC-1998)
18-DEC-1998 (Rel. 38-DEC-1998)
18-DEC-1998 (Rel. 38-DEC-1998)
18-DEC-1998 (Rel. 38-DEC-1998)
18-DEC-1998 (Rel. 38-DEC-1998)
18-DEC-1998 (Rel. 38-DEC-1998)
18-DEC-1998 (Rel. 38-DEC-1998)
18-DEC-1998 (Rel. 38-DEC-1998)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Rel. 37, Last sequence)
18-DEC-1998 (Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Two new genes, PHO86 and PHO87, involved in inorganic phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005315; F:inorganic phosphate transporter activity; IGI.
GO; GO:0006817; P:phosphate transport; IGI.
InterPro; IRR004331; SPX.
Pfam; PF03105; SPX; 1.
Phosphate transport; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=S288G / FY1679;
MEDLINE=91181345; PubMed=1964349;
Thierry A., Fairhead C., Dujon B.;
"The complete sequence of the 8.2 kb segment left of MAT on chromosome III reveals five ORFs, including a gene for a yeast
                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uptake in Saccharomyces cerevisiae.";

Curr. Genet. 29:344-351(1996).

-!- FUNCTION: Involved in the uptake of inorganic phosphate...
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potentia L. SIMILARITY: BELONGS TO THE SLC13A FAMILY OF TRANSPORTERS...
448 ZINC (CATALYTIC) (BY SIMILARITY).
551 ZINC (CATALYTIC) (BY SIMILARITY).
86285 MW; C6420C1F99001EFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bun-Ya M., Shikata K., Nakade S., Yompakdee C., Harashima S.,
                                                                                                                                                                          Length 762;
                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                      68;
                                                                                                                                                                               2.1%; Score 7; DB 1
100.0%; Pred. No. 68;
trive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96171517; PubMed=8598055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X56909; CAA40229.1; -. EMBL; X59720; CAA42304.1; -.
                                                                                                                                       Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keast 6:521-534(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S12919; MMBY7C.
GermOnline; 138943; -
SGD; S0000633; PHO87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHO87 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                        321 ADLQLID 327
             548 5
551 5
762 AA;
                                                                                                                                                                                                                                                                                                                                                 84 ADLQLID 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           584
628
668
708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ribokinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PH87_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oshima Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                             METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P25360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 39
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license@isb-sib.ch).
                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular characterization of the family of the N-methyl-D-aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92271257; PubMed=1350383;
Monyer H., Sprengel R., Schoepfer R., Herb A., Higuchi M., Lomeli H.,
Burnashev N., Sakmann B., Seeburg P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor subunits.";
J. Biol. (Gem. 268:2836-2843(1993).

J. Biol. (Gem. 268:2836-2843(1993).

-!- FUNCTION: NMDA RECEPTOR SUBTYPE OF GLUTAWATE-GATED ION CHANNELS POSSESSES HIGH CALCIUM PERMEABILITY AND VOLTAGE-DEPENDENT SERNSITYLYTY TO MAGNESIUM AND IS MODULATED BY GLYCINE.

-!- SUBUNIT: Heterodimer of an epsilon subunit and a zeta subunit.

-!- SUBUNITY: Belongs to the ligand-gated ionic channel family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Heteromeric NMDA receptors: molecular and functional distinction of
                                                                                                                                                                                                 Gaps
                                POLENTAL

POTENTIAL

POTENTIAL

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 41, Last annotation update)
38-FEB-2003 (Rel. 41, Last annotation update)
Glutamate [NMDA] receptor subunit epsilon 3 precursor (N-methyl D-aspartate receptor subtype 2C) (NR2C) (NMDAR2C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=91155102; PubMed=8428958;
IShii T., Moriyoshi K., Sugihara H., Sakurada K., Kadotani H.,
Yokoi M., Akazawa C., Shigemoto R., Mizuno N., Masu M.,
Nakanishi S.;
                                                                                                                                                                                                 ô
                                                                                                                                                                 DB 1; Length 923;
                                                                                                                                                                                                 0; Indels
                                                                                                                    372 N-LINKED (GLCNAC. . .) (POT 102549 MW; D168FC52FE26C5CB CRC64;
                                                                                                                                                                                                Mismatches
                                                                                                                                                                 2.1%; Score 7; D
100.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001320; Ion_glu receptor. InterPro; IPR001508; NMDA receptor. InterPro; IPR001311; SBP/\overline{g}lu_receptor.
POTENTIAL
                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D13212; BAA02499.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M91563; AAA41713.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 256:1217-1221(1992).
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
756
788
823
870
919
1162
202
                                                                                                                                                                                                                                                             784 SSGLLVT 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P19491; 1GR2.
                                                                                                                                                                                                                                75 SSGLLVT 81
                                                                                                                                                                                   Best Local Similarity
Matches 7; Conserv
                                                                                                                                       923 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
 736
768
803
850
899
162
202
274
                                                                                                                                                                                                                                                                                                                                     NME3 RAT
Q00961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subtypes.
                                                                          CARBOHYD
CARBOHYD
                                                                                                       CARBOHYD
CARBOHYD
                              TRANSMEM
TRANSMEM
                                                                                                                                       SEQUENCE
                                                                                                                                                                    Query Match
                                                             TRANSMEM
 TRANSMEM
                 FRANSMEN
                                                                                                                                                                                                                                                                                                          RESULT 40
                                                                                                                                                                                                                                                                                                                                         FT
FT
FT
FT
FT
FT
SO
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                           0
Pfam; PF00060; lig_chan; 1.
PRINTS; PR00177; NUMARECEPTOR.
SMART; SW00079; PBRe; 1.
Receptor; Postsynaptic membrane; lonic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92310564; PubMed=1377365;
Kutsuwada T., Kashiwabuchi N., Mori H., Sakimura K., Kushiya E.,
Araki K., Meguro H., Masaki H., Kumanishi T., Arakawa M.,
Mishina M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-UTN-1994 (Rel. 29, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutamate [NMDA] receptor subunit epsilon 3 precursor (N-methyl)
D-aspartate receptor subtype 2C) (NR2C) (NMDAR2C).
                                                                                                                                                                                    (GLCNAC. . ) (POTENTIAL)
(GLCNAC. . ) (POTENTIAL)
(GLCNAC. . ) (POTENTIAL)
(GLCNAC. . ) (POTENTIAL)
                                                                                                                                                                                                                                                                                           ;
0
                                                            POTENTIAL. GIMDA] RECEPTOR SUBUNIT
                                                                                                                                                              FUNCTIONAL DETERMINANT OF NMDA RECEPTORS (BY SIMILARITY).
N-LINKED (GLCNAC. ) (POTENTI
                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 1; Length 1237;
                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                         MW; B175993804B337A4 CRC64;
                                                                                    EPSILON 3. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular diversity of the NMDA receptor channel.";
Nature 358:36-41(1992).
                                                                                                                                                                                                                                                                               1.1e+02;
                                                                                                              1 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1239 AA.
                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                     N-LINKED
N-LINKED
                                                                                                                                                                                                                                N-LINKED
                                                   Calcium; Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D10694; BAA01536.1; -. PIR; I49705; I49705.
                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                             135271
                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                     337
                                                             1237
                                                                                                                                                                                                                               539 53
1237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                 101 TEAVAOL 107
                                                                                                                                                                                                                                                                                                                         63 TEAVAQL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                NME3 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVISIONS.
                                                                                                                TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                      RANSMEM
                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                              201098;
                                                               SIGNAL
                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 41
NME3 MOUSE
                                                                            CHAIN
                                                                                                                                                                     SITE
                                                                                                                                                                                                                                                                                                                                                                                                                  g
  챵
```

```
DOMAIN
RA MEDLINE-21846401; PubMed=11859360;
RA MEDLINE-21846401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Squorso Y., Peat N., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gonge P., Hornsby T., Howarth S., Hudtle E.J., Hunt S., Jagels K.,
A Mooney P., Moule S., Mingall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Noules S., Mingall K., Murphy L., Niblett D., Odell C.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Retton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Moodward J., Volckaert G., Tivey A., Walsh S.V., Warren T., Whitherd H.,
RA Mottiens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T. M.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T. M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert P., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Taloco A., Thode G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNG2_SCHPO STANDARD; PRT; 1489 AA.
014188; 9208G0;
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
Ras GTPase-activating-like protein rng2 (Ring assembly protein 2).
RNG2 OR SPAC4F8.13C.
                                                                                                                                                                                                                                                                                                                                                            FUNCTIONAL DETERMINANT OF NMDA RECEPTORS (BY SIMILARITY).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                           Receptor; Signal; Transmembrane; Postsynaptic membrane; Calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                             POTENTIAL.
GLUTAMATE [NMDA] RECEPTOR SUBUNIT
EPSILON 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 1239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          793E8E731E20C3C9 CRC64;
                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                    1 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
2.1%; Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.16
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
              MGD; MGI:95822; Grin2c.
InterPro; IRRO01120; Ion glu receptor.
InterPro; IPR001310; NMDA_receptor.
InterPro; IPR001311; SBP/Glu_receptor.
Pfam; PF00006; I.g. Chan; 1.
PRINTS; PR00177; NMDARECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135420 MW;
                                                                                                                                                                                  onic channel; Magnesium.
                                                                                                                                                                                                                        1239
                                                                                                                                                                                                                                                                                                                                           835
612
                                                                                                                                                                                                                                                                                                                                                                                                                          337
438
539
                                                                                                                                                                                                                                                                                                                          647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     539 53
1239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 TEAVAOL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 TEAVAQL 69
  HSSP; P19491; 1GR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                               438
                                                                                                                                                                                                                                                               20
554
597
627
815
                                                                                                                                                                                                                                                                                  TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                        TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 42
RNG2 SCHPO
                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                   SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HID DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DIT I DI
  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Large-scale screening of intracellular protein localization in living fission yeast cells by the use of a GFP-fusion genomic DNA library."; Genes Cells 5:169-190(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98298927; PubMed=9635188;
BDG K., Naqvi N.I., Wong K.C.Y., Balasubramanian M.K.;
Bng K., Naqvi N.I., Wong K.C.Y., Balasubramanian M.K.;
Bng K., Naqvi N.I., Wong K.C.Y., Balasubramanian M.K.;
Engles, a protein required for cytokinesis in fission yeast, is a component of the actomyosin ring and the spindle pole body.";
Curr. Biol. 8:611-621(1998).
-!- FUNCTION's Required for cytokinesis. Component of the contractile F-actin ring; required for its construction following assembly of F-actin ring; required for its construction following assembly of F-actin ring. Interestes with calmodulin.
-!- SUBMUIT: Interestes with calmodulin.
-!- SUBCELLULAR LOCATION: Localized to the F-actin ring and spindle pole body during interphase and mitosis. Also found in
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Userey D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00033; CH; 1.
SMART; SM00033; CB; 4.
SMART; SM000125; 1Q; 4.
SMOSTE; PS50021; CH; 1.
PROSITE; PS50016; IQ; 6.
PROSITE; PS50018; RAS GPPASE ACTIV 2; 1.
Cell division; Septation; Calmodulin-binding; Repeat; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                         Ding D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.
-!- SIMILARITY: Contains 6 IQ domains.
-!- SIMILARITY: Contains 1 Ras-GAP domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Geneba Spowbe, SPAC4F8.13c, -. Geneba Spowbe, SPAC4F8.13c, -. Go, GO:0030428, C:contractile ring (sensu Fungi); IDA. GO; GO:0030428, C:septum; IDA. GO; GO:0005448, C:septum; IDA. GO; GO:0005416; C:septum; IDA. GO; GO:005516; F:calmodulin binding; IPI. InterPro; IPR001715; Calponin.like. InterPro; IPR001936; RasGAAP. InterPro; IPR001936; RasGAAP. InterPro; IPR000593; RasGAAP. InterPro; IPR000593; RasGAAP. Fram; PP003077; CH; 1. Pfam; PP00317; CH; 1.
                                                                                                                                                                                                                                                                                    SEQUENCE OF 354-531 FROM N.A., AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                        STRAIN=968 h90;
MEDLINE=20223868; PubMed=10759889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1001.
1002.
1004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z98530; CAB11059.1; -.
EMBL; AB027779; BAA87083.1; -.
PIR; T38842; T38842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00616; RasGAP; 1.
Pfam; PF03836; RasGAP_C; 1.
ProDom; PD008735; RasGAP_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hiraoka Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                 ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: Involved in reticulocyte adhesion. Specifically binds to human reticulocyte cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL ATTACHMENT SITE (POTENTIAL)
CELL ATTACHMENT SITE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RETICULOCYTE BINDING PROTEIN 1. EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92315338; PubMed-1617731;
Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.;
"A reticulocyte-binding protein complex of Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 1; Length 2869; 00.0%; Pred. No. 2.2e+02;
                                                                    Length 1489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
         B54 1077 RAS-GAP.
1330 1364 COILED COLL (POTENTIAL).
1489 Aa; 171676 MW; 7D357FF9A7FED5EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2869 AA; 330213 MW; B9DBE442205EBCFF CRC64;
                                                                                                 0; Indels
COILED COIL (POTENTIAL).
                                                                    Score 7; DB 1; Ler
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                            (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 3433 AA.
                                                                                                                                                                                                                                PRT; 2869 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Preα. κ...
tive 0; Mismatches
                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malaria; Receptor; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: Homodimer (Potential).
-!- SUBCELLULAR LOCATION: Membrane-bound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC
                                                                                                                                                                                                                                                                                                        Reticulocyte binding protein 1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                    Plasmodium vivax (strain Belem)
                                                                      Query Match
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M88097; AAA29743.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                   7; Conservative
                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 69:1213-1226(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2869
2807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2826
2869
1032
2601
770
1077
1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 SLKLLGE 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 SLKLLGE 234
                                                                                                                             194 HKVLVAD 200
                                                                                                                                                        925 HKVLVAD 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=31273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2827
1030
2599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995
01-NOV-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                       merozoites."
                                                                                                                                                                                                                                                            01-APR-1993
                                                                                                                                                                                                                                RBP1 FLAVB
Q007<u>9</u>8;
                                                                                                                                                                                                                                                                             01-APR-1993
                                                                                                                                                                                                                                                                                         10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UTRO HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P46939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 44
UTRO_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
             DOMAIN
                                                                                                 Matches
                                                                                                                                                                                                                                                ò
FT
FT
SO
                                                                                                                              ð
                                                                                                                                                        g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96162017; PubMed=8576247; Ahn A.H., Feener C.A., Gussonh E., Yoshida M., Ozawa E., Kunkel L.M.; Ahn A.H., Feener C.A., Gussonh E., Yoshida M., Ozawa E., Kunkel L.M.; "The three human syntrophin genes are expressed in diverse tissues, have distinct chromosomal locations, and each bind to dystrophin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Crystal structure of the actin-binding region of utrophin reveals a head-to-tail dimer."; Structure 7:1539-1546(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The 2.0-A structure of the second calponin homology domain from the actin-binding region of the dystrophin homologue utrophin."; J. Mol. Biol. 285:1257-1264(1999).
                                                                                                                                                                                                                                                           INTERACTION WITH SNTB1.
MEDLINE-95146543; PubMed=7844150;
Ahn A.H., Kunkel L.M.;
Syntrophin binds to an alternatively spliced exon of dystrophin.";
J. Cell Biol. 128:363-371(1995).
                                                                                                                  SEQUENCE FROM N.A.
MEDILINE-39306045; PubMed=1461283;
Tinsley J.M., Blake D.J., Roche A., Fairbrother U., Ries J.,
Byth B.C., Knight A.E., Kendrick-Jones J., Suthers G.K., Love D.R.,
Edwards Y.H., Davies K.B.;
"Primary structure of dystrophin-related protein.";
Nature 360:591-593(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 31-256.
MEDDINE=20113481; Pubmed=10647184;
Keep N.H., Winder S.J., Moores C.A., Walke S., Norwood F.L.M.,
Rendrick-lones J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Contains 2 calponin-homology (CH) domains.
-!- SIMILARITY: Contains 1 WW domain.
-!- SIMILARITY: Contains 20 spectrin repeats.
-!- SIMILARITY: Contains 1 ZZ-type zinc finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99141377; PubMed=9887274;
Keep N.H., Norwood F.L.M., Moores C.A., Winder S.J.,
Kendrick-Jones J.;
(Dystrophin-related protein 1) (DRP1) (DRP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 144-261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDB; 1BHD; 16-FEB-99.

PDB; 1QAG; 01-JAN-00.
Genew, HGNC:12635; UTRN.
MIM; 128340; —
GO; GO:0005856; C:cytoskeleton; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 271:2724-2730(1996)
                                                                                                                                                                                                                                                                                                                                                                    INTERACTION WITH SNTA1 AND SNTB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X69086; CAA48829.1; -. PIR; S28381; S28381.
                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        its relatives.";
                                                                                 NCBI_TaxID=9606;
                  DMD
 Utrophin
```

```
TURN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  genes.";
                                                                                                                                                                                                                                                                                                                                                                                       ERRATUM
                                                                                                                RESULT 45
LYST MOUSE
    HELIX
                                                                                                                                SHR
                                                                          ð
                                                                                         셤
R GO; GO:0005624; C:membrane fraction; TAS.
R GO; GO:0005886; C:plasma membrane; TAS.
R GO; GO:0005886; C:plasma membrane; TAS.
R GO; GO:000517; P:muscle contraction; TAS.
R GO; GO:000517; P:muscle contraction; TAS.
R InterPro; IPR001715; Calponin-like.
R InterPro; IPR001202; WW Bectrin.
InterPro; IPR001202; WW PECTION.
R InterPro; IPR001202; WW PECTION.
R InterPro; IPR001202; WW PECTION.
R PFW, PF00397; CH; 2.
R PFW, PF00397; CH; 2.
R PfW; PF00397; CH; 2.
R PfW; PF00397; CH; 2.
R SWART; SM00150; SPEC; 19.
R SWART; SM00150; SPEC; 19.
R SWART; SM00150; ACTININ 1; 1.
R PROSITE; PS00109; ACTININ 2; 1.
R PROSITE; PS00101; ACTININ 1; 1.
R PROSITE; PS01159; WW DOMAIN 1; 1.
R PROSITE; PS01159; WW DOMAIN 1; 1.
R PROSITE; PS01159; WW DOMAIN 1; 1.
R PROSITE; PS01159; ZF ZZ 1; 1.
R PROSITE; PS01157; ZF ZZ 1; 1.
R PROSITE; PS01157; ZF ZZ 1; 1.
R PROSITE; PS01157; ZF ZZ 1; 1.
R PROSITE; PS01157; ZF ZZ 1; 1.
R PROSITE; PS01157; ZF ZZ 1; 1.
R PROSITE; PS01157; ZF ZZ 1; 1.
R PROSITE; PS01157; ZF ZZ 1; 1.
R PROSITE; PS01157; ZF ZZ 1; 1.
R PROSITE; PS01157; ZF ZZ 2; 1.
R PROSITE; PS01157; ZF ZZ 2; 1.
R PROSITE; PS01157; ZF ZZ 2; 1.
R PROSITE; PS01157; ZF ZZ 2; 1.
R PROSITE; PS01157; ZF ZZ 2; 1.
R PROSITE; PS01157; ZF ZZ 2; 1.
R PROSITE; PS01157; ZF ZZ 2; 1.
R PROSITE; PS01157; ZF ZZ 2; 1.
R PROSITE; PS01157; ZF ZZ 2; 1.
R PROSITE; PS01157; ZF ZZ 2; 1.
R PROSITE; PS01157; ZF ZZ 2; 1.
                                                                                                                                                                                                  Repeat, 3D-structure; Zinc-finger.
DOMAIN 1 246 ACTIN-BINDING.
DOMAIN 150 CH 1.
DOMAIN 150 252 CH 1.
REPEAT 253 308 SPECTRIN 1.
REPEAT 309 417 SPECTRIN 2.
REPEAT 418 526 SPECTRIN 2.
REPEAT 697 SPECTRIN 4.
REPEAT 697 SPECTRIN 4.
REPEAT 697 SPECTRIN 6.
                                                                                                                                                                                                                                                                                                                                                SPECTRIN 15.
SPECTRIN 16.
SPECTRIN 17.
                                                                                                                                                                                                                                                  SPECTRIN SPECTRIN SPECTRIN SPECTRIN SPECTRIN SPECTRIN SPECTRIN SPECTRIN SPECTRIN SPECTRIN SPECTRIN 1
                                                                                                                                                                                                                                                                                                                                                                              SPECTRIN SPECTRIN 2
                                                                                                                                                                                                                                                                                                                         SPECTRIN
                                                                                                                                                                                                                                                                                                                                         SPECTRIN
                                                                                                                                                                                                                                                                                                                                                                         SPECTRIN
                                                                                                                                                                                                                                                                                                                                 SPECTRIN
                                                                                                                                                                                                                                                                                                                                                                                                      ZZ-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                              1649
1753
1968
2081
2333
                                                                                                                                                                                                                                                                                                                                                        2440
2556
2636
2688
2797
                                                                                                                                                                                                                                                                                                                                                                                              2845
3111
                                                                                                                                                                                                                                                                                                                                                                                                                                                             103
1112
1118
1120
1136
1152
1164
1167
                                                                                                                                                                                                                                                                                                                                 1910
1976
2258
2399
2443
                                                                                                                                                                                                                                                                                                                                                                        2559
2658
2691
                                                                                                                                                                                                                                                                                                                                                                                              2812
                                                                                                                                                                                                                                                                                                          432
                                                                                                                                                                                                                                                                                                                         .652
                                                                                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
DOMAIN
ZN FING
HELIX
                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
                                                                                                                                                                                                                                                                                  REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                     TURN
TURN
HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                            TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TURN
HELIX
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TURN
HELIX
HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TURN
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      positional cloning.";
Nat. Genet. 13:303-308(1996).
-!- FUNCTION: May be required for sorting endosomal resident proteins into late multivesicular endosomes by a mechanism involving
                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96353977; PubMed=8717042; Barbosa M.D.F.S., Nguyen Q.A., Tchernev V.T., Ashley J.A., Detter J.C., Blaydes S.M., Brandt S.J., Chotai D., Hodgman C., Detter J.C., Blaydes S.M., Brandt S.J., Chotai D., Hodgman C., "Solari R.C.E.S., Lovett M., Kingsmore S.F.," "Identification of the homologous beige and Chediak-Higashi syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percu C.M., Moore K.J., Nagle D.L., Misumi D.J., Woolf E.A.,
Percu C.M., Monton L., Brody T.B., Dussault B.J., Monroe C.A.,
Duyk G.M., Pryor R.J., Li L., Justice M.J., Kaplan J.;
"Identification of the murine beige gene by YAC complementation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYST_MOUSE STANDARD; PRT; 3788 AA.
P97412.2 062403. OBVBS6;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Lysosomal trafficking regulator (Beige protein) (CHS1 homolog).
CHS1 OR LYST OR BG.
                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=97358584; PubMed=9215680;

Barbosa M.D.F.S., Barrat F.J., Tchernev V.T., Nguyen Q.A.,

Mishra V.S., Colnam S.D., Pastural E., Dufourcq-Lagelouse R.,

Fischer A., Holcombe R.F., Wallace M.R., Brandt S.J.,

De Saint Basile G., Kingsmore S.F.,

"Identification of mutations in two major mRNA isoforms of the
Chediak-Higashi syndrome gene in human and mouse.";

Hum. Mol. Genet. 6:1091-1098(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barbosa M.D.F.S., Nguyen Q.A., Tchernev V.T., Ashley J.A., Detter J.C., Blaydes S.M., Brandt S.J., Chotai D., Hodgman C., Solari R.C.E.S., Lovett M., Kingsmore S.F.;
                                                                                                                                                  DB 1; Length 3433;
5. 2.6e+02;
230 233
240 252
253 253
3433 AA; 394488 MW; EAEBDB409F858E5B CRC64;
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microtubules.
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1428-3788 FROM N.A. (ISOFORM 1).
STRAIN-C57BL/6J;
MEDLINE-96259558; PubMed-8673129;
                                                                                                                                                  2.1%; Score 7; DB 1
100.0%; Pred. No. 2.6
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=1;
IsoId=P97412-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                     Query Match
Best Local Similarity 10v...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 382:262-265(1996)
                                                                                                                                                                                                                                                                                                                                       1182 VKILKDN 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                              18 VKILKDN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=2;
```

```
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BD08 BOVIN
ID BD08 BOVIN
                                                                                                                                                                                                                                                                                                                       MOD RES
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                        PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P46166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WD 3.
WD 4.
WD 5.
WD 6.
WD 7.
WD 7.
SEGDRPEVTESINPGDRLIEDGCIHLISLGSKALMIQV ->
GMWAGSDLYTKILQIAACLSFKHIWQYFNVFFKCYSP (in
Isold=P97412-2; Sequence=VSP 006783, VSP 006784;
-!- DISEASE: Defects in CHS1 are the cause of beige, an autosomal recessive disorder characterized by hypopigmentation, bleeding, immune cell dysfunction, abnormal intracellular transport to and from the lysosome, and giant inclusion bodies in a variety of cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; WD repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anas platyrhynchos (Domestic duck).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0cT-1989 (Rel. 12, Created)
01-0cT-1989 (Rel. 12, Last sequence update)
10-0cT-2003 (Rel. 42, Last amnotation update)
Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VSP 006783.
Missing (In lsoform 2).
/FTId=VSP 006784.
W, F01BEB37C676A750 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Scor.
100.0%; Pred. No. 2...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 AA.
                                                                                                                 -!- SIMILARITY: Contains 7 WD repeats.
-!- SIMILARITY: Contains 1 BEACH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom, PD007848; Beige_BEACH; 1.
SMART; SM0320; WD40; 4.
PROSITE; PS50197; BEACH; 1.
PROSITE; PS500678; WD REPEATS 1; 1.
PROSITE; PS50082; WD REPEATS 2; 1.
PROSITE; PS50294; WD REPEATS 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            soform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WD 1.
WD 2.
BEACH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                             EMBL; L77884; AAL40134.1; -.
EMBL; U52461; AAB60778.1; -.
EMS.; T320851. T330851.
MOD; MGT:107448; Lyst.
InterPro; IPR000409; Beige_BEACH.
InterPro; IPR001680; WD40.
Pfam; PP02138; Beach; 1.
Pfam; PP02138; WD40; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3788 AA; 425283 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transport;
                                                                                                                                                                                                                                                                                                                             EMBL; U70015; AAC53011.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1620
3409
3589
3640
3686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1204 SLKLLGE 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 SLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3643
3687
3736
1509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIBA_ANAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P12801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIBA_ANAPL
           SOLUTION SOLUTION SELECTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SOLUTION SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

```
Sci. Sin., Ser. B, Chem. Biol. Agric. Med. Earth Sci. 28:31-35(1985).
-!- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet
                                                                                                                                                                                                                  -!-SUBBUTT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.-!- PTW: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neutrophils.";
J. Biol. Chem. 268:6641-6648(1993).
-!- FUNCTION: Has bactericidal activity. Active against B.coli ML35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93203264; PubMed-8454635; Seleted M.E., Tang Y.-Q., Morris W.L., McGuire P.A., Novotny M.J., Smith W., Henschen A.H., Cullor J.S., and antibacterial activities of beta-defensins, a new family of antimicrobial peptides from bovine
MEDLINE-85168193; PubMed=3983613; Min Y., Ping Z., Yaoshi Z., ^{\circ} Min Y., Ping Z., Yaoshi Z., ^{\circ} "purification and primary structures of duck fibrinopeptides A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                          PIR; JP0101; JP0101.
Blood coagulation; Plasma; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C7B94D6C341270C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and S.aureus 502A.
--- SUBCELIULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Neutrophilic granules.
--- SIMILARITY: Belongs to the beta-defensin family.
PIR; 145495; 145495.
HSSP; P46170; 1BNB.
InterPro; IPR001855; Defensin_beta.
InterPro; IPR006080; Defensin_mammal.
PF00711; Defensin_beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 15 15 15 15 15 15 AA; D78A51FF88B40373 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Beta-defensin 8 (BNDB-8) (BNBD-8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIBRINOPEPTIDE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 6; DB 1
Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 1
Similarity 100.0%; Pred. No. 23;
6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Hereford, TISSUE=Neutrophils;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4359 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00048; DEFSN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 SSFQKE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 SSFOKE 10
                                                                                                                                                                                                      aggregation.
```

```
NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPMC OR TP0197
                                                                                                                                                                               neutrophils.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RL29_TREPA
ID RL29_TREPA
AC 083227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD RES
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                 PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 50
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
ö
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 268:6641-6648(1993).
-!-FUNCTION: Has bactericidal activity. Active against E.coli ML35 and S.aureus 502A.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                        Bos taurus (Bovine).
Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia: Butheria, Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                        MEDLINE=93203264; PubMed=8454635; Selsted M.E., Tang Y.-Q., Morris W.L., McGuire P.A., Novotny M.J., Smith W., Henschen A.H., Cullor J.S.; "Purification, primary structures, and antibacterial activities of
                                                                                                                                                                                                                                                                                beta-defensins, a new family of antimicrobial peptides from bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
·,
                                                                                                                                                                                                                                                                                                                                                                                                                          Antibiotic; Pyrrolidone carboxylic acid.

MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BD09 BOVIN STANDARD; PRT; 55 AA.
P46167; O18814;
01-NOV-1995 (Rel. 32, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Beta-defensin 9 precursor (BNDB-9) (Bragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
EDC3486C3410CE24 CRC64;
                                                                                                                                                                                                                                                                                                                                       -!- TISSUB SPECIFICITY: Neutrophilic granules.
-!- SIMILARITY: Belongs to the beta-defensin family.
PIR; G45495; G45495.
 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
. 55;
                                                                                                                    01-FEB-1996 (Rel. 33, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Beta-defensin 7 (BNDB-7) (BNBD-7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; bccc.
100.0%; Pred. No. cc.
                                                                                        40 AA
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                       HSSP, P46170, 1BNB.
InterPro; IRPR01855;
InterPro; IRPR06080; Defensin_mammal.
Pfam; PF00711; Defensin_beta; 1.
                                                                                                                                                                                                                                STRAIN=Hereford; TISSUE=Neutrophils;
  ..
0
                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last seq
10-OCT-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4572 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 100.
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00048; DEFSN; 1
  6; Conservative
                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                              38
31
39
                                                                                                                                                                               Mammalia; Eutheria; Cel
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 RRQIGT 111
                   106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 RRQIGT 30
                                       23 RROIGT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9913;
                                                                                                                                                                                                 NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFB9 OR BNDB9.
                                                                             BD07 BOVIN
ID BD07 BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                       SEQUENCE
                                                                                                 P46165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 49
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                     g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
TISSUE-Small intestine;

TISSUE-Small intestine;

MEDLINE=98147718; PubMed=9488194;

MINDLINE=98147718; PubMed=9488194;

Tarver A.P., Clark D.P., Diamond G., Russell J.P.,

Erdjument-Ercomage H., Tempst P., Cohen K.S., Jones D.E., Sweeney R.W.,

Wines M., Hwang S., Bevins C.L.;

"Enteric beta-defensin: molecular cloning and characterization of a
gene with inducible intestinal epithelial cell expression associated
with Cryptosporidium parvum infection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rreponema pallidum.
Bacteria, Spirochaetes, Spirochaetales, Spirochaetaceae, Treponema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 268:6641-6648(1993).
                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Hereford; TISSUE=Neutrophils; MEDLINE=93203264; PubMed=8454635; Selereed M.B., Tang Y.-Q., Morris W.L., McGuire P.A., Novotny M.J., Smith W., Henschen A.H., Cullor J.S., "Purification, primary structures, and antibacterial activities of beta-defensins, a new family of antimicrobial peptides from bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
BETA-DEFENSIN 9.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 6; DB 1; Length 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A -> G (IN REF. 2).
48DAE6917DE366F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and S.aureus 502A.
--- SUBCELJULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY. Neutrophilic granules.
--- SIMILARITY: Belongs to the beta-defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibiotic; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
508 ribosomal protein L29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001865; Defensin_beta.
InterPro; IPR006080; Defensin_mammal.
Pfam; PF00711; Defensin_beta; 1.
SMART; SM00048; DEFSN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF016394; AAC48801.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6049 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 RROIGT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 AA;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 16-55
```

```
EMBL; U75930; AAC59059.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 VAQLAQ 71
                                                                                                                                                                                                                                                                                                                                          50 EQFADE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 VAQLAQ 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2190;
                                       Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                       SEQUENCE
                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P54009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P73882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RL31_METJA
                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y46S_SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RL31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOUR SERVING CONTROL OF STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
   SARB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                   Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDondid L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 281:375-388(1998).
-!- SIMILARITY: Belongs to the L29P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last amoncation update)
Hypothetical 9.7 kDa protein (ORF60).
Orgyla pseudoteugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dBDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97271300; PubMed=9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF6163F9E244D63A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: TO CORRESPONDING ORF IN ACMNPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 1.8%; Score 6; DB 1;
Local Similarity 100.0%; Pred. No. 93;
nes 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THAMAP; ME 00374; -; 1.
InterPro; IPR001854; Ribosomal L29.
TIGREAMS; TIGR00012; L29; 1.
PROSITE; PS0579; RIBOSOMAL L29; FALSE NEG.
SKIBOSOMAI Drotein; COmplete Protecome.
SEQUENCE 72 AA; 8654 MW; BF6163F9E244D6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                          STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001202; AAC65182.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyhedrosis virus genome.";
Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; G71355; G71355.
TIGR; TP0197; -.
HAMAP; MF 00374; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 ILRRQI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILRROI 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
          [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        spirochete.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YOSE NPVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DETACL DESCRIPTION OF STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND STREET AND 
          ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Okumura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803, II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 1; Length 83;
100.0%; Pred. No. 1.1e+02;
iive 0; Mismatches 0; Indels
                                                                                   Length 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanococcus jannaschii.
Archaea, Euryarchaeota, Methanococci, Methanococales,
Methanocaldococcaceae, Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S75083; S75083.
Hypothetical protein; Complete proteome.
SEQUENCE 83 AA; 9471 MW; B8C3711A1F798D2C CRC64;
al protein.
82 AA; 9686 MW; 37AC49CD76E1673B CRC64;
                                                                            1.8%; Score 6; DB 1; I
100.0%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-00T-1996 (Rel. 34, Created)
01-00T-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RPL31E OR MJ0049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 AA
                                                                                                                                                                                                                                                                                                                                                                                                                     83 AA
                                                                                                               100.0%; Pred. No. letive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein ssl0461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D90910; BAA17945.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                               Local Similarity 100.
Les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                         316 EQFADE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
```

```
MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIF4EBP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4BP3 MOU
Q80VV3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4BP3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HID DTT THE STAND TO THE STAND TO THE STAND TO THE STAND TO THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE STAND THE ST
SO THE WAR WENT TO THE COURSE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@iBb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

TO SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

TO SEQUENCE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE S
                                                                           MEDINE-5617999; PubMed-868087;
MEDINE-9637999; PubMed-868087;
MEDINE-9637999; PubMed-868087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness B.F., Weinstcok K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Ngnyen D.,
Utterback T.R., Kalley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        jannaschii.";
Science 273:1058-1073(1996).
-!- SIMILARITY: Belongs to the L31E family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 1; Length 87; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
Erythroid protein 4.1 (Band 4.1.) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U67463; AAB98030.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                band III protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A64306; A64306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 AEIVKI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 AEIVKI 50
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIGR; MJ0049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHICK
41 CHICK
P12264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SWARAN SW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              엄
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Testis;

X MEDINE=22388257; PubMed=12477932;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

R Alacknil S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

R Ana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Raha S.S., Worley Y.C., Hale S., Garcia A.M., Gabbs R.A.,

R Richards S., Worley V.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A27056; A27056.
InterPro; IPR000299; Band 4.1.
From: PR00373; Band 41; 1.
PROSITE; PS0066; FERM 1; PARTIAL.
PROSITE; PS00661; FERM 2; PARTIAL.
PROSITE; PS00661; FERM 2; PARTIAL.
PROSITE; PS0057; FERM 3; 1.
Structural protein; Alternative splicing; Cytoskeleton; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Bukaryotic translation initiation factor 4E binding protein 3 (4E-BP3)
(elf4E-binding protein 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6J;
Poulin F., Sonenberg N.;
Two overlapping reading frames in the second exon of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 6; DB 1; Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translational inhibitor 4E-BP3.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 AA; 10395 MW; 8938A0C88816604A CRC64;
Comment=A number of isoforms are produced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 AA.
                                                                     IsoId=P12264-1; Sequence=Displayed;
                                                                                                    -!- SIMILARITY: Contains 1 FERM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M16962; AAA48762.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1
>90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 SSGLLV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 SSGLLV 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ^1
```

```
RESULT 58
                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
       à
                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; More than 15,000 full-length human and mouse cDNA sequences."; -- FUNCTION: Regulates eIF4E activity by preventing its assembly into the EIF4E complex (By similarity).
-- FUNCTION: Regulates (By similarity).
-- SUBUNIT: EIF4EBP3 interacts will BIF4E (By similarity).
-- PIM: Phosphorylated (By similarity).
-- SIMILARITY: Belongs to the eIF4E binding protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Translation regulation, Protein synthesis inhibitor, Phosphorylation.
SEQUENCE 101 AA; 11018 MW; 78F82052696A9BD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Genomic organization and expression of the 3' end of the canine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Nonstructural protein 7 (11 kDa protein) (X3 protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Canine enteric coronavirus (strain K378) (CCOV) (CCV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    feline enteric coronaviruses.";
Virology 191:134-140(1992).
-!- FUNCTION: MAY FUNCTION IN THE FORMATION OF MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPLICATION COMPLEXES OR IN THE ASSEMBLY OF THE VIRUS. SUBCELLULAR LOCATION: Membrane-associated (Potential). SIMILARITY: Belongs to the coronavirus NS7 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.8%; Score 6; DB 1; Length 101; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILINE=93033103; PubMed=1329312;
Vennem H., Rossen J.W.A., Wesselling J., Horzinek M.C.,
Rottler P.J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003449; Corona_7.
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AY226182; AAO73448.1; -. EMBL; BC061242; AAH61242.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X66717; CAA47247.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; B44056; B44056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 TDDEQF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 TDDEOF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=33732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVCAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               004703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CVCAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Chlorophyta, Trebouxiophyceae, Chlorellales,
Chlorellaceae, Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                   Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Howell S.H., "Physical structure and genetic organisation of the genome of maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 1; Length 110;
100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                        Score 6; DB 1; Length 101;
Pred. No. 1.3e+02;
                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 110 AA; 12756 MW; FD028DB22508B037 CRC64;
Pfam; PF02398; Corona_7; 1.
ProDom; PD004733; Corona_7; 1.
Nonstructural protein; Membrane.
SEQUENCE 101 AA; 11491 MW; 1AB4641D94DB9BB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1988 (Rel. 09, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 12.7 kDa protein in 16S-23S DNA spacer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hajochetical 12.7 kDa protein.
Majace streak virus (Kenyan isolate) (MSV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 AA.
                                                                                                                                                                                                                                                                                                                                                  PRT; 110 AA.
                                                                                                      Ouery Match
1.8%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     streak virus (Kenyan isolate).";
Nucleic Acids Res. 12:7359-7375(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=86232622; PubMed=3714498;
Yamada T., Shimaji M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=85037917; PubMed=6493977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001191; Gemini_AL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000736; Gemini ALI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1988 (Rel. 09, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X01089; CAB37354.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlorella pyrenoidoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 PPTEAV 105
                                                                                                                                                                                                                                     96 LLVTLI 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PPTEAV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                            78 LLVTLI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI TaxID=3078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHLPY
                                                                                                                                                                                                                                                                                                                                                Y18K MSVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YCX1 CHI
P05720;
                                                                                                                                                                                                                                                                                                                                                                    P14988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YCX1 CHLPY
                                                                                                                                                                                                                                                                                                    RESULT 57
Y18K MSVK
```

113 AA; 12711 MW; 74350F5154B49E1A CRC64;

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               029357:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMIL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aplysia californica (California sea hare).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Heterobranchia; Buthyneura; Opisthobranchia; Anaspidea;
Aplysioidea; Aplysiidae; Aplysia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brunet J.-F., Shapiro E., Foster S.A., Kandel E.R., Iino Y.; "Identification of a peptide specific for Aplysia sensory neurons by PCR-based differential screening."; Science 252:856-859(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: May function as an inhibitory cotransmitter acting in conjunction with the fast excitatory transmitter released by sensory neurons. The peptide selectively inhibits certain postsynaptic cells probably by means of sensorin A release. SUBCELLULAR LOCATION: Throughout the neuronal cells (cell body, axon and presynaptic terminals). TISSUE SPECIFICITY: Seems to be specific to the mechanosensory neurons of the central nervous system.
"Peculiar feature of the organization of rRNA genes of the Chlorella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMIDATION (G-55 PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cleavage on pair of basic residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 110;
0. 1.4e+02;
ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A24444; A24444.
Chloroplast; Hypothetical protein.
SEQUENCE 110 AA; 12782 MW; 1F58A66055A1A377 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-BRA-2004 (Rel. 43, Last annotation update)
Sensorin A precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 33-54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 6; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SENSORIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEPTIDE B
                              chloroplast DNA.";
Nucleic Acids Res. 14:3827-3839(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Pleural sensory cells;
MEDLINE=91227915; PubMed=1840700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X56770; CAA40089.1; -. PIR; S23653; S23653.
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X03848; CAA27477.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Neurone; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32
54
54
113
54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 KLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 KLIEFL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33
46
58
54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SENA APLCA
P29233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SENA_APLCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HE TELEVISION OF COURSE SERVING COURSE BELLING COURSE BELLING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COURSE SERVING COUR
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@ibs-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klenchum K.A., Dodson R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Kichardson D.L., Kerlarvage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J. Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of the hyperthermophilic, sulphate-
                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 1; Length 124;
100.0%; Pred. No. 1.5e+02;
ive 0; Mismatches 0; Indels
1.8%; Score 6; DB 1; Length 113;
100.0%; Pred. No. 1.4e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55749C70EDCBC5B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Buryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the UPF0292 family.
                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                            124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Complete proteome.
SEQUENCE 124 AA; 13948 MW; 55749C70E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=VC-16 / DSM 4304 / ATCC 49558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical UPF0292 protein AF0905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF_01095; -; 1.
InterPro; IPR006171; Toprim dom.
InterPro; IPR006154; Toprim_sub.
Pfam; PF01751; Toprim; 1.
SMART; SM00493; TOPRIM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE001041; AAB90335.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A69363; A69363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGKKDV 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 EGKKDV 97
                                                                                                                                 26 AILEKQ 31
                                                                                                                                                                                             83 AILEKO 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF0905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter J.C.;
                                                                                                                                                                                                                                                                                          RESULT 60
Y905_ARCFU
ID _Y905_ARCFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and also as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=UTEX LB 555 / Pringsheim;
Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella M.,
Farley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C.,
Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
"The complete sequence of the cyanelle genome of Cyanophora paradoxa:
the genetic complexity of a primitive plastid.";
[In] Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequence of the cyanelle DNA from Cyanophora paradoxa.";
Plant Mol. Biol. Rep. 13:327-332(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryotism and Symbiosis, pp.40-48, Springer-Verlag, Heidelberg
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=UTEX LB 555 / Pringsheim;
Stirewalt V.L., Michalowski C.B., Loeffelhardt W., Bohnert H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=20504813; PubMed=11016950;
NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (strain NRC-1 / ATCC 700922 / JCM 11081).
                                                                                                                                                                                                                                                                                                       Eukaryota; Glaucocystophyceae; Cyanophoraceae; Cyanophora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 1; Length 128; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea, Euryarchaeota, Halobacteria, Halobacteriales,
Halobacteriaceae, Halobacterium.
NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 AA; 15317 MW; OFEA01CBDCB59BFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical 15.3 kDa protein ycf35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the ycf35 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 AA.
   128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cyanelle; Hypothetical protein. SEQUENCE 128 AA; 15317 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U30821; AAA81309.1; -. PIR; T06966; T06966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30S ribosomal protein S6e. RPS6E OR VNG2514G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                     Cyanophora paradoxa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (eds)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 LIADLO 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 LIADLO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Halobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schwemmler W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bryant D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSGE HALN1
YC35 CYAPA
P48275;
                                                                                                                                                                                                                                                                        Cyanelle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09HMJ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAMES OF COLOR OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Plson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; "Genome sequence of Halobacterium species NRC-1."; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12188 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            092750, 091003;
30.MAY-2000 (Rel. 39, Created)
30.MAY-2000 (Rel. 39, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
30S ribosomal protein S8
SESS ON Crowless ON CP0113 ON CPB0660.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiae; Chlamydiales; Chlamydophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 6; DB 1; Length 131;
Pred. No. 1.6e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01092; Ribosomal S6e; T.
PROSITE; PS00578; RIBOSOWAL, S6ES; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 131 AA; 13743 MW; 52FF77B556E2004B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                PIR; D84401; D84401.
HAMAP; MF_00512; -; 1.
Interpro; IPR001377; Ribosomal_S6E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99206606; PubMed=10192388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=AR39;
MEDLINE=20150255; PubMed=10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                                                                                EMBL; AE005129; AAG20576.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; £
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity luv...
Loca 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 EAVAQL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 EAVAQL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=83558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pneumoniae AR39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CWL029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-J138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RS8 CHLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RS8_CHLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94143474; PubMed=8310054;
Wolf A.H., Kirsch M., Wiessner W.;
Wolfectide sequence of a cDNA encoding ribosomal protein L27 from
"Nucleotide sequence of a cDNA encoding ribosomal protein L27 from
Chlamydobotrys stellata.";
Plant Physiol. 101:1123-1123 (1993).
-!- SIMILARITY: Belongs to the L27E family of ribosomal proteins.
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
Comparison of Whole genome sequences of Chlamydia pneumoniae J138
from Japan and CHLO29 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Spondylomoraceae, Pyrobotrys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prami Produity Ribosomal S8; 1.
Prodom; PD001098; Ribosomal S8; 1.
PROSITE; PS00053; RIBOSOMAL S8; 1.
Ribosomal protein; RNA-binding; RNA-binding; Complete proteome. SEQUENCE 133 AA; 15117 MW; 0EAE2623F9BE46A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.8%; Score 6; DB 1; Length 133; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-FBB-1996 (Rel. 33, Last annotation update)
60S ribosomal protein L27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrobotrys stellata (Chlamydobotrys stellata)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF_01302; -; 1.
InterPro; IPR000630; Ribosomal_S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AE001647; AAD18773.1; -.
BMBL, AE002173; AAR39861.1; -.
EMBL, AE017159; AAR9889.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; D72054; D72054.
PIR; G86569; G86569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P56209; 1SEI.
TIGR; CP0113; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 IVKILK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 İVKİLK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 002984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DATA DE DAT
    SOUR DEEP PROCESS OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial content is a license agreement (See http://www.isb-sib.ch/announce/
           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93347989; PubMed=8346031; Hallick R.B., Hong L., Drager R.G., Favreau M.R., Monfort A., Orsat B., Spielmann A., Stutz B.; "Complete sequence of Euglena gracilis chloroplast DNA."; Mucleic Acids Res. 21.3337-3544(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 1; Length 134;
100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 1; Length 134; 100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                 134 AA; 15408 MW; SODEBC32EF9C259E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Problem, Fruchous, Albohamaa, 29; 1.
Problem; PD001627; Ribosomal_S9; 1.
PROSITE; PS00360; RIBOSOWAL_S9; 1.
Ribosomal protein; Chloroplast.
SEQUENCE 134 AA; 15026 MW; 81C96A2E550E504F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
NCBI_TaxID=3039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Chloroplast 30S ribosomal protein S9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                            PIR; S26612; S26612.
InterPro; IPR05824; KOW
InterPro; IPR06646; KOW sub.
InterPro; IPR011141; Ribosomal L27e.
Pfam; PF00467; KOW: 1.
Pfam; PF01777; Ribosomal L27e; 1.
                                                                                                                                                                                                                                                                                     ProDom; PD009396; Ribbsomal L27e; 1. SMART; SM00739; KOW; 1. PROSITE; PS01107; RIBOSOMAL L27E; 1. Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z11874; -; NOT ANNOTATED CDS.
EMBL; X70810; CAA50120.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF 00532; -; 1.
InterPro; IPR000754; Ribosomal S9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00380; Ribosomal_S9;
                                                                                                                                                              EMBL; X68202; CAA48289.1; -.
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100..
Laga 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 VTKRQS 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 VTKRQS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euglena gracilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RR9 EUGGR
P32060;
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 65
à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
   ö
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Delta H.

X MEDLINE-98037514; PubMed-9371463;
X MEDLINE-98037514; DubMed-9371463;
X MEDLINE-98037514; DubMed-9371463;
X Math D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
A Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
A Adaredge T., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
A Jadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
A Jiwani N., Caruso A., Bubh D., Safer H., Patwell D., Prabhakar S.,
A Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
R. Complete genome sequence of Methanobacterium thermoautotrophicum
R. Geltah: functional analysis and comparative genomics.";
Geltah: T. Salare A., Pierrowski S., Church G.M.,
Bacteriol. 179:7135-7155(1997).
C. -!- FUNCTION: eIF-2 functions in the early steps of protein synthesis
C. Dy forming a ternary complex with GTP and initiator tRNA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Probable translation initiation factor 2 beta subunit (eIF-2-beta).
BIF2B OR MTH1769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heterotrimer composed of an alpha, a beta and a gamma
 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                 Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF 00232; -; 1.

InterPro; IPR004785; eIF5 eIF2B.

InterPro; IPR004488; TIF aIF-2Deta.

Pfam; PF01873; eIF5 eIF2B; 1.

ProDom; PD004078; eIF5 eIF2B; 1.

SMART; SM0653; eIF2B =; 1.

ITGRFAM8; ITGR00311; aIF-2Deta; 1.

Initiation factor; Protein biosynthesis; Complete proteome. SEQUENCE 135 AA; 15587 MW; 98AF22F6966CA0AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the eIF-2-beta / eIF-5 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 6; DB 1; Length 135;
Pred. No. 1.6e+02;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 AA.
                                                                                                                                                                  PRT; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. wc.
0; Mismatches
                                                                                                                                                                                                                                                                                                  Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE000932; AAB86235.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.00
The 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (By similarity)
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                  STANDARD:
                                   156 AKIILF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; B69103; B69103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 DYEKLL 217
                                                                    17 AKIILF 22
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYEKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT:
                                                                                                                                                                  IF2B METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YJAV_BACSU
ID YJAV_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 m
                                                                                                                                                 METTH
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 67
                                   à
                                                                      dd
                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
Runst F., Ogaswara N., Albertini A.M., Alloni G., Azevedo V., Bersieres P., Bolotin A., Borchert S., Ravedo V., Bersiero M.G., Bessieres P., Bolotin A., Borchert S., Ravedo V., Bersier I., Brans A., Bersieres P., Bolotin A., Borchert S., Bruschi C.W., Cannerton I.F., Cummings N.J., Daniel R.A., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Ratian K.D., Errington J., Fabret C., Ferrari B., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galarron N., Ghiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Holseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Hilbert H., Holseppel S., Hosono S., Hullo M.F., Itaya M., Jones I., Auria K., Lapidus A., Lardinois S., Runer-Blanchard M., Klein C., Robyashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Jones I., Auria K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Karria K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Auria M., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parecon E., Pujic P., Purnelle B., Ropoport G., Rey M., Reynolds S., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Scallan E., Schroeter R., Scoffone F., Schroeter R., Scoffone R., Sakouli, M., Tamakoshi A., Tanaka T., Tarpstra P., Tognoni A., Vareuchi M., Tamakoshi A., Tanaka T., Tarpstra P., Tognoni A., Vareuchi M., Tamakoshi A., Yanamoto H., Vannier F., Vasemoto K., Yata K., Wentlers P., Widpat A., Yanamoto H., Vamner K., Yasumoto K., Yata K., Wentlers P., Widpat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., The complete genome sequence of the Gram-positive bacterium Bacillus T., The Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                          Sacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete proteome. SEQUENCE 135 AA; 16149 MW; 5153D09CC417CF47 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 1; Ler
.00.0%; Pred. No. 1.6e+02;
                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein yjaV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.04; Pred. No. 1.0.
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                         MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 299109; CAB12970.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SubtiList, BG13125; yjaV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; E69842; E69842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 ONYDTI 209
                                                                                                                                    Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 QNYDTI 71
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                NCBI TaxID=1423;
                                                                                                               CLAV OR BSU11290
                                                                                                                                                                                                                                                        STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRS OENHO
Q9MTJ0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRB OENHO
ID RRB O
AC Q9MTJ
DT 28-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 68
ठ
```

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IF2B_PYRFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 70
      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=GES / Orsay;
MEDLINE=22511545; PubMed=12622808;
Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O., Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Myrtales; Onagraceae; Oenothera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Probable translation initiation factor 2 beta subunit (eIF-2-beta).
EIF2B OR PYRAB14410 OR PAB0959.
                                                                                                                                                                                                                                                   Mol. Gen. Genet. 263:881-585 (2000).
-1- FUNCTION: One of the primary rRNA binding proteins, it binds directly to 16S rRNA central domain where it helps coordinate assumily of the platform of the 30S subunit (By similarity).
-1- SUBUNIT: Part of the 30S ribosomal subunit.
-1- SUBCELLULAR LOCATION: Chloroplast.
-1- SIMILARITY: Belongs to the S8P family of ribosomal proteins.
                                                                                                                                                                                                              "Complete nucleotide sequence of the Oenothera elata plastid chromosome, representing plastome I of the five distinguishable Eucenothera plastomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                            STRAIN=cv. Johansen;
MEDIINE=2019318; PubMed=10852478;
Hupfer H., Swiatek M., Hornung S., Herrmann R.G., Maier R.M.,
Chiu W.L., Sears B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00410; Ribosomal_S8, 1.
ProDom; PD001098; Ribosomal_S8, 1.
PROSITE; PS00053; RIBOSOMAL_S8; 1.
Ribosomal protein; RNA-binding; rRNA-binding; Chloroplast.
SEQUENCE 138 AA; 15843 MM; B047635ECE213F29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 138;
. 1.7e+02;
ches 0; Indels
                                                  Oenothera hookeri (Hooker's evening primrose).
28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Chloroplast 30S ribosomal protein SB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No. 1.7
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF 01302; -; 1.
InterPro; IPR000630; Ribosomal_S8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ271079; CAB67195.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P56209; 1SEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 EIVKIL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 EIVKIL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=29292;
                                                                                                                   NCBI_TaxID=85636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrococcus abyssi
                                                                  Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IF2B_PYRAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9UY\overline{R}6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYRAB
 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an emmail to license@ib.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furitosus genome.";
submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: eIF-2 functions in the early steps of protein synthesis by forming a ternary complex with GTP and initiator tRNA (By
                                                                                                                                                -!- FUNCTION: eIF-2 functions in the early steps of protein synthesis by forming a ternary complex with GTP and initiator tRNA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MEA-2004 (Rel. 43, Last annotation update)
Probable translation initiation factor 2 beta subunit (eIF-2-beta).
EIF2B OR PF0481.
                                                                                                                                                                                                                                                                 SUBUNIT: Heterotrimer composed of an alpha, a beta and a gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Heterotrimer composed of an alpha, a beta and a gamma
Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.; "An integrated analysis of the genome of the hyperthermophilic archaeon Pyrococcus abyssi."; Mol. Microbiol. 47:1495-1512(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Initiation factor; Protein biosynthesis; Complete proteome. SEQUENCE 140 AA; 16247 MW; 9D40F2C556DB539A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 1; Length 140;
100.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                        chain (By similarity).
-!- SIMILARITY: Belongs to the eIF-2-beta / eIF-5 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chain (By similarity).
-!- SIMILARITY: Belongs to the eIF-2-beta / eIF-5 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. No. 1.7e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR, E72056; E75056.
HAWAP: MF 00232; -; 1.
Interpro; IPR00478; eIFS_EIF2B.
Interpro; IPR004489; TIF_AIF-2beta.
Pfam; PP01873; eIFS_EIF2B; 1.
SWART; SM00653; eIFS_EIF2B; 1.
SWART; SM00653; eIFS_E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ248287; CAB50346.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus furiosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 DYEKLL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 DYEKLL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                          similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYRFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IF2B_PYRI
Q8U3IS;
```

.. 0

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Probable translation initiation factor 2 beta subunit (eIF-2-beta).
EIF2B OR PH0605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Heterotrimer composed of an alpha, a beta and a gamma
                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF 00232; -; 1.
InterPro; IPR002735; eFF5 eIF2B.
InterPro; IPR004488; TIF aIF-2beta.
Pfam; PF01873; eIF5 eIF2B; 1.
ProDom; PD004078; eIF5 eIF2B; 1.
SMART; SM0653; eIF2B 5; 1.
INGREAMS; IGR00311; aIF-2beta; 1.
Initiation factor; Protein biosynthesis; Complete proteome. SEQUENCE 140 AA; 16247 MM; 9D40F2C1428A129A CRC64;
                                                                                                                               Initiation factor; Protein biosynthesis; Complete proteome.
SEQUENCE 140 AA; 16234 MW; 771153C98A871359 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the eIF-2-beta / eIF-5 family.
                                                                                                                                                                               Length 140;
                                                                                                                                                                                                             0; Indels
                                                                                                                                                                               Query Match 1.8%; Score 6; DB 1; Les Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                               140 AA.
                         HAWAP; MF 00232; -; 1.
InterPro; IPR002735; eIF5_eIF2B.
InterPro; IPR004498; TIF_aIF-2beta.
Pfam; PF01873; eIF5_eIF2B; 1.
ProDom; PD004078; eIF5_eIF2B; 1.
SMART; SM00653; eIF2B_5; 1.
TIGRFAM8; TIGR00311; aIF-2beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98344137; PubMed=9679194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP000003; BAA29694.1; -. PIR; D71104; D71104.
              EMBL; AE010171; AAL80605.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chain (By similarity).
                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrococcus horikoshii.
                                                                                                                                                                                                                                        212 DYEKLL 217
                                                                                                                                                                                                                                                                     DYEKLL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity
                                                                                                                                                                                                                                                                                                                                            IF2B PYRHO
058312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=OT3;
                                                                                                                                                                                                                                                                    <u>r</u>~
                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                               IF2B PYRHO
à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence determination and genetic content of an 8.9-kb restriction fragment in the short unique region and the internal inverted repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=86304344; PubMed=3017958; Jones D., Russnak R.H., Kay R.J., Candido E.P.M.; Jones D., Russnak R.H., Kay R.J., Candido E.P.M.; Structure, expression, and evolution of a heat shock gene locus in Caenorhabditis elegans that is flanked by repetitive elements.";
                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93118245; PubMed=1282282;
Sakaguchi M., Urakawa T., Hirayama Y., Miki N., Yamamoto M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 1; Length 142;
100.0%; Pred. No. 1.7e+02;
tive 0; Mismatches 0; Indels
                                      Length 140;
                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 AA; 15662 MW; 76D137DF02735E26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marek's disease herpesvirus (strain GA) (MDHV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Marek's disease-like viruses.
                               DB 1; Ler
. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
101-FEB-1995 (Rel. 31, Last annotation update)
Hypothetical 15.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HS16_CAEEL STANDARD; PRT; 143 AA. P06561; P02214; P0214; P0214; P0214; P0214; P0214; P0214; P0214AN-1988 (Rel. 06, Last sequence update) 28-FFB-2003 (Rel. 41, Last annotation update) Heat shock protein HSP16-41.
                                                                                                                                                                                                                                                                                                                                                                                                   142 AA.
                           1.8%; Score 6; DB 1
100.0%; Pred. No. 1.70
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment in the short unique region and of Marek's disease virus type 1 DNA."; Virus Genes 6:365-378(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M80595; AAB59898.1; -.
Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
                                                                                                                                                               212 DYEKLL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 SLKLLG 233
                                                                                                                                                                                                                         7 DYEKLL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 SLKLLG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                               HSVMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hirai K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HS16_CAEEL

DD HS18_C

O 0-0550

DT 01-JAN

DT 01-JAN

DT 01-JAN

DT 01-JAN

DT 08-FEB

DE HEAT 8

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO CAEA

CO 
                                                                                                                                                                                                                                                                                                                              RESULT 72
U426_HSVMG
                                                                                                                                                                                                                                                                                                                                                                                                   U426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

```
TAA1 VACCC
                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                 P20982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3oebel
                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                          SEQUENCE OF 47-143 FROM N.A.
MEDLINE-81220736; PubMed-6190129;
RUSSMAR R.H., Jones D., Candido E.P.M.;
"Cloning and analysis of cona sequences coding for two 16 kilodalton heat shock proteins (hsps) in Caenorhabditis elegans: homology with the small hsps of Drosophila."
Nucleic Acids Res. 11:3187-3205(1983).
-:- SIMILARITY: Belongs to the small heat shock protein (HSP20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen B.Y., Cassell G.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete sequence of the mucosal pathogen Ureaplasma urealyticum,",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 1; Length 143; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
                                            Stoneking T., Wohldmann P., Lennox S.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                           Waterston R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heat shock; Multigene family.
SEQUENCE 143 AA; 16252 MW; CID0F59D26E36C24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ureaplasma parvum (Ureaplasma urealyticum biotype 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 AA
                                                                                                                                                                                                                                                                                                                                                                                       WormPep; Y46H3A.2; CE22003.
InterPro; IPR001436; Crystallin_alpha.
InterPro; IPR002068; HSp20.
InterPro; IPR008978; HSP20_chap.
Pfam; PF00011; HSP20; 1.
Biol. Chem. 261:12006-12015(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20500219; PubMed=11048724;
                                                                                                                                                                                                                                                                                                                                           EMBL; M14334; AAA28070.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
                                                                                                                                                                                                                                                                                                                                                       EMBL, AC006774, AAF60616.1, --
EMBL, X01577, CAA25732.1, -.
PIR, A25199, HHKW41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00299; ACRYSTALLIN. PROSITE; PS01031; HSP20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50S ribosomal protein L9. RPLI OR RPL9 OR UU551.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 407:757-762(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 KPENLK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 KPENLK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                     SEQUENCE FROM N.A.
                                   STRAIN=Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Serovar 3;
                                                                                                                                                                                                                            family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RL9 UREPA
                                                                                REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    datches
à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
FUNCTION: Binds to the 23S rRNA (By similarity). SIMILARITY: Belongs to the L9P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Appendix to 'The complete DNA sequence of vaccinia virus'.";
Virology 179:517-563(1990).

    -!- FUNCTION: General late promoter trans-activator.
    -!- DEVELOPMENTAL STAGE: Intermediate stages of infection.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 1; Length 145; 100.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGRO0158; L9; "1."
PROSITE; PS00651; RIBOSOWAL, L9; 1.
Ribosomal protein; xRNA-binding; Complete proteome.
SEQUENCE 145 AA; 16420 MW; 3ESE203806EDF15F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete DNA sequence of vaccinia virus."; Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. wc. -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccinia virus (strain Copenhagen).
                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP, MF 00503, -; 1.
InterPro; IPR00912; L9 N like.
InterPro; IPR000244; Ribosomal L9.
Pfam; PP03948; Ribosomal L9.
Pfam; PF01281; Ribosomal L9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=91021027; PubMed=2219722;
                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE002153; AAF30964.1; -. HSSP; P02417; 1DIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; C42517; C42517.
InterPro; IPR004975; Pox_TAA1.
Pfam; PF03295; Pox_TAA1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M35027; AAA48116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trans-activator protein Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 IVEILL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 IVEIL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Orthopoxvirus.
NCBI_TaxID=10249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paoletti E.;
```

. 0

Gaps

ö

1.8%; Score 6; DB 1; Length 150; illarity 100.0%; Pred. No. 1.8e+02; Conservative 0; Mismatches 0; Indels

Local Similarity les 6; Conserva 260 NLLRDK 265 121 NLLRDK 126

Transcription regulation; Trans-acting factor; Activator;

150 AA; 16906 MW; 5569B1B78F0A9A8D CRC64;

Late protein. SEQUENCE 15

```
Query Match
                                                                                                                 Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                      N M N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation has bronched aboinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                    ò
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90263105; PubMed=2344616;
Keck J.G., Baldiack C.J. Jr., Moss B.;
"Role of DNA replication in vaccinia virus gene expression: a naked
Template is required for transcription of three late trans-activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carpenter M.S., belange A.M.; "Identification of a temperature sensitive mutant of vaccinia virus defective in late but not intermediate gene expression."; dirology 188:233-244(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccinia virus (strain WR).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Resistance of vaccinia virus to rifampicin conferred by a single uncleotide substitution near the predicted NH2 terminus of a gene encoding an Mr 62,000 polypeptide."; Virology 156:138-145(1887).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=86176781; PubMed=3008103;
Weinrich S.L., Hruby D.E.;
"A tandemly-oriented late gene cluster within the vaccinia virus
                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cell 61:801-809(1990).
-1- FUNCTION: General late promoter trans-activator.
-1- DEVELOPMENTAL STAGE: Intermediate stages of infection.
Transcription regulation; Trans-acting factor; Activator;
                                                                                      1.8%; Score 6; DB 1; Length 150; llarity 100.0%; Pred. No. 1.8e+02; Conservative 0; Mismatches 0; Indels
                                             150 AA; 16950 MW; 4DF6D39AC068AF5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 07, Last sequence update) (Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                            150 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 14:3003-3016(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=87122144; Pubmed=3811229; Baldick C.J. Jr., Moss B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92230221; PubMed=1566576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M16556; AAA44304.1; -.
EMBL; X03729; CAA27367.1; -.
EMBL; M86531; AAB59802.1; -.
PIR; C23768; WMVZR2.
InterPro; IPR004975; Pox_TAA1.
Pfam; PF03295; Pox_TAA1; -1.
                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1988 (Rel. 07, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trans-activator protein Al
                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                               260 NLLRDK 265
                                                                                                                                                                                                                             121 NLLRDK 126
                                                                                                     Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Orthopoxvirus
                          Late protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993
                                                                                                                                                                                                                                                                                                                                            TAA1 VACCV
P07610:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                             SEQUENCE
                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                            DEATH OF THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY AND THE PROPERTY A
SOWW
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN STAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Potential virulence determinants in terminal regions of variola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Bangladesh-1975;
MEDLINE=94088747; Pubmed=8264798;
MEDLINE=94088747; Pubmed=8264798;
MEDLINE=94088747; Esposito J.J., Liu L., Qi J., Utterback T.R.,
Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Garcia-1966;
Shchelkunov S.N., Totmenin A.V., Resenchuk S.M., Blinov V.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: General late promoter trans-activator.
-1- DEVELOPMENTAL STAGE: Intermediate stages of infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; B36848; B36848.

PIR; F72163; F72263.

PIR; P72163; F72263.

InterPro; IPR04975; Pox_TAA1.

Franscription = regulation; Trans-acting factor; Activator. SEQUENCE 150 AA; 16966 MW; IDE0A936061E6256 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X69198; CAA49045.1; -. EMBL; L22579; AAA60852.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X76262; CAA53826.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protective mechanisms."; FEBS Lett. 319:80-83(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Frans-activator protein Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   smallpox virus genome.";
Nature 366:748-751(1993).
                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=10255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sandakhchiev L.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Variola virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Orthopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter C.J.;
                                                                       TAA1_VARV
ID _TAA1_VARV
RESULT 77
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00732; YGGFC; 1.
TIGREAMs; TIGR00250; TIGR00250; 1.
Hydrolase; Nuclease; DNA repair; DNA recombination; Complete proteome.
SEQUENCE 151 AA; 16799 MW; 0F6618C1E0381E68 CRC64;
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
---- FUNCTION: Could be a nuclease that resolves Holliday junction
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21595285; PubMed=11759840; Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yasuda M., Tabata S.;
                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
   1.8%; Score 6; DB 1; Length 150; 100.0%; Pred. No. 1.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 1; Length 151;
100.0%; Pred. No. 1.8e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                               Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intermediates in genetic recombination.
-!- SUBCELLUIAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Belongs to the yqgF HJR family.
                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Putative Holliday junction resolvase (EC 3.1...).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-CCT-2003 (Rel. 42, Last annotation update)
SsrA-binding protein.
                                                                                                                                                                                                             151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; AE2193; AE2193.
HAMMP: MF 00651; -; 1.
InterPro; IPR005527; Cons_hypoth250.
InterPro; IPR006641; YqgFc.
Pfam; PF03652; UPF0081; 1.
                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP003591; BAB74799.1; -.
                                                                                                                                                                                                                                                                                                                                         Anabaena sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                          6; Conservative
                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 MTKYIS 250
                                                                            260 NLLRDK 265
                                                                                                           121 NLLRDK 126
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           I_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MTKYIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSRP HELPJ
                                                                                                                                                                                                           RUVX ANASP
                                                                                                                                                                                                                                                                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                        ALR3100
                                                                                                                                                                                                                              28YSIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 79
SSRP HELPJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9ZJHZ
                                                                                                                                                                                         RUVX ANASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                         Matches
                                                                                                                                                                                                           g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifised and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                  MEDLINE=99120557; PubMed=9923682; Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Trust T.J., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F., Trust T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97394467; PubMed=9252185;

MEDLINE=97394467; PubMed=9252185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Teleschmann R.D., Ketchun K.A., Klenk H.-P., Gill S., Dougherty B.A.,

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                    "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
          Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter pylori (Campylobacter pylori).
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                           --- FUNCTION: Binds specifically to the ssrA RNA (tmRNA) and in required for stable association of ssrA with ribosomes (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 1.8%; Score 6; DB 1; Length 152; Local Similarity 100.0%; Pred. No. 1.8e+02; Nes 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA binding, Complete proteome.
SEQUENCE 152 AA; 17814 MW; 2A07C14BB5E2C364 CRC64;
                                                                                                                                                                                                                                                                                                                                                     similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Belongs to the smpB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ssra-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001556; AAD06913.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD004488; SmpB; 1.
TIGRFAMB; TIGR00086; SMpB; 1.
PROSITE; PS01317; SSRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; G71820; G71820.
HAMAP; MF_00023; -; 1.
InterPro; IPR000037; SmpB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01668; SmpB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 KRQSLK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 KROSLK 134
                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                            NCBI_TaxID=85963;
SMPB OR JHP1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMPB OR HP1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSRP_HELPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       025985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSRP_HELPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     임
```

.; 0

ö

Gaps

..

DB 1; Length 153; . 1.8e+02; 0; Indels

1.8%; Score 6; DB 1 100.0%; Pred. No. 1.8 Live 0; Mismatches

Query Match Best Local Similarity 100.

61 PPTEAV 66

153 AA; 17768 MW; F08DAA3605CAB4ED CRC64;

SEQUENCE

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation -
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                       "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-85126910; PubMed-6526009;
Mullineaux P.M., Donson J., Morris-Krsinich B.A.M., Boulton M.I.,
                                                                                                            -!- FUNCTION: Binds specifically to the ssrA RNA (tmRNA) and is required for stable association of ssrA with ribosomes (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 1; Length 152;
100.0%; Pred. No. 1.8e+02;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD004488; SmpB; 1.
TIGRPAMs; TIGR00086; smpB; 1.
PROSITE; PS01317; SSRP; 1.
RNA-binding; Complete proteome.
SEQUENCE 152 AA; 17824 MW; 2CD90E775CE6C360 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleotide sequence of maize streak virus DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
Hypothetical 17, Kba protein.
Maize streak virus (Nigerian isolate) (MSV).
Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001191; Gemini ALI.
Pfam; PF00799; Gemini ALI; I.
ProDom; PD000736; Gemini ALI; I.
                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000644; AAD08482.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X01633; CAA25792.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF 00023; -; 1.
InterPro; IPR000037; SmpB.
Pfam; PF01668; SmpB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 3:3063-3068(1984).
                                                                        pylori.";
Nature 388:539-547(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                               D64700; D64700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 KRQSLK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 KROSLK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Davies J.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y18K MSVN
P14978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 81
Y18K MSVN
   à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=66205869; PubMed=3517854;
Cerretti D.P., McKereghan K., Larsen A., Cantrell M.A., Anderson D.,
Gallis S. Cosman D., Baker P.E.;
"Cloning, sequence, and expression of bovine interleukin 2.";
Proc. Natl. Acad. Sci. U.S.A. 83:3223-3227(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anikeeva N.N., Vinogradova T.V., Votoshin O.N.;
Anikeeva N.N., Vinogradova T.V., Votoshin O.N.;
Submitted (DEC-1985) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.
-: SUBCELLULAR LOCATION: Secreted.
-: SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reeves R., Spies A.G., Nissen M.S., Buck C.D., Weinberg A.D., Barr P.J., Magnuson N.S., Magnuson J.A.; "Molecular cloning of a functional bovine interleukin 2 cDNA.", Proc. Natl. Acad. Sci. U.S.A. 83:3228-3232(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0265; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; ILZ; 1.
PROSITE; PS00424; INTERLEUKIN 2; 1.
Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
                                                                                                                                   13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P01585, 3INK.
InterPro, IPR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M12791; AAA30586.1; -.
EMBL; M13204; AAA21143.1; ALT_INIT.
EMBL; X17201; CAA35062.1; -.
EMBL; X22687; CAA36912.1; -.
PIR; 145913; 145913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=86205870; PubMed=3486415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-22 FROM N.A.
                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                               Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                    IL2 OR IL-2.
Bos taurus (Bovine).
143 PPTEAV 148
                                                                                           ILZ BOVIN
P05016;
                                                            RESULT 82
                                                                        IL2_BOVIN
입
```

```
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumunogenet. 29:341-345(2002).

FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell the proliferation and other activities curcial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells (By
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sreekumar E., Premraj A., Saravanakumar M., Rasool T.J.; "Buffalo (Bubalus bubalis) interleukin-2: sequence analysis reveals high nucleotide and amino acid identity with interleukin-2 of cattle
                                                         . .) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                            Bubalus bubalis (Domestic water buffalo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bubalus.
                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00424; INTERLEUKIN_2; 1.
Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
                                                                                                                                                                                                                                                                                                     10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
                                                                                                                   Length 155;
                                                                                                                                              0; Indels
                                                                     V -> A (IN REF. 2).
816667DFEA052EDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1753173FE619946B CRC64;
                                                                                                                 DB 1; Len
                           INTERLEUKIN-2.
BY SIMILARITY.
O-LINKED (GALNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O-LINKED (GALNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                              155 AA
                                                                                                                         100.0%; Pred. ...
               BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERLEUKIN-2
BY SIMILARITY
                                                                                                                 Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF363786; AAK50039.1; -.
InterPro; IPR000779; Interleukin-2.
Pfam; PF00715; IL2; 1.
ProDom; PD00365; INTERLEUKIN2.
ProDom; PD003649; Interleukin-2; 1.
SMART; SM00189; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22117321; PubMed=12121282;
            20 BY
155 IN
127 BY
23 O-6
66 V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 O. 17541 MW;
                                                                                                                 1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%;
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
155
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and other ruminants.";
Eur. J. Immunogenet. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 1
79 1
23
155 AA;
                                                                                                                                                                          252 PENLKL 257
                                                                                   155 AA;
                                                                                                                          Local Similarity
                                                                                                                                                                                                  51 PENLKL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=89462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity)
                                                                                                                                           .
9
                                                                                                                                                                                                                                                                            IL2 BUBBU
                            CHAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                      CARBOHYD
                                                                                   SEQUENCE
                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        r-cell,
               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                            Matches
KW
FT
FT
FT
SO
                                                                                                                                                                          à
                                                                                                                                                                                                   g
```

DB 1; Length 155;

100.0%; Pred. No. 1.8e+02;

Best Local Similarity

Query Match

Score 6;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95367627; PubMed=7543777;
Bujdoso R., Williamson M.L., Roy D., Hunt P., Blacklaws B., Sargan D.,
McConnell I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20500438; PubMed=11048943;
Luehken G., Hiendleder S., Prinzenberg E.M., Erhardt G.;
"A single-strand conformation polymorphism in the ovine interleukin-2
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91088336; PubMed=2263496;
Seow H.F., Rothel J.S., Radford A.J., Wood P.R.;
"The molecular cloning of ovine interleukin 2 gene by the polymerase
Chain reaction.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokineactivated killer cells, natural killer cells, and glioma cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning and expression of DNA encoding ovine interleukin
                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
 0
                                                                                                                                                                                                                                                                                                                                                                                                                                          English L.S., Hall L.;
                                                                                                                                                            IL2 SHEEP STANDARD; PRT; 155 AA.
P19114; Q95MP4;
01-NOV-1990 (Rel. 16, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
 Indels
 .;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Goodall J.C., Emery D.C., Perry A.C.F., English "CDNA cloning of ovine interleukin 2 by PCR."; Nucleic Acids Res. 18:5883-5883 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the IL-2 family.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 18:7175-7175(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000779; Interleukin-2.
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=91016933; PubMed=2216781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anim. Sci. 78:2754-2755(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X53934; CAA37881.1; -. EMBL; X55641; CAA39165.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AF287479, AAK69554.1; -
EMBL, X60148; CAA42722.1; -.
EMBL, A19169; CAA01448.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 21-153 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine 7:223-231(1995).
6; Conservative
                                                                                                                                                                                                                                                                                                                                                Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S11488; S11488.
HSSP; P01585; 3INK.
                                252 PENLKL 257
                                                                    51 PENLKL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          Ovis aries (Sheep)
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chain reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene.";
Matches
                                    6
                                                                  g
```

CARBOHYD

-cell. SIGNAL

SEQUENCE CONFLICT

Matches

g

à

QBEVJO RL10_MYCPE

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swigs Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lockhart B.A.; Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine activated killer cells, natural killer cells, and glioma cells (By
                                                                                                                                                                                                                                                                                                                                          "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Cervoidea,
Cervidae, Cervinae, Cervus.
                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 24:4420-4449(1996).
-!- SIMILARITY: Belongs to the L10P family of ribosomal proteins.
                                                                                                                                                                               Bacteria, Firmicutes, Mollicutes, Mycoplasmataceae, Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interleukin-2 precursor (IL-2) (T-cell growth factor) (TGF)
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4A7C387BBA49D446 CRC64;
                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
50S ribosomal protein 110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 1.8%; Score 6; UD 1. Local Similarity 100.0%; Pred. No. 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L10eub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribosomal protein; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00466; Ribosomal L10; 1.
PROSITE; PS01109; RIBOSOMAL L10; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR, S73630; S73630.
HAMAP, MF 00362; -; 1.
INCER'S IPR001795; Ribosomal L10.
INCERPIC; IPR002363; Ribosomal_L10e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000028; AAB95952.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 AA; 17618 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cervus elaphus (Red deer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                           RPLJ OR MPN538 OR MP304.
                     STANDARD;
                                                                                                                                                                Mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 NNILRR 107
                                                                                                                                                                                                                                                                                                                                                                   pneumoniae.";
Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 NNILRR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9860;
                                                                                                                                                                                                  NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                           Herrmann R.;
                   RL10 MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IL2 CEREL
P51747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
  RL10 MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IL2 CEREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 87
                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstainnthe the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·.
                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22354719; PubMed=12466555; Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K., Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.; "The complete genomic sequence of Mycoplasma penetrans, an intracelular bacterial pathogen in humans."; Nucleic Acids Res. 30:5293-5300(2002).
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                            INTERLEUKIN-2.
O-LINKED (GALNAC. . .) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                 Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bāctēria; Fīrmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 1; Length 161;
100.0%; Pred. No. 1.9e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   DB 1; Length 155;
                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                     L -> P (IN REF. 1).
3F76C6CBB7B289C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 AA; 17949 MW; 1D95D1C29B5E87D3 CRC64;
                                                                                                                                                                                                                                                                                 Score 6; DB 1; Les
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00466; Ribosomal L10; T.
PROSITE; PS01109; RIBOSOMAL L10; FALSE NEG.
Ribosomal protein; Complete proteome.
                                                                                                                                                                                                                                                                                         100.0%; Pred. w...
                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAD; MF 00362; -; 1.
InterPro; IPR001790; Ribosomal L10.
InterPro; IPR002363; Ribosomal_L10eub.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP004172; BAC44364.1; ALT_INIT.
                   PRINTS; PRO0265; INTERLEUKIN2.
PRODOM; PRO03649; Interleukin-2; 1.
SMART; SMO0189; IL2; 1.
PROSITE; PSO0424; INTERLEUKIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 42, Created)
(Rel. 42, Last sequ
(Rel. 42, Last anno
                                                                                                                                                                                                                     6 6 6 L
155 AA; 17678 MW;
                                                                                                                                                                                                                                                                                 1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50S ribosomal protein L10. RPLJ OR MYPE5740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                         20
155
23
127
Pfam; PF00715; IL2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma penetrans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 NNILRR 107
                                                                                                                                                                                                                                                                                                                                                             252 PENLKL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNILRR 62
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       51 PENLKL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=28227;
                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L0-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RL10 MYCPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
```

ö

Gaps

ò

0; Indels

similarity).

Query Match

Matches

à ద RESULT 86

ö

Gaps

٠.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseseisb.sib.ch).
  the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
HYPOTHETICAL PROTEIN C28H8.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
Hypothetical protein (228H8.2 in chromosome III precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                  162 AA; 18261 MW; AC4CC72724389AEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 AA; 19547 MW; D4B9BAE3E209752F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               // Match
1.8*; Score 6; DB 1; Let
Local Similarity 100.0*; Pred. No. 1.9e+02;
nes 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Lei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.8%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No. 1.9
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                Lioeub.
                                                                                                                                                                                                                                                                                                                                  Pfam; PF00466; Ribosomal L10; I. PROSITE; PS01109; RIBOSOMAL L10; 1. Ribosomal protein; Complete proteome.
                                                                                                                                                                                                                                                        HAMAÞ; MF 00362; -; 1.
InterPro; IPR001790; Ribosomal L10.
InterPro; IPR002363; Ribosomal L10e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Signal.
SIGNAL 1 21
                                                                                                                                                      EMBL; U39718; AAC71587.1; -.
EMBL; U02206; AAD12496.1; -.
PIR; 164239; 164239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U20861; AAA62290.2; -.
PIR; C88470; C88470.
WormPep; C28H8.2; CE32812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 NNILRR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 FAIMTK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 FAIMTK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 NNILRR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                                                                                                                                                                                                                                      TIGR; MG361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YP92_CAEEL
ID _YP92_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miller N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-ATCC 33330 / G-37;

STRAIN-ATCC 33530 / G-37;

Fraser C.M., Gocayne G.D., White O., Adams M.D., Clayton R.A.,

Fraser C.M., Gocayne J.D., White O., Sutton G., Kelley J.M.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchman J.L., Weidman J.F., Sanal R.V., Sandusky M., Fuhrmann J.L.,

Ngvyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERLEUKIN-2.

BY SIMILABRIY?

O-LINKED (GALNAC. .) (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing.";
J. Bacteriol. 175.7918-7930(1993).
-!- SIMILARITY: Belongs to the L10P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; PubMed-8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A Burvey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 1; Length 162;
100.0%; Pred. No. 1.9e+02;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 20 BY SIMILARITY.
21 162 INTERLEUKIN-2.
79 134 BY SIMILARITY.
23 23 O-LINKED (GALNAC. . .) (BY
70 70 N-LINKED (GCNAC. . .) (PO
162 AA; 18389 MW, 6E572799BLB6E799 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-FRB-1996 (Rel. 33, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Sols ribosomal protein L10.
RPLJ OR RPLIO OR MG361.
                       -:- SIMILARITY: Belongs to the IL-2 family.
                                                                                                                                                                                                                                                                                                                  hase; rolls, commercial problem, property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of t
                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00189; IL2; 1.
PROSITE; PS00424; INTERLEUKIN_2; 1.
SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 92-162 FROM N.A.
                                                                                                                                                                                                                                                                             EMBL; U14682; AAA61733.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 PENLKL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 PENLKL 56
                                                                                                                                                                                                                                                                                                        P01585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RL10 MYCGE
P36263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RL10_MYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
```

ö

Gaps

ö

```
Gas vesicle; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SODC CAUCR STANDARD; F P20379; 01-FEB-1991 (Rel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL939106; CAB61167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 19089 / CB15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 ELILDR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ELILDR 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SODC OR CC1579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SODC_CAUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOW WERE THE STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the S16P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                             Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 6; DB 1; Length 165; Pred. No. 2e+02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00886; Ribosomal_S16; 1.
ProDom; PD003791; Ribosomal_S16; 1.
TIGREPANS; TIGR0002; S16; 1.
PROSITE; PS00732; RIBOSOMAL_S16; FALSE_NEG.
Ribosomal protein; Complete proteome.
SEQUENCE 165 AA; 17837 MW; 61DD81961BC30846 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable gav vesicle structural protein 2 (GVP)
GVPA2 OR SCO0650 OR SCF91.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomycineae, Streptomycetaceae, Streptomyces,
                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sols ribosomal protein S16.
RPSP OR CGL2054.
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
Nakagawa S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP; MF_00385; -; 1.
InterPro; IPR000307; Ribosomal_S16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP005280; BAB99447.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 PTEAVA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 PTEAVA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                     NCBI TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVA2 STRCO
                                                                                        CORGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D9RJB4;
                                                                                                              QBNNX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRCO
                                                                   RS16_CORGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 91
                                        RESULT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATC 1089 / CB15,
MEDLINE=21173699; PubMed=11259647;
MEDLINE=21173699; PubMed=11259647;
MEDLINE=21173699; PubMed=11259647;
Mistram W.C., Peldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Bisen J.A., Heidelberg J.R., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.E., Smit J., Crawen M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steinman H.M., Ely B.; "Copper-zinc superoxide dismutase of Caulobacter crescentus: cloning, sequencing, and mapping of the gene and periplasmic location of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                     -i- FUNCTION: Gas vesicles are small, hollow, gas filled protein structures that are found in several microbial planktonic microorganisms. They allow the positioning of the organism at the favorable depth for growth. GvpA type proteins form the essential core of the structure.

-i- SUBCELLULAR LOCATION: Gas vesicle membrane.

-i- SIMILARITY: Belongs to the gas vesicle protein type A family.
Seeger K., Saunderв D., Sharp S., Squares R., Squares S., Taylor 1
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                   Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)."; Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 1.8%; Score 6; DB 1; Length 170; Local Similarity 100.0%; Pred. No. 2e+02; es 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 AA; 19422 MW; 57C97217BE59ACDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MF_00576; -; 1.
InterPro; IPR000638; Gas vesicle.
Pfam; PF00741; Gas vesicle.
ProDom; PD003598; Gas vesicle; 1.
PROSITE; PS00234; GAS_VESICLE_A_1; 1.
PROSITE; PS00669; GAS_VESICLE_A_2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90264275; PubMed=2345128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriol, 172:2901-2910(1990)
```

°

us-10-025-730-1.oligo.rsp

```
Bukaryota; Metazoa;
Mammalia; Butheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 94
    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                     InterPro; IPR001424; SOD CU_ZN.
Pfam; PF00080; Sodcu; 1.
ProDom; P0000469; SOC CU_ZN, 1.
PROSITE; PS00087; SOD CU_ZN, 1: 1.
PROSITE; PS00312; SOD CU_ZN, 2; 1.
Antioxidant; Oxidoreductage; Metal-binding; Copper; Zinc; Periplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps

    -!- SUBUNIT: Homodimer.
    -!- SUBCELLULAR LOCATION: Periplasmic.
    -!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COPPER (BY SIMILARITY).
COPPER (BY SIMILARITY).
COPPER AND ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 1; Length 174;
100.0%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUPEROXIDE DISMUTASE [CU-ZN]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F3B3C79EF3E3642C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COPPER (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Prec. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                         STRAIN=ATCC 19089 / CB15;
MEDLINE=82265686; PubMed=7050107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE005832; AAK23558.1; -. PIR; A35383; A35383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17100 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M55259; AAA23054.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      285 HKTQPI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P00446; 1YAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         similarity)
                                                                                                                                                       Steinman H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIGR; CC1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
    SOLUTION OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF THE SET OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            and heme 2 (or BH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR005798; Cytb b6 C.
InterPro; IPR005797; Cytb b6 C.
InterPro; IPR005797; Cytch b6 N.
Pfan; PF000133; cytochrome D N; 1.
PROSITE; PS00192; CYTOCHROME B HEME; 1.
PROSITE; PS00193; CYTOCHROME B QO; PARTIAL.
Mitochondrion; Electron transport; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: Binds two heme groups non-covalently. Heme 1 (or BL or b562) is low-potential and absorbs at about 562, and heme 2 (or E or b566) is high-potential and absorbs at about 566 (By
                                                                                                                                                                STRAIN-ISOLAGE LISUMZ 23913; TISSUE-Kidney, and Liver;
Sudman P.D., Barkley L.J., Hafner M.S.;
"Familial affinity of Tomopeas ravus (Chiroptera) based on protein
electrophoretic and cytochrome b sequence data.";
J. Mammal. 75:365-377(1994).
-!- FUNCTION: Component of the ubiquinol-cytochrome c reductase
complex (complex III or cytochrome b-cl complex), which is a
respiratory chain that generates an electrochemical potential
coupled to ATP synthesis (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=Mu50 / ATCC 700699, and N315;
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchlyama I., Baba T., Yuzawa H., Kobayashi I.,
Chordata, Craniata, Vertebrata, Euteleostomi;
Chiroptera, Microchiroptera; Vespertilionidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
-!- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable DNA-directed RNA polymerase delta subunit (RNAP delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRON 1 (HEME BS62 AXIAL LIGAND).
IRON 2 (HEME BS66 AXIAL LIGAND).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytochrome c1 and the Rieske protein (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 83 IRON 1 (HEME B562 AXIAL LI
97 97 IRON 2 (HEME B566 AXIAL LI
176 176 176 0M; 0D271F45A3880F5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879, 196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus (strain Mn50 / ATCC 700699)
Staphylococcus aureus (strain N315), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 1; Ler
Local Similarity 100.0%; Pred. No. 2.1e+02;
es 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tactor).
RPOE OR SAV2128 OR SA1930 OR MW2052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq.
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L19727; AAA17773.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 PLAKII 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 PLAKII 14
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                    NCBI_TaxID=27670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPOE STAAM
ID RPOE STAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   099800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor)
```

ö

15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)

STANDARD;

CYB NYCHU

RESULT 93 CYB_NYCHU Nycticeius humeralis (Evening bat)

Mitochondrion.

Cytochrome b (Fragment) MTCYB OR COB OR CYTB.

OCCEPTO

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matuyama A., Mharuyama A., Mharuyama A.,
Mizuteani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba 'Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Baba T., Tawama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatau K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP003364; BAB58290.1; -.
EMBL; AP00336; BAB43214.1; -.
EMBL; AP004829; BAB5917.1; -.
EINBL; AP004829; BAB5917.1; -.
EINBL; BP0006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E90006; E9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) (HPRT)
HPT OR B0125 OR C0154 OR SF0122 OR S0124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 1; Length 176;
100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae, Escherichia.
NCBI TaxID=562, 217992, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                       Lancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli,
Escherichia coli 06, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 LKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 ÍKLLGE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shigella flexneri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acquired MRSA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MW2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPRT ECO
                                                                                                                                                                                                                                                                                                                       aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 datches
         SO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-
alpha-D-ribose 1-diphosphate.
-!- COFACTOR: Binds 2 magnesium ions per subunit. One of the ions does
not make direct protein contacts (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234. PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Bouttin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S.-R., Schartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-22065829; PubMed-12070315; Guddat LW., vos S., Martin U.L., Keough D.T., de Jersey J.; Guddat LW., vos S., Martin U.L., Keough D.T., de Jersey J.; Crystal structures of free, iMP-, and GMP-bound Escherichia coli hypoxanthine phosphoribosyltransferase."; Protein Sci. 11:1626-1638(2002).

-i- FUNCTION: THIS ENZYME ACTS EXCLUSIVELY HYPOXANTHINE; IT DOES NOT ACT ON GUANINE (EN SIMILABLIX).
                                                                                                                                                                                   SEQUENCE FROM N.A.
SPECIESE.CO.01; STRAIN=KI2 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Ribey M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
SEQUENCE FROM N.A. STAIN-KI2 / W3110;
SPECIRES-B.coli; STAIN-KI2 / W3110;
MEDLINES-94261430; PubMed-8202364;
Fujita N., Mori H., Yura T., Ishihama A.;
Fystematic sequencing of the Bacharichia coli genome: analysis of the 24-4.1 min (110, 917-193, 643 bp) region.";
Nucleic Acids Res. 22:1637-1639(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a; MEDLINE=22990274; PubMed=12704152; Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Man B., Perran M.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; Complete genome sequence and comparative genomics of Shigella
                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Bscherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: Belongs to the purine/pyrimidine phosphoribosyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  flexneri serotype 2a strain 2457T.
Infect. Immun. 71:2775-2786(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
```

```
ö
 oved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
     and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=LTZ / GSG1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCG1elland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: THIS ENZYME ACTS EXCLUSIVELY HYPOXANTHINE, IT DOES NOT ACT ON GUANINE (BY SIMILARITY).
-1- CATALYIIC ACTIVITY: IMP + diphosphate = hypoxanthine + 5-phospho-alpha-D-ribose 1-diphosphate.
-1- COFACTOR: Binds 2 magnesium ions per subunit. One of the ions does
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98198059; PubMed=9521670;
Lee C.C., Craig S.P. III, Bakin A.E.;
"A single amino acid substitution in the human and a bacterial
Mypoxanthine phosphoribosyltransferase modulates specificity for the
binding of guanine.";
                                                                                                                                                      PDB; 1G95; 28-AUG-02.

R PDB; 1G95; 28-AUG-02.

RDB; 1G8V; 13-DEC-02.

RN SS-2DPAGE; P36766; CCLI.

R MISS-2DPAGE; P36766; CCLI.

R InterPro; IPR00599; Hxn phspho trans.

R InterPro; IPR00599; FXTransferase.

R InterPro; IPR001375; PXTransferase.

R ITGRPAMS; TIGR01203; PRTRATSFER; 1.

R PGM; PF001153; PW PYR PR TRANSFER; 1.

R PROSITE; PS00103; PUR PYR PR TRANSFER; 1.

R Transferase; Glycosyltransferase; Purine salvage; Metal-binding; Magnesium; Complete proteome; 3.3-structure.

T GRPAM: 159 159 MAGNESTUM (BY SIMILARITY).

SEQUENCE 178 AA; 20115 MW; ELA75EB66231DC32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-0CT-2003 (Rel. 42, Last annotation update)
Hypoxanthine phosphoribosyltransferase (BC 2.4.2.8) (HPRT).
HPT OR STM0170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 AA.
 this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match
Local Similarity 100.0%; Pred. No. 2.1.
es 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                    EMBL, AE000122; AAC73236.1; ALT INIT.
EMBL; AE016755; AAN78648.1; ALT_INIT.
EMBL; AE015050; AAN41785.1; ALT_INIT.
EMBL; AE016978; AAP15666.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                       EMBL; D26562; BAB96700.1; ALT INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 37:3491-3498(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=LT2 / GP660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 VKILKD 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=602;
modified and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPRT SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPRT
ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. Columbia;

MEDLINE=21016720; bubMed=11130713;

MEDLINE=21016720; bubMed=11130713;

Alanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,

Balanoubat M., Lemcke K., Rieger M., Perez-Alonso M., Obermaier B.,

Balanoubat M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

Bolsimone V., Choisne N., Artiguenave F., Robert C., Brottier P.,

Mincker P., Catcolico L., Waissenbach J., Saurin W., Quetier P.,

Mincker P., Catcolico L., Waissenbach J., Saurin W., Benes V.,

Rohaeller M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,

Wurmbach E., Drzonek H., Berlle H., Holland R., Bangert S.,

Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,

Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,

Reichelt J., Scharfe M., Schoon O., Bargues M., Terol J., Climent J.,

A Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Verdoucg L., Meyer Y.; "Characterisation of the Arabidopsis thaliana thioredoxin f family."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THEI ARATH STANDARD; PRT; 178 AA.

O9XFR18; O9MFR5;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2003 (Rel. 41, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

Thioredoxin F-type 1, chloroplast precursor (TRX-F1).

Arabidopsis thaliana (Mouse-ear cress).

Arabidopsis thaliana (Mouse-ear cress).

Arabidopsis thaliana (Mouse-ear cress).

Subermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosaids II; Brassicales; Brassicaceae; Arabidopsis.

NCBL TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRPAMS; TIGR01203; HGPRTase; 1.
PROSITE; PS00103; PUR PYR PR TRANSFER; 1.
Transferase; Glycosyltransferase; Purine salvage; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAGNESIUM 1 (BY SIMILARITY).
5A52B93CAB331357 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 178; . 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
not make direct protein contacts (By similarity).
                 -!- PATHWAY: Purine Balvage.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUMILARITY: Belongs to the purine/pyrimidine phosphoribosyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Scor.
100.0%; Pred. No. 2....
                                                                                                                                                                                                                                                                                                                           HSSP; Q26997; 1QK3.
StyGene; SG10756; hpt.
InterPro; IPR005904; Hxn_phepho_trans.
InterPro; IPR0023075; Pr/py_rp_transf.
InterPro; IPR000836; PRTransferase.
Pfam; PF00156; Pribosyltran,
                                                                                                                                                                                                                                                                                        EMBL; AF008931; AAC46255.1; -. EMBL; AE008702; AAL19134.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Magnesium, Complete proteome.
METAL 159 159 M
SEQUENCE 178 AA, 20068 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity luv...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 VKILKD 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THF1_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 97
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
```

0;

Gaps

ö

0; Indels

Score 6; DB 1; Length 178; Pred. No. 2.1e+02;

100.0%; Pred. No. 2.1 tive 0; Mismatches

Local Similarity 100. Les 6; Conservative

Matches

1.8%;

A -> P (IN REF. 1). ; 7B4E6CFE8F2714BD CRC64;

134 134 A 178 AA; 19325 MW;

SEQUENCE Query Match

CONFLICT

FT

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the between the Swiss Institute of Bioinformatics Institute. There are or estrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta B.,
Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
Monnhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
Mannhaupt G., Raizo M., Walts A., Utterback T., Fujic C.Y., Shea T.P.,
Rooney T., Rizzo M., Walts A., Utterback T., Fujic C.Y., Shea T.P.,
A Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
Pruess D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
Rasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
Kiyokawa C., Kohara M., Mateumoto M., Matsuno A., Muraki A.,
Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
Watanabe A., Yamada M., Yasuda M., Tabata S.,
H., Hailing M., Yasuda M., Tabata S.,
H., Hailing M., Yasuda M., Tabata S.,
H., Hailing M., Tabata S.,
H., Hailing M., Tabata S.,
H., Hailing M., Tabata S.,
H., Hailing M., Tabata S.,
H., Hailing M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE=22954850; Pubmed=14593172;
A WEDILINE=22954850; Pubmed=14593172;
A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
A Karlin-Newmann G., Liu S.K., Lam B., Sakano H., Wu T., Yu G.,
Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
A Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akryama K., Ansari Y.,
A Rakawa T., Banh J., Banno F., Boweer I., Brooks S.Y., Carninci P.,
A Rakawa T., Dannon-Hopson C., Hsuan V.W., Iida K., Karnes M.,
A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
A Khan S., Koesema E., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
A Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
T. Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Redox-active center; Electron transport; Chloroplast; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 302:842-846(2003).

-!- FUNCTION: Participates in various redox reactions through the reversible oxidation of the active center dithiol to a disulfide. The F form is known to activate a number of enzymes of the photosynthetic carbon cycle (By similarity).
-!- SUBCELLULAR LOCATION: Chloroplast (By similarity).
-!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY. PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell Feldmann K.A.; "Full-length cDNA from Arabidopsis thaliana."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHLOROPLAST (POTENTIAL). THIOREDOXIN F-TYPE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006663; Thioredox_dom2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00194; THIOREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF144385, AAD35003.1; -... EMBL, AC018363; AAF26987.1; -... EMBL, AY084778, AAM61345.1; -... EMBL, AY065391; AAL38822.1; -... EMBL, AX066721; AAM20355.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00421; THIOREDOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P10599; 1AIU.
InterPro; IPR006662; Thiored
                                                                                                                                                                                                                                                                                                                                                                                                     Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00085; thiored; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
178
102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSIT
```

REDOX-ACTIVE (BY SIMILARITY).

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=RIMD 2210633 / Serotype O3:K6;
MEDLINE=22208454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Ijijima Y., Najima M., Nakano M., Yanashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                  Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.8%; Score 6; DB 1; Length 179;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 protein, Complete proteome.
179 AA; 20742 MW; F016FB0E5F63AAD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               distinct from that of V. cholerae.";
Lancet 361:743-749(2003).
-!- SIMILARITY: Belongs to the UPF0227 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P60085; Q8XFC9;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                       [0-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP005076; BAC59232.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF_01047; -; 1.
InterPro; IPR008886; UPP0227.
Pfam; PP065728; UPP0227; 1.
Hypothetical_protein; Complete
                                                                                                                                                                                                             Hypothetical protein VP0969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Syd protein.
SYD OR STY3106 OR T2875.
                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                 parahaemolyticus.
                                                                                                                                                                                                                                                                                     Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 LOAMKE 175
                                 146 KILKDN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 LOAMKE 51
19 KILKON 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhi
                                                                                                                                                                                                                                                                                                     NCBI_TaxID=670;
                                                                                                                                                                          10-OCT-2003
                                                                                                                       VIBPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYDP SALTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                    Q87R29;
                                                                                                                                                                                                                                                   Vibrio
                                                                                                        Y969 VIBPA
ID Y969 V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYDP_SALTI
                                                                                                                         ò
```

```
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rudd K.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YHCE_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 101
  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·
0
                                                              Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chlingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Choulingworth T., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Mhitchead S., Barrell B.G., "Complete genome sequence of a wultiple drug resistant Salmonella enterica servar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 185:2330-2337(2003).

-!- FUNCTION: Interacts with the secY protein in vivo. May bind preferentially to an uncomplexed state of secY, thus functioning either as a chelating agent for excess secY in the cell or as a regulatory factor that negatively controls the translocase function (By similarity).

-:- SUBCELBULAR LOCATION: Loosely associated with the cytoplasmic side
                                                                                                                                                                                                                                       STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                          of the inner membrane, probably via secY (By similarity) SIMILARITY: Belongs to the Syd family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 1; Length 181; 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AA; 20518 MW; B5A36E754F43C8D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYDP_SALTY STANDARD; PRT; 181 AA. P60084; QBXFC9; Created) 15-MAR-2004 (Rel. 43, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=LT2 / SGSC1412 / ATCC 700720;
                                                   MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE016843; AAO70431.1; -. EMBL; AL627276; CAD06080.1; -.
                                                                                                                                                                                                      Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_01104; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 QFADEK 322
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 QFADEK 97
                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Syd protein.
SYD OR STM2967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=602;
 NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYDP SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -I-FUNCTION: Interacts with the secy protein in vivo. May bind preferentially to an uncomplexed state of secy, thus functioning either as a chelating agent for excess secy in the cell or as a regulatory factor that negatively controls the translocase function (By similarity).

-I-SUBCELLULAR LOCATION: Loosely associated with the cytoplasmic side of the inner membrane, probably via secy (By similarity).
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nauyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished observations (APR-1995).
-!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THIS PROTEIN IS
TRUNCATED BY AN ISS ELEMENT WHICH IS INSERTED BETWEEN POSITION 123
                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.8%; Score 6; DB 1; Length 181;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AA; 20518 MW; B5A36E754F43C8D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THEE ECOLI STANDARD; PRT; 181 AA. P4542; P76674; P6674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7674; P7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE008836; AAL21846.1; -.
StyGene; SG????; syd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONCEPTUAL TRANSLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF 01104; -; 1.
Complete proteome.
SEQUENCE 181 AA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      317 QFADEK 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 OFADEK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
```

```
ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the EMBL outstation.

the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Redox-active center; Electron transport; Chloroplast; Transit peptide. TRANSIT 1 ? CHLOROPLAST (POTENTIAL). CHAIN ? 182 THIOREDOXIN F-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mora-Garcia S.E.F., Rodriguez-Suarez R.J., Wolosiuk R.A.;
Submitted (Aug-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Participates in various redox reactions through the reversible oxidation of the active center dithiol to a disulfide.
The F form is known to activate a number of enzymes of the photosynthetic carbon cycle (By similarity).
-!- SUBCELLULAR LOCATION: Chloroplast (By similarity).
-!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY. PLANT F-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 105 REDOX-ACTIVE (BY SIMILARITY).
182 AA; 19757 MW; 9EE3E6AC7C0F3SA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 181; 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                         Ecodene, EG12811; yhcE.
Hypothetical protein, Complete proteome.
SEQUENCE 181 AA; 19192 MW; 6CE38D142ED90B5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-B-SEB-2003 (Rel. 41, Last amonotation update)
Thioredoxin F-type, chloroplast precursor (TRX-F).
                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 1
100.0%; Pred. No. 2.1.
tive 0; Mismatches
                                                                                                                                                                                                                             EMBL; U18997; AAA58019.1; ALT SEQ.
EMBL; AE000401; AAC76249.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P10599; IAIU.
InterPro, IPR006662; Thiored.
InterPro, IPR006663; Thioredox dom2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00085; thiored; 1.
PRINTS; PR00421; THIOREDOXIN.
PROSITE; PS00194; THIOREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF018174; AAC04671.1; -.
PIR; T07837; T07837.
                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity luv..
Fra 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica napus (Rape)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Thes 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 IASDAF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 IASDAF 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THIF BRANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THIP BRANA
THIP BRANA
THIP BRANA
THIP BRANA
AC 0488 JF
DT 16-OCT-
DT 28-FEB-
DE Thiore
GN SPERSION
OC SPERSION
OC SPERSION
OC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC SPERSION
CC 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 048897
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHINTELE TATE OF THE PROPERTY OF THE PRINTS; PRO0421; THIOREDOXIN.

PROSITE; PS00194; THIOREDOXIN.

REGOX-active center; Electron transport; Chloroplast; Transit peptide.

TRANSIT 1 69 CHLOROPLAST (POTENTIAL).

CHAIN 70 182 THIOREDOXIN F-TYPE.

DISULFID 106 109 REDOX-ACTIVE (BY SIMILARITY).

SEQUENCE 182 AA; 19775 MW; 158FC352C89E0FF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lepiniec L., Hodges M., Gadal P., Cretin C.,
"Isolation, characterization and nucleotide sequence of a full-length
pea cDNA encoding thioredoxin-f in the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Mol. Evol. 42:422-431(1996).
-!- FUNCTION: Participates in various redox reactions through the reversible oxidation of the active center dithiol to a disulfide. The F form is known to activate a number of enzymes of the photosynthetic carbon cyole.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY. PLANT F-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                  Thioredoxin F-type, chloroplast precursor (TRX-F).
Pienm sativum (Garden pea).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Bermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96215867; PubMed=8642611;
Sahrawy M., Hecht V., Lopez Jaramillo J., Chueca A., Chartier Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meyer Y.; Intron position as an evolutionary marker of thioredoxins and "Intron position as an evolutionary marker of thioredoxins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 1; Le1
100.0%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last Beguence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 100.0%; Pred. No. 4.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X63537; CAA45098.1; -.
EMBL; U35830; AAC49357.1; -.
PIK; S20929; S20329.
INFSP; PLO559; LAIU.
InterPro; IPR006662; Thiored.
InterPro; IPR006663; Thioredox_dom2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92256804; PubMed=1581563;
                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thioredoxin domains."
                                                               149 KILKDN 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 KILKDN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
KILKDN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 KILKDN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3888;
                                                                                                                                                                                   THIF PEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                   P29450;
                                                                                                                                                                 RESULT 103
                                                                                                                                                                                                                                                                   QC
```

. 0

Gaps

. 0

1.8%; Score 6; DB 1; Length 182; 100.0%; Pred. No. 2.1e+02; live 0; Mismatches 0; Indels

Conservative

```
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00085; thiored;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185
                SEQUENCE FROM N.A.
Verdoucg L., Meyer Y.;
"Characterisation of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 KILKDN 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 KILKDN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=11264;
                                                                                                                                                                                                                                                                                         Pl clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VMA2_TRTV
ID VMA2_TRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 106
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gen. Genet. 258:363-372(1998).
FUNCTION: Involved in peptide bond synthesis. Stimulates efficient FUNCTION: Involved in peptide-bond synthesis on native or reconstituted 708 ribosomes in vitro. Probably functions indirectly by altering the affinity of the ribosome for aminoacyl-tRNA, thus increasing their reactivity as acceptors for peptidyl transferase (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99XEMS.
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last sequence update)
Thioredoxin F-type 2, chloroplast precursor (TRX-F2).
AFSG16400 OR MOK4.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; NCBI_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Abratt V.R., Mbewe M., Woods D.R., "Cloning of an EF-P homologue from Bacteroides fragilis that increases B. fragilis glutamine synthetase activity in Bscherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                            Bacteroides fragilis.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- PATHWAY: Frotein biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the elongation factor P family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 185;
. 2.2e+02;
ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01132; EFP; 1.
TIGRFAMS; TIGR00038; efp; 1.
PROSITE; PS01275; EFP; 1.
Protein biosyntheels; Elongation factor.
SEQUENCE 185 AA; 20812 MW; 2457150F941A240E CRC64;
                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
08-EBE-2003 (Rel. 41, Last annotation update)
Elongation factor P (EF-P).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.8%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No. 2.2
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98311074; PubMed=9648740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U75509; AAC26328.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF_00141; -; 1.
InterPro; IPR001059; EF-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 KLIEFL 305
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 KLIEFL 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
                                                                                                                                                                                                                                                                                NCBI_TaxID=817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THF2 ARATH
                                                                                                                                                                                                                                                                                                                                                 STRAIN-BF1
                                                       EFP BACFR
           RESULT 104
EFP BACFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOW THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ሯ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                       STRAIN=cv. Columbia; MEDLINE=97471969; PubMed=9330910; Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M., Miyalima N., Tabbata S.; "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Redox-active center; Blectron transport; Chloroplast; Transit peptide;
"Characterisation of the Arabidopsis thaliana thioredoxin f family."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                          PUNDA Res. 4:215-230(1997).

-!- FUNCTION: Participates in various redox reactions through the reversible oxidation of the active center dithiol to a disulfide. The F form is known to activate a number of enzymes of the photosynthetic carbon cycle (By similarity).
-!- SUBCELLULAR LOCATION: Chloroplast (By similarity).
-!- SIMILARITY: BELONGS TO THE THIOREDOXIN FAMILY. PLANT F-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=9233325; PubMed=1629697;
Ling R., Easton A.J., Pringle C.R.;
"Sequence analysis of the 22K, SH and G genes of turkey
rhinotracheitis virus and their intergenic regions reveals a gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
1-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1995 (Rel. 32, Last senotation update)
Matrix glycoprotein M2 (Envelope-associated 22 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 185 THIOREDOXIN P-TYPE 2.
109 112 REDOX-ACTIVE (BY SIMILARITY).
185 AA; 19999 MW; DB7EA3FAA35EDDSC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; BBRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Metapneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Ler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AB005242; BAB09607.1; -.
HSSP, P10599; IANU.
InterPro; IPR006662; Thiored.
InterPro; IPR006663; Thioredox_dom2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Turkey rhinotracheitis virus (TRTV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00421; THIOREDOXIN.
PROSITE; PS00194; THIOREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF144386; AAD35004.1; -.
```

ö

```
between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 403:665-668(2000).
-!- FUNCTION: Links a guanosine 5' phosphate to molydopterin (MPT)
forming molybdopterin guanine dinucleotide (MGD) (By similarity).
-!- PATHWAY: Molybdenum cofactor biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the mobA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAINE-NCTC 11168;
MEDIATE-2012; PubMed=10688204;
MEDIATE-2012; PubMed=10688204;
Barkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.W., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Ouail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.,
The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Probable molybdopterin-guanine dinuclectide blosynthesis protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
                                                                                                                                             MEDITNE=92300329; PubMed=1607858;
Yu Q., Davis P.J., Brown T.D.K., Cavanagh D.;
"Sequence and in vitro expression of the M2 gene of turkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 1; Length 186;
100.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
      other pneumoviruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 4.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reveals hypervariable sequences.";
                                                                                                                                                                                                                                                                                    J. Gen. Virol. 73:1355-1363(1992).
                                Gen. Virol. 73:1709-1715(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                       rhinotracheitis pneumovirus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S40185; AAB22544.1; -. EMBL; X63408; CAA45004.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campylobacter jejuni.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 LAKIIL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAKIIL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                         STRAIN=UK/3BV/85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOBA CAMJE
Q9PMU9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE RRENE R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C2A / ATCS 3535 / DSM 2834;

MEDLINE=21929760; PubMed=11932334;

MEDLINE=21929760; PubMed=11932334;

RA dalagan J.B., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

RA Linton L., McEwan P., McKernan K., Talrell A., Ye W.,

RA Linton L., McMaram-Smith C., Kuettner H.C., Krzycki J.A.,

RA Hedderich R., Ingaram-Smith C., Kuettner H.C., Krzycki J.A.,

RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.M., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

Rerry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,

Rerry J.G., Jarrell K.F., Swanson R.V., Zinder S.H., Lander E.,

RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Pritchet M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA The genome of Methanosarcina acetivorans reveals extensive metabolic

RT and physiological diversity.";

Genome Res. 12:532-542(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
    There are no restrictions on
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                 PIR; C81279; C81279.

HAMAP; MF 00316; -; 1.

Molybdenum cofactor biosynthesis; GTP-binding; Complete proteome. SEQUENCE 191 AA; 22341 MW; 98521199C79C1B46 CRC64;
                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                Score 6; DB 1; Lengtu ...;
Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 1; Length 198;
100.0%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9D5B2C3A07DC6918 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the UPF0228 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 AA
                                                                                                                                                                                                                                                                     Match
Local Similarity 100.0%; Pred. No. 2.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 2...
Matches 6; Conservative 0; Mismatches
                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Complete proteome.
SEQUENCE 198 AA; 23463 MW; 9D5B2C3AC
    the European Bioinformatics Institute.
                                                                                                                                 EMBL; AL139078; CAB73777.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE011115; AAM07380.1; -. InterPro; IPR008887; UPF0228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein MA4032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanosarcina acetivorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF05727; UPF0228;
                                                                                                                                                                                                                                                                                                                                                              201 FLEONY 206
                                                                                                                                                                                                                                                                                                                                                                                                         112 FLEONY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y4D2 METAC
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MA4032
SSSSSSR##¥8
                                                                                                                                                                                                                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

ð

139 LAILEK 144

d

ö

Gaps

1.8%; Score 6; DB 1; Length 199; 100.0%; Pred. No. 2.3e+02; ive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100...
6; Conservative

60 EPPTEA 65

ð

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=2238257; PubMed=12477932;

RESUE=Ovary;

RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.D., Collins P.S., Wagner L. Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Bhat N.K.,

Hopkins R.E., Jordan H., Moore T., Max S.I., Wang J., Habie F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rab Diatchenko L., Wagner T.B., Toshhyuki S., Carninoir P., Prange C.,

Rab S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley R.C., McKernan K.J., Malek J.A., Gunarathe P.H.,

Raba S.S., Worley K.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schwuck J., Myers R.M.,

Blakesley R.W., Touchman J.W., Schwuck J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Ruden and mouse CDNA sequences.",

"Generation and initial analysis of more than 15,000 full-length

Ruman and mouse CDNA sequences.",

"Generation M.A., Might play a role in mitosis. Antigenic molecule. Could

"C., ProcTION: Might play a role in mitosis. Antigenic molecule.

"C., Antibonies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98145811; PubMed=9486406;
Muro Y., Yamada T., Himeno M., Sugimoto K.;
"cDNA cloning of a novel autoantigen targeted by a minor subset of
                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                              15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Sjogren's syndrome/scleroderma autoantigen 1 (Autoantigen p27).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO-RICH:
SER/THR-RICH:
EF08439FDFFAlDAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASP/GLU-RICH (ACIDIC)
                                                               199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clin. Exp. Immunol. 111:372-376(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 606044; -.
GO; GO:0007067; P:mitosis; TAS.
Antigen; Mitosis.
                                                                                                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB001740; BAA25263.1; -.
EMBL; BC014791; AAH14791.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21474 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-centromere antibodies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:11328; SSCAl.
GK; 060232; -.
                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
122
145
177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
113
138 1
170
199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibodies.
                                                               AA27 HUMAN
060232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                     AA27 HUMAN

1D AA27 H

AA27 HUMAN

DT 10-JUL

DT 10-JUL

DE SSCA1

OC MAMMAN

OC MAMMAN

OC MAMMAN

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

OC BUKARY

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
RESULT 109
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                     30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sjogren's syndrome/scleroderma autoantigen 1 homolog (Autoantigen p27
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                STRAIN=ICR; TISSUE=Forebrain;
MEDLINE=99443733; PubMed=10512749;
Sakuma-Takagi M., Tohyama Y., Kasama-Yoshida H., Sakagami H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 1; Length 199;
100.0%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB012727; BAA87048.1; -.
SEQUENCE 199 AA; 21336 MW; 13A5222048009E00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMI CAMJE

TO 99PMS6; Q9ZF65;

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DD 28-FEB-2003 (Rel. 41, Last sequence update)

DD 28-FEB-2003 (Rel. 41, Last sequence update)

DD 28-FEB-2003 (Rel. 41, Last annotation update)

DE HAMI protein homolog.
                                                                            199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 2.3
                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campylobacteraceae; Campylobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 6; Conservative
                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Campylobacter jejuni.
 14 EPPTEA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 EPPTEA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 EPPTEA 19
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=OH4384;
                                                                         AA27 MOUSE
P56873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                            RESULT 110
AA27 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 111
g
                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                    STATE TENTE TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD TO COULD 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
Gilbert M., Michniewicz J., Wakarchuk W.W., "Cloning of a multidrug-efflux transporter homolog from Campylobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                            MEDITRE 20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11 midazole glycerol phosphate synthase subunit hisH (BC 2.4.2.-) (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hisH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-AND9 / DSM 6324 / JCM 9639;
MEDLINE=21927647; PubMed=11930014;
MEDLINE=21927647; PubMed=11930014;
MEDLINE=21927647; PubMed=11930014;
SLesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
Natale D.A., Rogozia I.B., Tatusov Y.E., Wolf Y.I., Stetter K.O.,
Malykh A.G., Koonin E.V., Kozyavkin S.A.;
"The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaeal methanogens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 1; Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                 Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y -> H (IN REF. 1).
; 02F29AF6FEB0FBA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the HAM1 NTPase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 2.3e+02; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, Q57679; 1B78.
HWARP, MF 01405; -; 1.
InterPro; IPR002637; Hamlp_like.
Fram; FF01725; Hamlp_like; 1.
FroDom; PD004952; Hamlp_like; 1.
TIGREAMS; TIGRO0042; TIGRO0042; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF113952; AAD10059.1; -. EMBL; AL139078; CAB73801.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 AA; 22375 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanopyrus kandleri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C81282; C81282.
; Q57679; 1B78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 LAKIIL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 LAKIIL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                               STRAIN=NCTC 11168;
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR MKISIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HISS METKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBTVB3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
    RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRER RRARRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
               -!- FUNCTION: IGPS catalyzes the conversion of PRFAR and glutamine to IGP. AICAR and glutamate. The hish subunit provides the glutamine amidotransferase activity that pracduces the ammonia necessary to hisp for the synthesis of IGP and AICAR (By similarity).
-!- CATALYTIC ACTIVITY: 5- [(5-phospho-1-deoxyribhlos-1-ylamino)methylideneamino]-1-[-5-phosphoribosyl)imidazole-4-carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-aminoimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)0.
                                                                                                                                                                                                                -1- PATHWAY: Histidine biosynthesis; fifth step.
-1- SUBUNT: Heterodimer of hisH and hisk [8] similarity).
-1- SUBCELLULAR LOCATION: Cytoplasmic [8] similarity).
-1- SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=S2886 / AB972;
MEDLINE=97313268; PubMed=9169872;
Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Oddll C., Pearson D., Rajandream M.A. Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical 23.2 Exb protein in ABF2-CHL12 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.3e+02;
nes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 BY SIMILARLIL.
22013 MW; E46FEAD5E28EA035 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: Belongs to the cytochrome b5 family.
Natl. Acad. Sci. U.S.A. 99:4644-4649(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 1
100.0%; Pred. No. 2.3
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP; MF_00278; -; 1.
InterPro; IPR000991; GATase_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE010441; AAM02723.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 387:90-93(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 1
200 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 LKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 LKLLGE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome. ACT_SITE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79
179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YMW3_YEAST
ID YMW3_YEAST
AC Q04772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
```

```
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 423:87-91(2003).
-!- CATALYNIC ACTIVITY: N-(5-phospho-beta-D-ribosyl)-anthranilate = 1-(2-CATALYNIC ACTIVITY: N-(5-phospho-beta-D-ribosyl) -anthranilate = 1-(2-CATALYNIC ACTIVITY: N-(5-CATALYNIC ACTIVITY: Tryptophan biosynthesis; third step.
-!- SAMILARITY: Belongs to the trpF family.
                                                                                                                                                                                                                                                                                               IRON (HEME AXIAL LIGAND) (BY SIMILARITY). IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T., Overbeek N., Ypuides N., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Kyrpides N., "Genome sequence of Bacillus cereus and comparative analysis with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
W. (5'-phosphoribosyl)anthranilate isomerase (EC 5.3.1.24) (PRAI).
TRPF OR BC1236.
                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 1; Length 201;
100.0%; Pred. No. 2.3e+02;
7ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus,
                                                                                                                                                                                                                                                                                                                                      7686ElDEF08DDDFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isomerase; Tryptophan biosynthesis; Complete proteome.
SEQUENCE 202 AA; 22556 MW; 42EB66CEE351304B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus cereus (strain ATCC 14579 / DSM 31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 AA.
                                                                                           PIR; S52833; S52833.
HSSP; P00175; 1FCB.
GermOnline; 142739; -.
SGD; S0004677; YMRO73C.
InterPro; IRR001199; Cyt_B5.
Pfam; PF00173; heme_l; 1.
ProDom; P000173; heme_l; 1.
PROSITE; PS00191; CYTOCHROME_B5_1; 1.
PROSITE; PS0191; CYTOCHROME_B5_1; 1.
HYPORITE; PS0191; CYTOCHROME_B5_2; 1.
HYPORTE; PS0191; CYTOCHROME_B5_2; 1.
HYPORTEI protein; Heme.
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22608415; PubMed=12721630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE017001; AAP08221.1; -.
                                                                                                                                                                                                                                                                                                                                  201 AA; 23182 MW;
                                                                               EMBL; Z48952; CAA88798.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF 00135; -; 1.
InterPro; IPR001240; PRAI.
Pfam; PF00697; PRAI; 1.
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity luv...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus anthracis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 YEKLLQ 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 YEKLLO 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=226900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRPF BACCR
                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              081666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRPF BACCR
  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
```

1.8%; Score 6; DB 1; Length 202; 100.0%; Pred. No. 2.3e+02;

Best Local Similarity

Query Match

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                        Sandmeier H., Iida S., Huebner P., Hiestadt-Nauer R., Arber W.;
"Gene organization in the multiple DNA inversion region min of plasmid
pl5B of E.coli 15T-: assemblage of a variable gene.";
Nucleic Acids Res. 19:5831-5838 (1991).
-!- SIMILARITY: BELONGS TO THE TPA FAMILY.
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97313264; Pubmed=9169868;
Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical 23.5 kDa protein in LCD5-PAK1 intergenic region.
YER128W OR SYGP-ORF44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 1; Length 203; 100.0%; Pred. No. 2.4e+02; Live 0; Mismatches 0; Indels
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 AA; 22198 MW; 7D7245C2BE2403DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetales; Saccharomycetaceae; Saccharomyces
 .;
                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 AA.
 0; Mismatches
                                                                                                                                                                                                                         Tail fiber assembly protein homolog
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92051368; PubMed=1945872;
                                                                                                                                                                                                                                                                                                           Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X62121; CAA44047.1; -. PIR; S18684; S18684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003458; DUF144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02413; Caudo_TAP; 1.
6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 6; Conservat
                                                              182 EGKKDV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 TKRQSL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 TKRQSL 229
                              92 EGKKDV 97
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                            NCBI TaxID=562;
                                                                                                                                                                                                                                                                              Plasmid p15B.
                                                                                                                                                                                                                                                                                                                                                                             STRAIN=15T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEV8_YEAST
ID _YEV8_YEAST
                                                                                                                                             TFAB ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                              047427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P40080:
                                                                                                              RESULT 115
TFAB_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 116
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                              ઠે
                                                             g
                                                                                                                                                              g
```

or send an email to license@isb-sib.ch).

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation --
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.L.,
Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Buncan M., Guzana E., Hartzell G., Huncke-Smith S., Hyman R.W., Kayer A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 423:81-86(2003).
-!- CATALYTIC ACTIVITY: N-(5-phospho-beta-D-ribosyl)-anthranilate = 1-
(2-carboxyphenylamino)-1-deoxy-D-ribulose 5-phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T., Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Holtzapple B.K., Okstad O.A., Helgason E., Rilstone J., Wu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M., DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F., Hazen X., Chine R.D., Wolf A.M., Watkins K.L., Nierman W.C., Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L. Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome sequence of Bacillus anthracis Ames and comparison to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 41, Last annotation update)
N-(5'-phosphoribosyl)anthranilate isomerase (BC 5.3.1.24) (PPAI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 1; Length 203; 100.0%; Pred. No. 2.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus anthracis (strain Ames).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                    Germonline; 139207; -.
SGD; S0000930; YER128W.
Hypothetical protein.
SEQUENCE 203 AA; 23488 WW; 819930CSODDS6B1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: Tryptophan biosynthesis; third step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22608414; PubMed=12721629;
                                                                                                                                                                                                                                                                                                                                                                         EMBL; U18916; AAC03226.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             closely related bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                        Nature 387:78-81(1997).
                                                                                                                                                                                                                                                                                                                                                                                             PIR; S43222; S43222.
GermOnline; 139207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 EAVAOL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 EAVAOL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI TaxID=198094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRPF OR BA1252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINE-2388257; PubMed=12477932;

MEDINE-2388257; PubMed=12477932;

MEDINE-2388257; PubMed=12477932;

MEDINE-2388257; PubMed=12477932;

MARALINE-22388257; PubMed=12477932;

MARALINE-22388257; PubMed=12477932;

MARALINE-2388257; PubMed=12477932;

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE-25.

MARALINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Immature colon cardinoma transcript 1 (Digestion substraction 1) (DS-
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96163468; PubMed=8575443; van der Made A.C.J., Nozawa Y., van Belzen N., Diesveld M.P.G., van der Made A.C.J., Nozawa Y., Dinjens W.N.M., Vlietstra R., Trapman J., Bosman F.T.; "Identification of mRNAs that show modulated expression during colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- TISSUE SPECIFICITY: Down-regulated during the in vitro differentiation of HT29-D4 colon carcinoma cells.
-!- SIMILARITY: TO C.ELEGANS RO2F2.2 AND YEAST YOL114C.
                                                                                                                                                                                                                                                                           DB 1; Length 204;
                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                  Isomeraee, Tryptophan biosynthesis, Complete proteome. SEQUENCE 204 AA, 22619 MW; F153422997A4D765 CRC64;
                                                                                                                                                                                                                                                                                                  100.0%; Pred. No. 2.4e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                              Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      carcinoma cell differentiation.";
Eur. J. Biochem. 234:843-848(1995).
                                              EMBL; AE017028; AAP25210.1; -.
                                                                                                                                                                                                                                                                           1.8%;
                                                                                                 HAMAP, MF 00135; -; 1.
InterPro; IPR001240; PRAI.
Pfam; PF00697; PRAI; 1.
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                       184 EGKKDV 189
                                                                                                                                                                                                                                                                                                                                                                                      92 EGKKDV 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CT1 OR DS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICT1 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 118
ICT1_HUMAN
SS####₩8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

206 AA; 22617 MW; 3D9F4E9DFDB34DAD CRC64;

SEQUENCE

Š

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as Inspected and this statement is not removed. Usage by and for commercial
       oved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- FUNCTION: Removes 5-oxoproline from various penultimate amino acid
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           residues except L-proline (By similarity).
-!- CATALYTIC ACTIVITY: 5-oxoprolyl-peptide + H(2)0 = 5-oxoproline +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MB4 / JCM 11007;
MEDLINE=21992816; PubMed=11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chan Y., Xua Y., Lai X., Huang L., Dong X., Ma Y., Ling L.
Tan H., Chen R., Wang J., Yu J., Yang H.,
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700[2002].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pyrrolidone-carboxylate peptidase 2 (BC 3 4.19.3) (5-oxoprolyl-peptidase_2) (Fyroglutamyl-peptidase I 2) (FGP-I 2) (Fyrase 2).
                                                                                                                                                                                                                                                                     ,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
                                                                                                                                                                                                                            1.8%; Score 6; DB 1; Length 206;
100.0%; Pred. No. 2.4e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                            206 AA; 23630 MW; 663BF52443D41540 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide.
-!- SUBUNIT: Homotetramer (By similarity).
-!- SUBCELIULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to peptidase family C15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Thiol protease; Complete proteome.
ACT_SITE 78 78 BY SIMILARITY.
ACT_SITE 141 141 BY SIMILARITY.
ACT_SITE 165 165 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermoanaerobacteriaceae, Thermoanaerobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                  206 AA.
modified and this statement is not removed.
                  entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                     InterPro; IPR000352; Pep_rel_factor_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probom, PD008480, Peptidase C15; 1.
TIGRHAMS; TIGR00564; Dyro pdase; 1.
PROSITE; PS01334; PYRASE CYS; 1.
PROSITE; PS01333; PYRASE GLU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF_00417; -; 1.
InterFro; IPR000816; Peptidase_C15.
Pfam; PF01470; Peptidase_C15; 1.
                                                               EMBL; X81788; CAA57387.1; -.
EMBL; BC015335; AAH15335.1; -.
PIR; S63540; S63540.
Genew; HGNC:5359; ICT1.
MIM; 603000; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE013116; AAM24815.1; -.
                                                                                                                                                                                                                                              Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                        Pfam, PF00472; RF-1; 1
                                                                                                                                                                                                                                                                                                   232 LGELIL 237
                                                                                                                                                                                                                                                                                                                                      130 LGELIL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCP2 OR TTE1612
                                                                                                                                                                                                                                                                                                                                                                                                                              PCP2_THETN
O8R9J6;
                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                Best Loca
Matches
ð
```

```
..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                    Cruciere C., Laporte J.; "Sequence and analysis of bovine enteritic coronavirus (F15) genome. "Sequence and analysis of coding for the nucleocapsid protein; analysis of the predicted protein.";
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                   01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein in nucleocapsid ORF (IORF).
Byoine cronavirus (strain F15) (BCOV) (BCV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae, Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
18-FEB-2004 (Rel. 43, Last annotation update)
Probable translation initiation factor 2 beta subunit (eIF-2-beta).
EIF2B OR TA0665.
                                    .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
1.8%; Score 6; DB 1; Length 206; 100.0%; Pred. No. 2.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 1; Length 207;
100.0%; Pred. No. 2.4e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al protein.
207 AA; 23001 MW; A4E5DE61171BAB50 CRC64;
                                                                                                                                                                                     207 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ann. Inst. Pasteur Virol. 139:123-138(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=89087718; PubMed=3207501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M36656; AAA42759.1; -..
PIR; S06869; S06869.
InterPro; IPR004876; Corona_nucl.
Pfam; PF03187; Corona_1; 1.
Hypothetical_protein.
                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
les 6; Conservative
                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermoplasma acidophilum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
             Best Local Similarity
Matches 6: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 NLLRDK 265
                                                                  15 AEIVKI 20
                                                                                               33 AEİVKI 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 NLLRDK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2303;
                                    9
                                                                                                                                                                                 YIOR CVBF
P22654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IF2B THEAC
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29нклз;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IF2B_THEAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                          FUNCTION: eIF-2 functions in the early steps of protein synthesis by forming a ternary complex with GTP and initiator tRNA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Bufonidae, Bufo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutathione S-transferase P 2 (EC 2.5.1.18) (BBGSTP2-2) (GST class-
                                                                                                                                                                                                                                                                                                                                                similarity).
SUBUNIT: Heterotrimer composed of an alpha, a beta and a gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Int. J. Biochem. Cell Biol. 34:1286-1290(2002).
-!- FUNCTION: Conjugation of reduced glutathione to a wide number of exogenous and endogenous hydrophobic electrophiles.
-!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
-!- SUBUNIT: Homodimer.
-!- TISSUE SPECIFICITY: Liver, kidney, muscle, skin, lung and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-22123471; PubMed-12127579; Bucciarelli F., Petruzzelli R., Bucciarelli T., Sacchetta P., Amicarelli F., Petruzzelli R., Melino S., Rotilico D., Celli N., Di Ilio C.; "Amino acid sequence of the major form of toad liver glutathione
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01873; eIFF, eIFF8; 1.
Pfam; PF01873; EIFF, eIFF8; 1.
Probom; PD004078; eIFF8; 1.
SMART; SM00653; eIF28 5; 1.
TIGRFAM8; TIGR00311; aIF-2beta; 1.
PR0SITE; PS50926; TRAM; 1.
Initiation factor; Protein biosynthesis; Complete proteome.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, SUBUNIT, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the eIF-2-beta / eIF-5 family. -!- SIMILARITY: Contains 1 TRAM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 1; Length 209; 100.0%; Pred. No. 2.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 209 AA; 23899 MW; 577234B9BEC61B8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF_00232; fused; 1.
INCEYPRO; PRO022735; EIFS EIF2B.
INCEYPRO; IPR004488; TIF_AIF-2beta.
INCEYPRO; IPR002792; TRAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL445064; CAC11744.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FBB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                           chain (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pi).
Bufo bufo (European toad)
                                                                                                                                                                                                      Nature 407:508-513(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 DYEKLL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 DYEKLL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transferase.";
                                                                                                                                                             acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTP2_BUFBU
AC P89325;
DT 28-FEB-2003 (9 P89325;
DT 28-FEB-2003 (9 P89325;
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P89326)
DT 28-FEB-2003 (9 P893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
          SETWENT THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bitchiformatics and the BMBL outstation — the Buropan Bitchiformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=96127529; PubMed=8590279;

MEDLINE=96127529; PubMed=8590279;

MEDLINE=96127529; PubMed=8590279;

Mankor T., Tabata S.;

Suginta M., Tabata S.;

"Sequence analysis of the genome of the unicellular cyanobacterium
Syncehocystis ap. strain PCC6803. I. Sequence features in the 1 Mb
region from map positions 64% to 92% of the genome.";

DNA Res. 2:153-166(1995).

-! GATALYTIC ACTIVITY: 1-(5-phospho-D-ribosyl)-ATP + diphosphate =
ATP + 5-phospho-alpha-D-ribose 1-diphosphate.

-! PATHWAY: Histidine biosynthesis; first step. Very important in the
regulation of histidine metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Homohaxamer (By similarity). Binds to hisz possibly to allow the regulation of hisG transferase activity by histidine (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTITION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gabs

    -!- SIMILARITY: Belongs to the ATP phosphoribosyltransferase family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                         -!- SIMILARITY: Belongs to the GST superfamily. Pi family. InterPro; IPRO04046; GST Cterm.
InterPro; IPRO04045; GST Cterm.
InterPro; IPRO03082; GST_Nterm.
InterPro; IPRO03082; GST_Di.
Pfam; PR02708; GST_C; 1.
Pfam; PR01208; GST_N; 1.
PRINTS; PR01268; GST_N; 1.
PRINTS; PR01268; GSTRNSFRASEP
Transferase; Multigene family.
SEQUENCE 210 AA; 24178 MM; 3D233F9AE53F3F8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF 01018; -; 1.
InterPro; IPR001348; ATP_phspho_trans.
Pfam; PF01634; HisG; 1.
ProDom; PD003516; ATP_phspho_trans; 1.
TIGRPAMs; TIGRO0070; hisG; 1.
PROSITE; PS01316; ATP_P_PHORIBOSYLTR; 1.
Histidine blosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.8%; Score 6; DB 1; Length 210;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 AA; 23436 MW; CBCEBDIEC8CIABF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ATP phosphoribosyltransferase (EC 2.4.2.17).
HISG OR SLL0900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D64006; BAA10855.1; -. PIR; S76008; S76008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Short subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 IRDLKK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 IRDLKK 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome
SEQUENCE 210 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIS1 SYNY3
Q555503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by hisz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 123
SSEREEREESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    엄
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and flor statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:2157899; Pr1.
Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                             Klugbauer N., Dai S., Specht V., Lacinova L., Marais E., Bohn G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                          0
                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Voltage-dependent calcium channel gamma-like subunit (Neuronal voltage-gated calcium channel gamma-like subunit).
PRI OR PR OR CACNGS.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 1; Length 211;
100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0; Indels
               Length 210;
                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 151 POTENTIAL.
155 175 POTENTIAL.
211 AA; 23230 MW; A1A05270E971CC03 CRC64;
              DB 1; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 19, Created)
(Rel. 20, Last sequence update)
           1.8%; Score 6; DB 1
100.0%; Pred. No. 2.4
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20200313; PubMed=10734232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ272046; CAB86387.1; -.
Ouery Match
Best Local Similarity Tuv...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 ILLKNQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 ILLKNQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                 65 AVAQLA 70
                                                                                            81 AVACLA 86
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                           NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calcium channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subfamily.
                                                                                                                                                                                                                                                                                                                                                TISSUE=Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P229<u>1</u>5;
01-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1991
                                                                                                                                              CCGX MOUSE
                                                                                                                                                                                                                                                                                                                                                                                          Hofmann F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOTA_BPT4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOTA BPT4
ID MOTA
AC P2291
DT 01-AU
                                                                                                                                   RESULT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                              셤
                                                                   à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22514363; PubMed=12626685;
Miller E.S., Kutter E., Mosig G., Arisaka F., Kunisawa T., Ruger W.;
"Bacteriophage T4 genome.";
Microbiol. Mol. Biol. Rev. 67:86-156(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mota binds directly to Mota boxes.
15-MAR-2004 (Rel. 43, Last annotation update)
Transcription regulatory protein moth (Middle transcription protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacteriophage T4.";

EMBO J. 16:1992-2003(1997).

-1- FUNCTION: Required for the transcriptional activation of

middle promoters. Middle promoters are characterized by the

presence of the conserved sequence [AT]3TGCTINA (MotA box).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription regulation; Activator; DNA-binding; 3D-structure. DNA BIND 23 42 H-T-H MOTIF (BY SIMILARITY). MUTÄGEN 140 A->D: TEMPERATURE-SENSITIVE.
                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Finnin M.S., Cicero M.P., Davies C., Porter S.J., White S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kreuzer K.N.; "The activation domain of the MotA transcription factor from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 1; Length 211; 100.0%; Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                             Uzan M., Brody E., Favre R., "Nucleotide sequence and control of transcription of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23574 MW; 841625941A194E3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.19 ANGSTROMS) OF 2-96.
MEDLINE=97299876; PubMed=9155025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and stops abruptly some 4-5 min later.
                                                                                                                                                                                                                                                                    MEDLINE=91141300; PubMed=2287273;
                                                                                                                                                                                                                                                                                                                                               bacteriophage T4 motA regulatory Mol. Microbiol. 4:1487-1496(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z48569; CAA88453.1; -.
EMBL; AF158101; AAD42607.1; -.
PIR; JV0101; ZKBPT4.
PDB; 1BJA; 18-NOV-98.
PDB; 111S; 18-APR-01.
PDB; 1KAF; 24-APR-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                     NCBI_TaxID=10665;
                                                                                                    Bacteriophage T4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HELIX
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTĀGEN
HELIX
TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAND
HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TURN
SOLUTION TO THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTION OF THE SELECTI
```

```
the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: 10-formyltetrahydrofolate + N(1)-(5-phospho-D-ribosyl)glycinamide = tetrahydrofolate + N(2)-formyl-N(1)-(5-phospho-D-ribosyl)glycinamide.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Finchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fräser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Phosphoribosylglycinamide formyltransferase (BC 2.1.2.2) (GART) (GAR transformylase) (5'-phosphoribosylglycinamide transformylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
   .
0
                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: De novô purine biosynthesis; third step.
-!- SUBUNIT: Homodimer (By similarity).
-!- SIMILARITY: TO OTHER GART FROM BACTERIA AND EUKARYOTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 1; Length 212;
100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0; Indels
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 145 BY SIMILARITY. 212 AA; 23463 MW; D1AE249CDDB879C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purine biosynthesis; Transferase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JB l;
2.4e+02;
0;
0;
   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00551; formyl transf; 1.
TIGRFAMS; TIGR00639; PurN; 1.
PROSITE; PS00373; GART; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002376; formyl tr
InterPro; IPR001555; GART AS.
InterPro; IPR004607; PurN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U32822; AAC23075.1; -.
PIR; F64122; F64122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 269:496-512(1995)
   6; Conservative
                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P08179; 1GAR.
                                                                            139 LAILEK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 LKDNLA 26
                                       25 LAILEK 30
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; HI1428;
                                                                                                                                                                                                                                                                                                    PURN OR HI1428
                                                                                                                                                                      PUR3 HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                 PUR3_HAEIN
                                                                                                                                   RESULT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
   Matches
                                                                                                                                                                      d
```

192 LKDNLA 197

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                        SERUMENTE FROM N.A.

STRAIN-JAL-1 DSM 2661 / ATCC 43067;

MEDLINE=9633799; PubMed=8688087;

MEDLINE=96337999; PubMed=8688087;

Buil C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness B.F., Weinstcok K.G., Merrick V.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 273:1058-1073(1996).
-1- FUNCTION: Involved in DNA repair and in homologous recombination.
May regulate the cleavage reactions of the branch-structured DNA.
Has a very weak ATPase activity that is not stimulated by DNA.
Binds DNA but does not promote DNA strands exchange (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity)
SIMILARITY: Belongs to the eukaryotic recA-like protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 1; Length 212; 100.0%; Pred. No. 2.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50162, RECA 2; 1.
DNA damage; DNA recombination; ATP-binding; DNA-binding;
                                                                                                                                                              Archaea; Euryarchaeota; Methanococci; Methanococcalea; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 212 AA; 23842 MW; OBDIC9D5D68579CB CRC64;
                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL)
                                                                                                  DNA repair and recombination protein radB
RADB OR MJ0254.
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR; MJ0254; -.
HAMAP; MF 00350; -; 1.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR001553; RecĀ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MMC1 METAC STANDARD;
P58867;
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U67480; AAB98241.1; -. PIR; G64331; G64331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.0
  STANDARD;
                                                                                                                                             Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00382; AAA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RadB subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 LAILEK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 LAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                       NCBI_TaxID=2190;
RADB METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MMC1 METAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                   ð
```

```
ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STATE | STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and a its content is no modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 12:532-542(2002).
-!- FUNCTION: Acts as a methyl group carrier between mtmB and mtbA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The genome of Methanosarcina acetivorans reveals extensive metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Can form a complex with mtmB (By similarity).
-!- SIMILARITY: Belongs to the methylamine corrinoid protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                  Archaea; Buryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 1; Length 217;
100.0%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 AA; 23016 MW; A4266EEE52DD53E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: Methanogenesis from monomethylamines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-00T-2001 (Rel. 40, Created)
16-00T-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                  Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical metal-dependent hydrolase MJ1163
                                          Monomethylamine corrinoid protein 1 (MMCP 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 AA.
  28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02607; B12-binding_2; 1.
Cobalt; Methanogenesis; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE010671; AAM03598.1; -.
InterPro; IRR006158; B12-binding.
InterPro; IPR003759; Comet synth_B12.
B4m; PF02310; B12-binding; 1.
Pfam; PF02607; B12-binding_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and physiological diversity."
                                                                             Methanosarcina acetivorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 AQLAQE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQLAQE 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2190;
                                                                                                                                            NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YB63 METUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INIT MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          058563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MJ1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YB63_METUA
11D YB63_M
YB63_M
T 16-OCT
DT 16-OCT
DT 18-PEB
DE Hypotha
GN M1163
GN M1163
GN M1163
CO Methan
OC Methan
OX NGBL
RN 11]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE-9637999; PubMed=868087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fleizderaid L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Boordovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=95350630; PubMed=7542800;
Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Finchman J.L., Ruhrmann J.L., Geoghagen N.S.M., Geneb C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 269:496-512(1995).
-!- FUNCTION: NOT KNOWN, IS CODED IN AN OPERON ESSENTIAL FOR
CELL DIVISION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.8%; Score 6; DB 1; Length 217;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF 00457; -; 1.
InterPro; IPR001279; Blactmase-like.
Pfam; PF00753; lactamase B; 1.
Hypothetical protein; Hydrolase; Complete proteome.
SEQUENCE 217 AA; 23516 MW; A2FE84E3BD9EC616 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 273:1058-1073(1996).
-!- SIMILARITY: Belongs to the UPF0173 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
FTSE OR H10769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U67558; AAB99165.1; -. PIR; B64445; B64445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 APQIAL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 APQIAL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTSE HAEIN
P44871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       jannaschii.
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as long as its content is no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIRE 1 TOV NISS61 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: Necessary for normal cell division and for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 1.8%; Score 6; DB 1; Length 218; Local Similarity 100.0%; Pred. No. 2.5e+02; Local 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 218 AA; 24349 MW; 6E3DFE39C03F33EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            maintenance of normal septation (By similarity).
-!- SIMILARITY: Belongs to the engB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
Cell division; ATP-binding; Complete proteome.
NP_BIND 36 43 ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 40, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                          or send an email to license@igb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transporter; 1.
SWART; SW00382; AAA; 1.
TIGRRAMs; TIGR00960; 3a0501802; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probable GTP-binding protein engB.
ENGB OR VC0111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003593; AAA ATPASE.
InterPro; IPR003439; ABC_transpo
InterPro; IPR005286; IISP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U32760; AAC22427.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; H64091; H64091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 LRRQIG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 LRRQIG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR; HI0769; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cholerae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9KVÑO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
SO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE PER MAN TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DATO DE LA COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR C
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
Fiers M.W.B.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
De Vos W.M., Siezen R.J.,
"Complete genome sequence of Lactobacillus plantarum WCFS1.",
Proc. Natl. Acad. Sci. U.S.A. 100:199-1995 [2003].
-: FUNCTION: Phosphorylation of dTMP to form dTDP in both de novo and
salvage pathways of dTTP synthesis (By similarity).
-: CATALYTIC ACTIVITY: ATP + thymidine 5'-phosphate = ADP + thymidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP; MF_00165; -; 1.
PiterPro; IPR000062; Thymidylate kin.
Pro2223; Thymidylate kin; I.
PROSITE; PS01331; THYMIDYLÄTE KINASE; 1.
Transferase; Kinase; Nucleotide biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 221;
5. 2.5e+02;
cches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the thymidylate kinase family.
                                                                                                                                                                                                                                                         0; Indels
                                                                                                       Cell division; Septation; GTP-binding; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 18 ATP (POTENTIAL).
221 AA; 24314 MW; C18351577FD252A3 CRC64;
                                                                                                                                                                                220 AA; 24343 MW; D4926E9E5073E37C CRC64;
                                                                                                                                                                                                                     Query Match
1.8%; Score 6; DB 1; Le:
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          [5-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
17-MAR-2004 (Rel. 43, Last annotation update)
Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)
                                                                                                                           GTP (POTENTIAL)
GTP (POTENTIAL)
GTP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                         221 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.8%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No. 2.5
Matches 6; Conservative 0; Mismatches
                                                 HAMAP; MF 00321; -; 1.
InterPro; IPR005289; GTP-bindding dom.
TIGRFAMS; TIGR00650; MG442; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=NCIMB 8826 / WCFS1;
MEDLINE=22480296; PubMed=12566566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL935253; CAD63305.1; -.
EMBL; AE004101; AAF93289.1;
PIR; E82364; E82364.
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactobacillus plantarum.
                                                                                                                                                                                                                                                                                            225 KRQSLK 230
                                                                                                                                                                                                                                                                                                                                 106 KRQSLK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5'-diphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0703.
                                      TIGR; VC011
                                                                                                                                                                                                                                                                                                                                                                                                                         KTHY LACPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TMK OR LP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                SEQUENCE
                                                                                                                           NP BIND
NP BIND
                                                                                                                                                               NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                          OBBYP6;
                                                                                                                                                                                                                                                                                                                                                                                                        KTHY_LACPL
                                                                                                                                                                                                                                                                                                                                                                                                                         SET TY SET TO SE
                                                                                                                                                                                                                                                                                              ਨੇ
                                                                                                                                                                                                                                                                                                                               qq
```

```
SPECIES=E.coli; STRAIN=C157:H7 / RIMD 0509952; MEDLINB=21156231; PubMed=11258796; MEDLINB=21156231; PubMed=11258796; MEDLINB=21156231; PubMed=11258796; Murata T., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Xasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Complete genome sequence of enterchemorrhagic Beoherichia coli CO157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLINE=94316500; PubMed=8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
"Analysis of the Escherichia coli genome. V. DNA sequence of the
region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=E.COli; STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=2288234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-E. coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller I.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                              01-MAR-1989 (Rel. 10, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Cell division ATP-binding protein ftsE.
FTSE OR B3463 OR C4256 OR Z4837 OR ECS4312 OR SF3481 OR S4282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-E.coli, STRAIN-K12;
MEDLINE-87089083; PubMed=3025556;
Gall D.R., Hatfull G.F., Salmond G.P.C.;
An new cell division operon in Escherichia coli.";
Mol. Gen. Genet. 205:134-145(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 83334, 623;
                                                                                                                                                                                                                                                                                                             01-MAR-1989 (Rel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli,
Escherichia coli 06,
Escherichia coli 0157:H7, and
                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 8:11-22(2001)
236 ILDRHN 241
                                                              55 ILDRHN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       FTSE ECOLI
                                                                                                                                                                                                          FTSE_ECOLI
                                                                                                                                                                                                                                               HERETT BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BE
                                                          셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                        "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441 (2002).
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                     SPECIES-S.flearneri; STRAIN-2457T / ATCC 700930 / Serotype 2a; MEDLINE-22590274; PubMed=12704152; MEDLINE-22590274; PubMed=12704152; Med J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Pernier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payre S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; Complete genome sequence and comparative genomics of Shigella fleareri serotype 2a atrain 2457T."; Infect. Immun. 71:2775-2786(2003).

-I. FUNCTION: NOT KNOWN. IS CODED IN AN OPERON ESSENTIAL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 1; Length 222;
100.0%; Pred. No. 2.6e+02;
tive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSCO0211; ABC_TRANSPORTER 1; 1.
PROSITE; PSCO093; ABC_TRANSPORTER 2; 1.
Cell division; ATP-binding; Complete proteome.
NP BIND 35
ATP (BY SIMILARITY).
SEQUENCE 222 AA; 24439 MW; 13CFCDECD8FE7590 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000422; AAC76488.1; -.
EMBL; AE016768; AAN82692.1; -.
EMBL; AE005569; AAG5872.1; -.
EMBL; AP005565; BAB37735.1; -.
EMBL; AE015366; AAN44940.1; ALT_INIT.
EMBL; AE016992; AAP19242.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EcoGene; EG10340; ftsE.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR005286; IISP.
Pfam; PF00005; ABC_tran; I.
ProDom; PD000006; ABC_transporter; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00382; AAA; Ī.
TIGRFAMS; TIGR00960; 3a0501802; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X04398; CAA27985.1; -. EMBL; U00039; AAB18438.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity lvv..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; H86013; H86013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; H91167; H91167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 LRRQIG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S03131; CEECFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 LRROIG 82
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GL14 ARATH
Q9M8X4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GL14_ARATH
       SO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44444
```

```
A Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
Salanoubat M., Lemcke K., Rieger M., Perez-Alonso M., Obermaier B.,
Bertmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
De Simone V., Choisne N., Artiguenave F., Robert C., Bucottier P.,
Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
Wurmbach E., Drzonek H., Fifle H., Holland R., Brandt P., Nyakatura G.,
Corzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
Conrad A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordalek G.,
A Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
A Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta B.,
Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
Mannhaupt G., Haase B., Maiti R., Wu D., Peterson J., Van Aken S.,
Crasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
Rasentco S., Kimhra T., Idesawa K., Kabhida Y.,
Sasmato S., Kimhra T., Idesawa K., Kashida Y.,
Kivokawa C., Kohara M., Matenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., Marenno A., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: May play a role in plant defense. Has probably no oxalate oxidase activity even if the active site is conserved.
-!- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROBABLE NON-FUNCTIONAL MANGANESE-BINDING
                      AT3G04180 OR TGKI2.20.

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00325; GERMIN.
PROSITE; PS00725; GERMIN; FALSE NEG.
Apoplast; Cell wall; Signal; Glycoprotein; Manganese; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GERMIN-LIKE PROTEIN SUBFAMILY 1 MEMBER
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; "Sequence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MANGANESE (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Apoplast (By similarity).
     Germin-like protein subfamily 1 member 4 precursor.
                                                                                                                                                                                                                                     STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P45850; IFI2.
InterPro; IPR006145; Cupin.
InterPro; IPR007113; Cupin sup.
InterPro; IPR001929; Germin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AC016829; AAF26795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00190; Cupin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multigene family.
                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
METAL
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
```

```
RA MEDILE-2101 Pubmed-11130713;

RA MEDILE-21020; Pubmed-11130713;

RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,

Ra Janoubat M., Lamcke K., Rieger H., Perez-Alonso M., Obermaier B.,

Belseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech F.,

RA Wincker P., Cattolico L., Weisgenbach J., Saurin W., Quetier P.,

RA Wincker P., Cattolico L., Weisgenbach J., Saurin W., Quetier P.,

RA Wincker P., Cattolico L., Weisgenbach J., Saurin W., Quetier P.,

RA Wincker B., Drzonek H., Erfle H., Holland R., Brandt P., Nyakatura G.,

RA Wedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

RA Wedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

RA Navarro P., Collado C., Perez-Perez A., Ottenwealder B., Duchemin D.,

RA Navarro P., Collado C., Perez-Perez A., Ottenwealder B., Duchemin D.,

RA Mantaro P., Collado C., Perez-Perez A., Ottet A., Caascuberta E.,

RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D., Mewes H.-W.,

RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D., Mewes H.-W.,

RA Roomey T., Rizzo M., Walter A., Utterback T., Fujil C.Y., Shea T.P.,

RA Roomey T., Rizzo M., Walter A., Utterback T., Fujil C.Y., Shea T.P.,

RA Preuss D., Linn X., Nierman W.C., Salzbergs S.L., White O., Venter J.C.,

R Fraser C.M., Kaneko T., Nakamura Y., Satto S., Kato T., Asamizu B.,

RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,

RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,

RA Kaparama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,

RA Rachama M., Wasuda M., Tabata S.,

RH Requence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 408:820-822(2000).
-!- FUNCTION: May play a role in plant defense. Has probably no oxalate oxidase activity even if the active site is conserved.
-!- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
     N-LINKED (GLCNAC. . .) (POTENTIAL)
                                 (POTENTIAL)
                                                                                                                                                  ;
0
                                                                                                   DB 1; Length 222;
                                                                                                 1.8%; Score 6; DB 1; Length 222;
100.0%; Pred. No. 2.6e+02;
ive 0; Mismatches 0; Indels
38 38 N-LINKED (GLCNAC. . .) (PO 139 139 N-LINKED (GLCNAC. . .) (PO 222 AA; 24102 MW; 036F2D1F6B6C3537 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (By similarity)
-1- SUBCELLULAR LOCATION: Apoplast (By similarity).
-1- SIMILARITY: Belongs to the germin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Last sequence update)
[6-OCT-2001 (Rel. 40, Last annotation update)
Germin-like protein subfamily 1 member 5 precursor.
AT3G04190 OR T6K12.19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                  155 LAKIIL 160
                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                9 LAKIIL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thaliana.";
                                                                                                                                                    .
9
                                                                                                                                                                                                                                                                                                                                                                         GL15 ARATH
                            CARBOHYD
     CARBOHYD
                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                             Q9M8X5;
                                                                                                                                                                                                                                                                                                                        RESULT 135
                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                  GL15 ARATH
```

```
Pfam; PF01381; HTH_3; 1.
                                                                                                                                                                     Query Match
                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                        RESULT 137
                                                                                                                                                                                                            Matches
    SO FFF SOR
                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                       YAN DEN NA DEN NA DECECTO COUNTY AND DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA DEN NA 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. The European Bioinformatics Institute. The European Bioinformatics on the European Bioinformatics are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ileb.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Farinha M.A., Allan B.J., Gertman E.M., Ronald S.L., Kropinski A.M., "Cloning of the early promoters of Pseudomonas aeruginosa bacteriophage D3: sequence of the immunity region of D3."; J. Bacteriol. 176:4809-4815(1994).
                                                                                                                                                                                                 Apoplast; Cell wall; Signal; Glycoprotein; Manganese; Metal-binding; Multigene family.

SIGNAL 1 24 POTENTIAL.
                                                                                                                                                                                                                                                                GERMIN-LIKE PROTEIN SUBFAMILY 1 MEMBER MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 1 HTH cro/C1-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kropinski A.W.;
"Sequence of the genome of the temperate, serotype-converting, Pseudomonas aeruginosa bacteriophage D3.";
J. Bacteriol. 182:6066-6074(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 1; Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           24051 MW; 334DBBF1BAA4F0A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. No. 2.6e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Repressor protein Cl.
                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20485557; PubMed=11029426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94327444; PubMed=8050993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF165214; AAA53553.1; -.
                                        EMBL; AC016829; AAF26794.1; -.
                                                                           InterPro; IPR006045; Cupin.
InterPro; IPR007113; Cupin su
InterPro; IPR001929; Germin.
                                                                                                                                                               PRINTS; PR00325; GERMIN.
PROSITE; PS00725; GERMIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro, IPR001387; HTH_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
Les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                   222
1112
1114
119.
50
38
                                                                                                                                         Pfam; PF00190; Cupin;
                                                                                                                                                                                                                                                                                                                                                                                                                                 139 1
222 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 LAKIIL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 LAKIIL 14
                                                              P45850; 1FI2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=31535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriophage D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPC1_BPD3
Q37906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                    CHAIN
METAL
METAL
                                                                                                                                                                                                                                                                                                                              METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPC1 BPD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibe.sib.ch).
                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Linzer D.I.H., Mordacq J.C.;
"Transcriptional regulation of proliferin gene expression in response
"to serum in transfected mouse cells.";
EMBO J. 6:2281-2288(1987).
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: May have a role in embryonic development. It is likely to provide a growth stimulus to target cells in maternal and fetal tissues during the development of the embryo at mid-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nucleotide sequence of a growth-related mRNA encoding a member of
the prolactin-growth hormone family.";
Proc. Natl. Acad. Sci. U.S.A. 81:4255-4259(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Belongs to the somatotropin/prolactin family.
                                                                                                                                                                                                                                    DB 1; Length 223; 2.6e+02;
                                                                                                                                    18 37 H-T-H MOTIF (POTENTIAL).
223 AA; 24558 MW; B74F89FE0EB3E781 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1986 (Rel. 03, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Proliferin 1 precursor (Mitogen-regulated protein 1).
PLF OR PLFI OR MRP1.
                                                                                                      HTH CRO/C1-TYPE.
H-T-H MOTIF (POTENTIAL)
SMART; SMO530; HTH XRE; 1.
PROSITE; PS50943; HTH CROC1; 1.
Repressor; Transcription regulation; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 AA.
                                                                                                                                                                                                                                / Match 1.8%; Score 6; DB 1 Local Similarity 100.0%; Pred. No. 2.6 nes 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00266; SOMATOTROPIN 1; 1. PROSITE; PS00338; SOMATOTROPIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, Q28632; 1AN3.
MgD, MGI:97618; Plf.
InterPro; IPR001400; Somatotropin.
Pfam; PF00103; hormone; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hormone; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=84272617; PubMed=6087314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88029317; PubMed=3478191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1986 (Rel. 03, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X05787; CAA29231.1; -. EMBL; K02245; AAA39946.1; -. EMBL; X05786; CAA29230.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Linzer D.I.H., Nathans D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-10 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A05086; A05086.
                                                                                                                                                                                                                                                                                                                                                                     250 SKPENL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                   122 SKPENL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLF1 MOUSE
P04095;
                                                                                                                                 DNA BIND
SEQUENCE
```

us-10-025-730-1.oligo.rsp

79 LRDKSP 84

RESULT

```
use by non-profit institutie. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Linzer D.I.H., Lee S.-J., Ogren L., Talamantes F., Nathans D.;
"Identification of proliferin mRNA and protein in mouse placenta.";
Proc. Natl. Acad. Sci. U.S.A. 82:4356-4359(1985).
-!- FUNCTION: May have a role in embryonic development. It is
likely to provide a growth stimulus to target cells in maternal
and fetal tissues during the development of the embryo at mid-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 1; Length 224;
100.0%; Pred. No. 2.6e+02;
                                                                                                                                                                                                    DB 1; Length 224; . 2.6e+02;
                                                                                                                                                                                                                                                      0; Indels
                       PROLIFERIN 1.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
3786P100C338374B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1EB34BEA21433B82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
16-OCT-201 (Rel. 40, Last annotation update)
Proliferin 2 precursor (Mitogen-regulated protein 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROLIFERIN 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. ...
                                                                                                                                                                                           1.8%; Score 6; DB 1 100.0%; Pred. No. 2.6 ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS, PRO0836, SOMATOTROPIN.
PROSITE, PRO0366, SOMATOTROPIN 1;
PROSITE, PS00338; SOMATOTROPIN 2; 1.
Hormone; Signal; Multigene family.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=85242683; PubMed=3859868;
29
224 PRC
40 BY
199 BY
224 BY
25367 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25312 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; K03235; AAA39945.1; -. HSSP; Q28632; 1AN3.
                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00103; hormone; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1341833; Plf2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLF2 OR MRP2. Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                            262 LRDKSP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        LRDKSP 84
                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gestation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLF2 MOUSE
                             CHAIN
DISULFID
                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                     79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                           SEQUENCE
                                                                                                                                                                                              Query Match
Best Local
     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P04768
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 138
                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A PART OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE 
  FT
FT
FT
FT
SO
                                                                                                                                                                                                                                                                                                                  à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb.ch).
                                                                                                                                                                                                                                                                                    "Characterization of a mouse mitogen-regulated protein/proliferin gene and its promoter: a member of the growth hormone/prolactin gene superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94319082; PubMed=8043949;
Ko M.S., Wang X., Horton J.H., Hagen M.D., Takahashi N., Maezaki Y.,
Nadeau J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genetic mapping of 40 cDNA clones on the mouse genome by PCR.";

Mamm. Genome 5:349-355(1994).

-!- FUNCTION: May have a role in embryonic development. It is

likely to provide a growth stimulus to target cells in maternal and fetal tissues during the development of the embryo at mid-
                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the somatotropin/prolactin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 1; Length 224;
100.0%; Pred. No. 2.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C87F3A2310C91320 CRC64;
                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CD-1; TISSUE=Fibroblast;
MEDLINE=90001249; PubMed=2790033;
Connor A.M., Waterhouse P., Khokha R., Denhardt D.T.;
                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Proliferin 3 precursor (Mitogen-regulated protein 3).
MRPPLE3 OR PLE3 OR MRP3.
   224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROLIFERIN 3.
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                           iochim. Biophys. Acta 1009:75-82(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0836; SOMATOTROPIN.
PROSITE; PS00266; SOWATOTROPIN. 1; 1.
PROSITE; PS00338; SOWATOTROPIN. 2; 1.
HOTMONE; Signal; Multigene family.
1.
29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S05648; S05648.
HSSP; Q26632; LAN3.
MGI:1347041; MTPDJE3.
InterPro; IPR001400; Somatotropin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, X16009, CAA34146.1, ...
EMBL, X16010, CAA34146.1, JOINED.
EMBL, X16011, CAA34146.1, JOINED.
EMBL, X16012, CAA34146.1, JOINED.
EMBL, X16013, CAA34146.1, JOINED.
EMBL, U05747, AAB60482.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25338 MW;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 208-224 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00103; hormone; 1
                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 2
224 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gestation
PLF3 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                  P18918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
```

ö

Gaps

. 0

6; Conservative

Matches

·.

Gaps

ö

0; Indels

Conservative

و:

Matches

262 LRDKSP 267

```
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VATE MANSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 142
VATE MANSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
3-dehydroquinate dehydratase (EC 4.2.1.10) (3-dehydroquinase) (Type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCHIFF-BASE INTERMEDIATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              third step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF 00214; -; 1.

InterPro; IPR001381; DHquinase_I.

ProDom; P01487; DHquinase_I; 1.

PROSITE; PS01028; DEHYDROQUINASE_I; FALSE_NEG.

Aromatic amino acid biosynthesis; Lyase; Complete proteome.

ACT_SITE 120 120 BY SIMILARITY.

ACT_SITE 146 SCHIFF-BASE INTERMEDIATE (BY SI SEQUENCE 226 AA; 23048 MW; 0054520FIEFB9468 CRC64;
                                                                                                                                                                                                                                                                                                              Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 1; Length 226; 100.0%; Pred. No. 2.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 43, Created)
(Rel. 43, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE004992; AAG18893.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A84191; A84191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      221 LIADLQ 226
                LRDKSP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 LIADLO 87
                                                    79 LRDKSP 84
                                                                                                                                                                                                                                                                                            AROD OR VNG0314G.
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-2004
15-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RADC STAEP
QBCNZ4;
                                                                                                                                                      AROD HALNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                         O9HSB4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RADC_STAEP
                                                                                                                                 AROD HALNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                      DDT THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO THE TERM TO TH
                                                  PP
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingiodea;
Sphingidae; Sphinginae; Manduca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94153976; PubMed=8110816; Graef R., Harvey W.R., Wieczorek H.; Graef R., Harvey W.R., Wieczorek H.; Clonding, sequencing and expression of cDNA encoding an insect "Clonding, sequencing and expression of cDNA encoding an insect Biochim. Biophys. Acta 1190:193-196(1994)

-!- FUNCTION: The vacuolar ATPase is responsible for acidifying a variety of intracellular compartments in eukaryotic cells. This subunit is essential for its assembly or catalytic function. VATPase is responsible for energizing electrophoretic K+/2H+
                                                                                                                                                                                                                                                                                                                              Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J., Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z., Yana Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.; "Wara E-Based analysis of virulence genes in a non-biofilm-forming Staphylococcus epidermidis strain (ATCC 12228).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 41, Last annotation update)
Vacuolar ATP synthase subunit E (EC 3.6.3.14) (V-ATPase E subunit)
(Vacuolar proton pump E subunit) (V-ATPase 28 kDa subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 1; Length 226;
100.0%; Pred. No. 2.6e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flami, Forsca, Macd; 1.
Probon; PD00415; Radc; 1.
TIGRPAMs; TIGR00608; radc; 1.
PROSITE; PS01302; RADc; 1.
DNA repair; Complete proteome.
SEQUENCE 226 AA; 25319 MW; 16DE9D290C98F005 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Microbiol. 49:1577-1593(2003).
-!- FUNCTION: Involved in DNA repair (By similarity).
-!- SIMILARITY: Belongs to the radC family.
                                                                                                          Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 AA.
DNA repair protein radC homolog.
RADC OR SE1336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE016748; AA004935.1; -.
                                                                          Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_00018; -; 1.
InterPro; IPR001405; RadC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF04002; RadC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 IRDLKK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=ATCC 12228; PubMed=12950922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 IRDLKK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                 NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI TaxID=7130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Midgut;
```

.. 0

```
ARDINES-21016720; PubMed=11130713;

MEDLINE=21016720; PubMed=11130713;

RABIATOWDAR M., Lemcke K., Raeger M., Ansorge W., Unseld M.,

RABATOWDAR M., Lemcke K., Raeger M., Perez-Alonso M., Obermaier B.,

RA Balanowdar M., Lemcke K., Bloecker H., Perez-Alonso M., Obermaier B.,

RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,

RA Delseny M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,

RA Wincker P., Cattolico L., Weigsenbach J., Saurin W., Queeier F.,

RA Wincker P., Cattolico L., Weigsenbach J., Saurin W., Ouerier F.,

RA Wincker P., Cattolico L., Weigsenbach J., Saurin W., Ouerier F.,

RA Wincker P., Cattolico L., Weigsenbach J., Saurin W., Dandert B.,

RA Wincker P., Cattolico L., Pallavicini A., Toppo S., Simionati B.,

RA Wedelmann R., Kraner G., Lochnert T.-H., Nordeiek G.,

RA Cooke R., Landiec M., Schoen O., Barques M., Terol J., Climent J.,

RA Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Climent J.,

RA Reichelt J., Scharfe M., Schoen O., Barques M., Vitale D.,

RA Mayer K.F., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,

RA Mayer K.F., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,

RA Rooney T., Rizzo M., Walts A., Wierman W.C., Salzberg S.L., White O., Venter J.C.,

RA Rae G., Miltescher J., Salzberg S.L., White O., Venter J.C.,

RA Fraser C.M., Kaneko T., Nakamura Y., Saro S., Karo T., Asamizu E.,

RA Fraser C.M., Kaneko T., Nakamura Y., Saro S., Kato T., Asamizu E.,

RA Sagamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
antiport by generating a transmembrane voltage of more than 200mV
                                                                                                                                                      peripheral catalytic V1 complex (components \hat{\mathbf{A}} to H) attached to an integral membrane V0 proton pore complex (components: a, c, c'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                         CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
                                                                      H(+) (Out).
SUBUNIT: V-ATPage is an heteromultimeric enzyme composed of a norinheral catalytic VI complex (components A to H) attached to norinheral catalytic VI complex (components 3. c. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 1; Length 226; 100.0%; Pred. No. 2.6e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the V-ATPase E subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002842; ATPsynt_Bsub.
Pfam; PF01991; vATP-synt_B; I.
Hydrolase; ATP synthesis; Hydroen ion transport.
BSEQUENCE 226 AA; 26090 MW; DF7AR42E01067400 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Germin-like protein subfamily 1 member 3 precursor. AT3G04170 OR T6K12.21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 40, Last sequence update) (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X67131; CAA47610.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 LLVTLI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 LLVTLI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eurosids II; Bra:
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GL13 ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , EX8M6C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HERE REPAREMENT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                               Nature 408:820-822(2000).
-!- FUNCTION: May play a role in plant defense. Has probably no oxafate oxidase activity even if the active site is conserved.
-!- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
GERMIN-LIKE PROTEIN SUBFAMILY 1 MEMBER 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98037514; PubMed=9371463; Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00325; GERMIN.
PROSITE; PS00725; GERMIN; 1.
Apoplast; Cell wall; Signal; Glycoprotein; Manganese; Metal-binding;
Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S., Nakazaki N., Shinpo S., Tabeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S., "Sequence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanobacterium thermoautotrophicum.
Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -LINKED (GLCNAC. . .) (P(C42948B9F92F9304 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MANGANESE (BY SIMILARITY)
MANGANESE (BY SIMILARITY)
MANGANESE (BY SIMILARITY)
MANGANESE (BY SIMILARITY)
                                                                                                                                                                 -!- SUBCELLULAR LÔCATION: Apoplast (By similarity). -!- SIMILARITY: Belongs to the germin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 2.6 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6;
                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPRO06045; Cupin.
InterPro; IPRO007113; Cupin sup.
InterPro; IPRO01929; Germin.
Pfam; PF00190; Cupin; 1.
                                                                                                                                                                                                                                                                                                                                                    EMBL; AC016829; AAF26796.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24424 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein MTH685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
227
109
111
116
160
50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109
111
116
160
34
136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 LAKIIL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Delta H;
                                                                     thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y685 MET
026781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

ö

```
ö
                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Berkeley;
MEDINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Gocrge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Gorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B Sutton G.G., Worthan J.R., Yandell M.D., Champe M., Pfeiffer B.D.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bhandari D., Bolshakov S.,
Beson K.Y., Bence P.V., Berman B.P., Bhandari D., Botchan M.R., Bouck J., Srokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saville K.J., Belote J.M.; "Identification of an essential gene, 1(3)73Ai, with a dominant temperature-sensitive lethal allele, encoding a Drosophila proteasome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSB1_DROME STANDARD; PRT; 235 AA.
P40304; Q9YV84;
01-FEB-1995 (Rel. 31, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Profeasome subunit beta type 1 (EC 3.4.25.1) (Profeasome 26 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta, Pterygota;
Neoptera, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 1; Length 232; 100.0%; Pred. No. 2.7e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMS; TIGR00291; TIGR00291; 1.
PROSITE; PS01287; UPP0023; 1.
HYDChhetical protein; Complete proteome.
SEQUENCE 232 AA; 26193 MW; 80ACC4306A5BF1AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 90:8842-8846(1993).
                                                                                 -!- SIMILARITY: Belongs to the UPF0023 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROS26 OR PROS-26 OR L(3)73AI OR CG4097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94022270; PubMed=8415617;
                                                                                                                                                                                                                                                                                                                                            InterPro, IPR009022; EFG_III_V.
                                                                                                                                                                                                                                                                                                 EMBL; AE000848; AAB85190.1; -. PIR; C69191; C69191.
                                                                                                                                                                                                                                                                                                                                                                   IPR002140; UPF0023.
                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01172; UPF0023; 1.
ProDom; PD009796; UPF0023; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Rest Local Similarity
6, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 DKASEE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 DKASEE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subunit."
                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subunit)
```

```
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Durbin K.J., Evagelista C.C., Ferraz C., Ferraca S., Felsischmann W.,
Rosler C., Gabriellan A.E., Gargen N.S., Gelbart W.M., Glasser K.,
A Harris N.L., Harvey D.A., Heiman T.J., Hermandez J.R., Houck J.,
A Harris N.L., Harvey D.A., Heiman T.J., Hermandez J.R., Houck J.,
A Harris N.L., Howland T.J., Herming C.J., Liang W. C.J.,
Jali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
A Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
A Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Nerulov G., Milshina N.V., Mobarry C., Morris J., Noshrefi A.,
A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Shue B.C., Spradling A.C., Stapleton M., Strong R., Sun K.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Miljams S.M., Moodage T., Worley K.C., Mu D., Yang S., Yao Q.A.,
A Hilliams S.M., Moodage T., Worley K.C., Mu D., Yang S., Yao Q.A.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Berkeley; TISSUE=Embryo; Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chawpe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., ii P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: The proteasome is a multicatalytic proteinage complex which is characterized by its ability to cleave peptides with Arg, Phe, Tyr, Leu, and Glu adjacent to the leaving group at neutral or slightly basic pH. The proteasome has an ATP-dependent proteolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: The protessome is composed of at least 15 non identical subunits which form a highly ordered ring-shaped structure (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULÂR LOCATION: Cytoplasmic and nuclear (By similarity). SIMILARITY: Belongs to peptidase family T1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity.
CATALYTIC ACTIVITY: Cleavage at peptide bonds with very broad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: Involved in an ATP/ubiquitin-dependent non-lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interruc,
Interpro; IPR001353; reput.
Interpro; IPR001353; reput.
Pfan; PF0027; proteasome; 1.
PROSITE; PS00854; PROTEASOME_B; 1.
PROSITE; PS00854; Protease, Threonine protease.
Proteasome; Hydrolase; Protease; Threonine protease.
Proteasome; 192 192 R -> W (IN REF. 1).
192 192 ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ... > ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001243; Pept TIA subB.
InterPro; IPR001353; Peptidase_T1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE003526; AAF49435.1; -. EMBL; AY051697; AAK93121.1; -. HSSP; P23724; 1RYP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0002284; Pros26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U00790; AAC46465.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteolytic pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; T01.986; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specificity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity)
```

Length 235;

DB 1;

1.8%; Score 6;

Query Match

us-10-025-730-1.oligo.rsp

239 AA

STANDARD;

Y247 MYCPN

RESULT 147

212 RHKVLV 217

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -- the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RACALNEWLY, STATULE 21949401; PubMed=11859360;
RA MEDLINE=21949401; PubMed=11859360;
RA WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Squoros U., Peat N., Hayles J., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraer A.,
RA Gonlins M., Connor R., Cronin A., Davis P., Hiddell T., Fraer A.,
RA Gonos P., Moules M., Leather S., McDonald S., McLean J.,
RA James K., Jones M., Jones M., Murphy L., Niblett D., Odell C.,
RA James K., O'Neil S., Pearson D., Seeger K., Sharp S.,
RA Doliver K., O'Neil S., Parson D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreans S., Lehrach H., Reinhardt R., Pohl T.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gillardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armetrong J., Forsburg S.D.,
RA Cerrutti L., Lower T., McCombie W.R., Paulsen I., Potashkin J.,
RA Granter 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                             ö
                                         Gaps
                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 1; Length 236;
100.0%; Pred. No. 2.7e+02;
ative 0; Mismatches 0; Indels
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ll protein.
236 AA; 26869 MW; 3F74841306935F40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                         0
   100.0%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-REB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C22G7.03 in chromosome I.
                                                                                                                                                                                                                                                                                                                                                                 236 AA.
                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; T11613; T11613.
GeneDB_SPombe; SPAC22G7.03; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z54328; CAA91127.1; -.
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces
                                                                                                                                                                                  105 TEAVAQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                              63 TEAVAQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPAC22G7.03
                                                                                                                                                                                                                                                                                                                                                                     YAA3 SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     SOW RRY REPARANCE SOUTH REPART REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS REPARTS
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Dethiobictin synthetase (EC 6.3.3.3) (Dethiobictin synthase) (DTB synthetase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
-!- SUBCELIULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the UPF0078 family.
                                                                                                                                                                                Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                    Himmelreich R., Hilbert H., Plagens H., Pirkl B., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0078 protein MG247 homolog (H91_orf239).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AE000047, AAB96134.1; -.
PIR, 573812, 573812.
HAMAP: MF 0.1043; -.
InterPro; IPR003811; DUF205.
Pfam; PF02666; DDF205; ..
TIGRPAMS; TIGR00023; TIGR00023; 1.
Hypothetical protein; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6D4110A8253C9EBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 1
100.0%; Pred. No. 2.7
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                           PubMed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27439 MW;
                                                                                                                                                                                                                                                                                                                      STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135
159
199
239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 LLVTLI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 LLVTLI 83
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     NCBI_TaxID=2104;
                                                                                                                                                    MPN350 OR MP486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIOD OR CAC1361
                                                                                                                                                                                                                                                                                                                                                                                                                         Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOD CLOAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          097705;
P75428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 148
BIOD CLOAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOLUTION DE LA PRESENTATION DE LA PRESENTATION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROPERTION DE LA PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

ö

ö

Gaps

; 0

6; Conservative

Matches

193 RHKVLV 198

```
NCBI_TaxID=2096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strain S6."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLPF MYCGA
ID GLPF MYCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=S6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P52280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 150
       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
                                      STRAIN=AICC 824 / DSM 792 / VKM B-1787;
MEDLINB=213925; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Glabson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennet G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=RIMD 2210633 / Serotype 03:K6;
MBDLINE=22508454; PubMed=12620739;
Makino K., Obhima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Ilijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
Lancet 361:743-749(2003).
                                                                                                                                                                                                                         J. Bacteriol. 183:4823-4838(2001).-!- CATALYTIC ACTIVITY: ATP + 7,8-diaminononanoate + CO(2) = ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                    phosphate + dethiobiotin.
--- CORACTOR: Magnesium (By similarity).
--- PATHWAY: Bioconversion of pimelate into dethiobiotin.
--- SIMILARITY: Belongs to the dethiobiotin synthetase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 HTH LytTR-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 1; Length 240; 100.0%; Pred. No. 2.7e+02; ttive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 16 ATP (BY SIMILARITY).
240 AA; 26677 MW; 2FA903A8C23E4AD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01656; CbiA; 1.
TIGRFAMs; TIGR00347; bioD; 1.
Biotin biosynthesis; Ligase; Magnesium; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical response regulatory protein VP0539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP: WF 00336; -; 1. InterPro; IPR004472; BioD_synth. InterPro; IPR002586; CbiA_P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE007647; AAK79329.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-2003 (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      parahaemolyticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F97067; F97067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 EDYEKL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
NP BIND 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 EDYEKL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y538 VIBPA
Q87S86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
HER REPRESENTATION OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF
```

```
between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Forsyth M.H., Saoud S., Geary S.J.;
"Gene encoding a gycerol uptake protein from Mycoplasma gallisepticum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: Aquaporins contain two tandem repeats each containing three membrane-spanning domains and a pore-forming loop with the signature motif Asn-Pro-Ala (NPA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microbiology 149:2307-2316(2003).
-I-FUNCTION: Glycerol enters the cell via the glycerol diffusion facilitator protein. This membrane protein facilitates the movement of glycerol across the cytoplasmic membrane (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22830409; PubMed=12949158; Papazisi L., Gorton T.S., Kutish G., Markham P.F., Browning G.F., Rayven D.K., Swartzell S., Madan A., Mahairas G., Geary S.J.; "The complete genome sequence of the avian pathogen Mycoplasma gallisepticum strain R(Iow).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycoplasma gallisepticum.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the MIP/aquaporin (TC 1.A.8) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50930; HTH LYTTR; 1.
PROSITE; PS50110; RESFONSE REGULATORY; 1.
HYPOCHELical protein; Transcription regulation; DNA-binding;
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN 139 240 HTH LYTTR-TYPE.
SEQUENCE 242 AA; 26992 MW; A7264E539FID4CD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESPONSE REGULATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-Dabble glycerol uptake facilitator protein.
GLFF OR MYCGA0140 OR MGA_0641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.8%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No. 2.8
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                          EMBL), AP005074; BAC58801.1; -.
InterPro; IPR007492; LytIR.
InterPro; IPR001789; Response_reg.
                                                                                                                                                                                                                                                                                                                                                            Pfam; PF04397; LytTR; 1. _ _ _ Pfam; PF004397; LytTR; 1. _ _ ProDom; PD000039; Response_reg; 1. SWART; SM00448; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116
240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 DDEQFA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 DDEOFA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
```

```
Herrmann R., Frank R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H(+) (Out)
                                                                                                                                                                                                                                                                                                                                      01-NOV-1995
28-FEB-2003
                                                                                                                                                                                                                                                                                                        ATP6 MYCLE
P45829;
                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                      RESULT 152
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                  DDTTDDDDTTDDDDTTDDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDD
ö
oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hilbert H., Himmelreich R., Plagens H., Herrmann R.; "Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma pneumoniae comprising the dnaA region, the atp operon and a cluster of ribosomal protein genes."; Nucleic Acids Res. 24:628-639(1996).
                                                                                                                                                                                                                                                              AFNKKLONPVSADFRYGLVPLLAPIAAGLIMGGFSLLINQ
-> VV (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Regula J.T., Ueberle B., Boguth G., Goerg A., Schnoelzer M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                        DB 1; Length 243;
                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                              PRINTS; PR00783; MINTRINSICP.
ProDom; PD000295; MIP_family; 1.
PROSITE; PS00221; MIP; 1.
Glycerol metabolism; Transport; Repeat; Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                   43594672BCE4990C CRC64;
                                                                                                                                                                                                                                                                                                                 ; Pred. No. 2.8e+02; 0; Mismatches 0;
                                                                                                                                                                                                                   S -> C (IN REF. 1).
K -> E (IN REF. 1).
L -> F (IN REF. 1).
N -> H (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
modified and this statement is not removed.
        entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                        1.8%; Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996)
                                     EMBL; U35010; AAA79047.1; -.
EMBL; AE016967; AAP56364.1; ALT_INIT.
HSSS; P1244; 1FXB.
InterPro; IPR000425; MIP.
                                                                                                                                                                                                NPA 1.
NPA 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION BY MASS SPECTROMETRY.
STRAIN=ATCC 29342 / M129;
MEDLINE=21088919; PubMed=11271496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FACE 29342 / M129;
STRAIN=ATCC 29342 / M129;
...nr tND-97105885; PubMed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=96177562; Pubmed=8604303;
                                                                                                                                                                                                                                                                                   243 AA; 26194 MW;
                                                                                                                                                                                                                                                                                                                 100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (K05 or£250).
                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4ycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                 231 LLGELI 236
                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                   LLGELI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OR MP155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein MPN687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                         YG87 MYCPN
                                                                                                                                             TRANSMEM
TRANSMEM
                                                                                                                                                                            TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                   TRANSMEM
                                                                                                                                                                  FRANSMEM
                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swies Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: F-type AFPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(1) has five subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0) has three main subunits: a, b and c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21128722; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Holroyd S., Hornsby T., Jagels K., Felewell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
-!- FUNCTION: Key component of the proton channel; it may play a direct role in the translocation of protons across the membrane.
-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
"Towards a two-dimensional proteome map of Mycoplasma pneumoniae.";
Electrophoresis 21:3765-3780(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 1; Length 250;
100.0%; Pred. No. 2.8e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith D.R., Robison K.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 AA; 28662 MW; 4378A2834BBB7877 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: Belongs to the ATPase A chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterineae, Mycobacteriaceae, Mycobacterium
NCBI TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) ATP synthase A chain (EC 3.6.3.14) (Protein 6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000017; AAB95803.1; -. PIR; S62838; S62838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U34816; AAC43647.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 TOPIVE 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 TOPIVE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
tes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome. SEQUENCE 250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATPB OR ML1139.
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                            ö
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: Plays an important role in several metabolic pathways.
-!- SUBUNIT: Homodimer (By similarity).
-!- SIMILARITY: Belongs to the triosephosphate isomerase family.
                                                                                  EMBL; AL58350; CAC31520.1; -.
PIR; T09980; T09980.
IMSP; P00855; IC17.
Leproma; ML1139; -.
InferPro; IRR000568; ATPsynt Asub.
PEan; PF001919; ATP-synt A; 1.
PRINTS; PR00123; ATP-Synt A; 1.
TIGRRAMS; T1GR01131; ATP-Synt Gor A; 1.
Hydrogen in transport; GF(0); Transmembrane; Complete protecome.
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Nine Mile phase I / RSA 493;
MEDLINE=22608657; PubMed=12704232;
Seshadri R., Paulsen I.T., Elsen J.A., Read T.D., Nelson K.E.,
Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J.,
DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.,
"Complete genome sequence of the Q-fever pathogen, Coxiella
burnetii."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
-!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 251; . 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                        BCCF2AE7FC158DF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
17-MAR-2004 (Rel. 43, Last annotation update)
Triosephosphate isomerase (EC 5.3.1.1) (TIM).
                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                Score 6; Di
                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                        27558 MW;
                                                                                                                                                                                                                                                                                                                                                                                        1.8%;
                                                                                EMBL; U15186; AAA63110.1;
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coxiellaceae; Coxiella.
NCBI_TaxID=777;
                                                                                                                                                                                                                                                                                        150
174
212
240
                                                                                                                                                                                                                                                                                                                     192
220
251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 LVTLIA 203
                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 LUTLIA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coxiella burnetii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPIA OR CBU1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                       . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COXBU
                                                                                                                                                                                                                                                                                       TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            burnetii.
                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                         FRANSMEM
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q83BQ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 153
TPIS COXBU
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
 à
```

EMBL; AE016964; AA090947.1; -.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hong Y.G., Robinson D.J., Harrison B.D.; Mulleotidate sequence evidence for the occurrence of three distinct whitefly-transmitted genuiniviruses in cassava."; J. Gen. Virol. 74:2437-2443(1993).
          HAMAP; MF_00147; -; 1.
InterPro; PR000652; Triophos_ismrse.
Pfan; PF00121; TIM: 1.
ProDom; PF00121; TIM: 1.
ProDom; PF00121; TIM: 1.
PROSITE; PF00171; TIM: 1.
Isomerase; Glycoly1; TIM: 1.
Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis; Pentone shunt; Complete proteome.
ACT_SITE 169 169 BY SIMILARITY.
ACT_SITE 169 169 BY SIMILARITY.
                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                         . Match 1.8%; Score 6; DB 1; Length 255; Local Similarity 100.0%; Pred. No. 2.9e+02; les 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.8%; Score 6; DB 1; Length 256;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                  96 96 BY SIMILARITY.
169 169 BY SIMILARITY.
255 AA, 28172 MW, 82780F6A8985D2C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 AA; 29910 MW; 0FA4FD4AE48A702A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            viruses; Geminiviridae; Begomovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Z24758; CAA80885.1; -.
PIR; JQ2326; JQ2326.
InterPro; IPR000650; Gem_coat_ARI.
InterPro; IPR000263; GV_A/BRI_coat.
Pfam; PF00844; Gemini_coat; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00223; GEMCOATARBRI.
ProDom; PD000901; Gem_coat_ARI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indian cassava mosaic virus (ICMV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=94065670; PubMed=8245859;
                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                            139 ALRCGI 144
                                                                                                                                                                                                                                                                                                                             117 ALRCGI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 VTKRQS 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 VTKRÓS 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssDNA vi
TIGR; CBU1450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coat protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCNA NPVAC
ID PCNA NPVAC
AC P11038;
                                                                                                                                                                                                                                                                                                                                                                                                                     COAT ICMV
008583;
                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 155
                                                                                                                                                                                                                                                                                                                                                                                RESULT 154
                                                                                                                                                                                                                                                                                                                                                                                                  COAT
ð
```

100.08;

Best Local Similarity

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- DEVELOPMENTAL STAGE: WAS FOUND TO BE TRANSCRIBED EARLY (FROM 2 THROUGH 6 HOURS POST-INFECTION) BUT NOT LATE (12 TO 24 HOURS POST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Passarelli A.L., Todd J.W., Miller L.K.;
"A baculovirus gene involved in late gene expression predicts a large polypeptide with a conserved motif of RNA polymerases.";
J. Virol. 68:4673-4678(1994).
                                                                                                                                                                                                                                           "Characterization of an early gene accelerating expression of late genes of the baculovirus Autographa californica nuclear polyhedrosis virus.";
                                                                                                                                                                                                                                                                                                                                                                                              Nyres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
The complete DNA sequence of Autographa californica nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - FUNCTION: REQUIRED FOR TIMELY EXPRESSION OF MANY OTHER ACNPY
              01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Proliferating cell nuclear antigen (EcoRI-T site protein ETL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA-binding; Nuclear protein; DNA replication; Early protein.
                                                                                  Autographa californica nuclear polyhedrosis virus (AcMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73A8A9887AD9E532 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY TO PCNA, AND FUNCTION.
MEDLINE=89143717; Pubmed=2563897;
O'Reilly D.R., Crawford A.M., Miller L.K.;
Wiral proliferating cell nuclear antigen.";
Nature 337:606-606(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the PCNA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; Pl2004; IAXC.
InterPro; IPR000730; Pr_cel_nuc_antig.
Pfam; PF00705; PCNA; 1.
                                                                                                                                                                                               STRAIN=L1;
MEDLINE=88275045; PubMed=3292791;
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94303173; PubMed=8030224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94267933; PubMed=8207843;
 01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 AA; 28635 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PF02747, PCNA_C, 1.
PRINTS, PRO0339, PCNAYCLIN.
Probom, PD002673, Pr_Col_nuc.
TIGRFAMs; TIGR00590; pcna, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, M20718; AAA21097.1; -. EMBL, 122858; AAA20059.2; -. EMBL, U04879; AAA20059.1; -- PIR; A28147; WMAVET.
                                                                                                                                                                                                                                                                                                     Virol. 62:2773-2781(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFECTION) IN INFECTION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-126 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virology 202:586-605(1994).
                                                                                                                                                                                                                                Crawford A., Miller L.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00293; PCNĀ
PROSITE; PS01251; PCNĀ
                                                                                                                       Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                 polyhedrosis virus."
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                          NCBI_TaxID=46015;
                                                                   PCNA OR ETL.
                                                                                                                                                                                                                                                                                                                                                                                               Ayres M.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA BIND
SEQUENCE
```

1.8%; Score 6; DB 1; Length 256;

Query Match

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires allicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Phosphate import ATP-binding protein pstB 2 (BC 3.6.3.27) (Phosphate-transporting ATPase 2) (ABC phosphate transporter 2).
                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser C.M., Norris S.J., Weinetock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalbath H., Richardson D., Howell J.K., Chidambaram M., Utterback T., Khalbath H., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                     Gaps
                                                                                                                                                                                                                                                                                                                     Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 258; .. 2.9e+02; ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL PROTEIN TP0789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 AA; 29040 MW; 5CE4E6C09FC240B1 CRC64;
Pred. No. 2.9e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE001250; AAC65764.1; -.
PIR; D71280; D71280.
TIGR; TP0789; -.
Hypothetical protein; Signal; Complete proteome.
SIGNAL
                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypochetical protein TP0789 precursor.
TP0789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 1
100.0%; Pred. No. 2.9
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 LIEFLS 306
                                                   186 TFKDLL 191
                                                                                                                                                                                                                                                                                                 Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 LIEFLS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Cyanobaci
NCBI_TaxID=103690;
                                                                                       18 TFKDLL 23
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSTB2 OR ALL0908.
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTB2 ANASP
                                                                                                                                                                            Y789 TREPA
                                                                                                                                                                                                                                                                                                                       Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                          083768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBYYE2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTB2 ANASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE DIT DE OX OX OX OX OX
                                                                                                                                                                                              염
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifised and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                cyanobacterium Anabaena sp. strain PCC 7120.";

DNA Res. 8:205-213(2001).

-!- FUNCTION: Part of the ABC transporter complex pstSACB
(TC 3.A.1.7.1) involved in phosphate import. Responsible for energy coupling to the transport system (By similarity).

-!- CATALYTIC ACTIVITY: ATP + H(2)O + phosphate(Out) = ADP + phosphate

    + phosphate(In).
    -!- SUBUNT: The complex is composed of two ATP-binding proteins (pstB), two transmembrane proteins (pstC and pstA) and a solute-binding protein (pstS) (Probable).
    -!- SUBCELLUIAR LOCATION: Inner membrane-associated (By similarity).
    -!- SIMILARITY: Belongs to the ABC transporter family. PstB subfamily.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS051893; ABC_TRANSPORTER_2; 1.
Hydrolase; Transport; Prosphate transport; Membrane; Inner membrane; ATP-binding; Complete proteome.
                                                        Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                "Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 1; Length 260; 100.0%; Pred. No. 2.9e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 48 ATP (By similarity).
260 AA; 28967 MW; E379845A40320F7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Thiazole biosynthesis protein thig.
THIG OR ML0297 OR MLCB1450.26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00005; ABC tran; 1.
Probom; PD000006; ABC transporter; 1.
SWART; SM00382; AAA; 1.
[1]
SEQUENCE FROM N.A.
MEDLINE=21S95285; Pubmed=11759840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AP003584; BAB72865.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; AI1919; AI1919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 LRRQIG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 LRROIG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THIG MYCLE
Q9ZBL2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=IN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THIG MYCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Stutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome.";
Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: Required for late and very late gene expression (By
                                                                                                                                              Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Orgyia pseudotaugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thiamine biosynthesis; Flavoprotein; FWN; Complete proteome. SEQUENCE 261 AA; 27138 MW; A8CC3CAD6F5DE49D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S., Rohrmann G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the baculoviruses LEF-5 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 1; Length 261;
100.0%; Pred. No. 2.98+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                 thiamine (By similarity).
--- CORACTOR: FMN (Potential).
--- PATHWAY: Thiamine biosynthesis.
--- SUBCELIJULAR LOCATION: Cytoplaemic (By similarity).
--- SIMILARITY: Belongs to the thiG family.
                                                                                                                          "Massive gene decay in the leprosy bacillus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 42, Last annotation update)
Late expression factor 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97271300; PubMed=9126251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL035159; CAA22710.1; -.
EMBL; AL583918; CAC29805.1; -.
PIR; T44741; T44741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leproma; ML0297; ---
HAMAR; MF 00443; -; 1.
InterPro; IPR001909; FMN enz:
InterPro; IPR008867; ThiG.
Pfam; PF05690; ThiG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 NLAILE 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 NLAILE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bimilarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEFS NPVOP
010344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEFS_NPVOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

ö

Length 264;

1.8%; Score 6; DB 1; Length 264; 100.0%; Pred. No. 3e+02; tive 0; Mismatches 0; Indels

6; Conservative

64 EAVAQL 69

Best Local Similarity

Matches

264 AA; 29394 MW; 7740A65424B6AFEB CRC64;

SEQUENCE Query Match

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                            ·;
 entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              deltaH: functional analysis and comparative genomics.";
J. Bacteriol, 179:7135-7155 (1997).
-!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the archaebacteria RPOD / eukaryotic RPB3 RNA polymerase subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
                                                                                                                                        1.8%; Score 6; DB 1; Length 263; 100.0%; Pred. No. 3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00446; RNA POL D 30KD; 1.
Transferase; DNA-directed RNA polymerase; Transcription;
                                        EMBL, U75930, AAC59099.1; -.
InterPro; IPR006923; Baculo LEF5.
Pfam; PF04838; Baculo LEF5. 1.
Transcription regulation.
SEQUENCE 263 AA; 30323 MW; 3FE59420A6BDB1D4 CRC64;
                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase subunit D (EC 2.7.7.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; G69147; G69147.
HAMAP; MF_00320; -; 1.
InterPro; IPR009025; RBP11-like RNApo.
InterPro; IPR001700; RNA pola bac_org.
InterPro; IPR001514; RNA polb.
Pfam; PF01000; RNA pol Abac; 1.
Probom; PD002883; RNA_polD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000796; AAB84545.1; -.
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00662; RPOLD
                                                                                                                                                                                                        300 KLIEFL 305
                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                   42 KLIEFL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome.
                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                 RPOD METTH
                                                                                                                                                                                                                                                                                                                               026144;
                                                                                                                                                                        Matches
```

```
REALINE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND THE STATES AND TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    264 AA; 30665 MW; DOEE75C409F09F0B CRC64;
                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-EEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein C737.05 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL031546; CAB44773.1; -. PIR; T41578; T41578.
GeneDB_SPombe; SPCC737.05; -.
                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68
                                                                                                                                                                                                                                                                                       Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4896;
                        YJ15 SCHPO
013679;
                                                                                                                                                                                  SPCC737.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
SEQUENCE
SCHPO
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swies Institute of Bioinformatics and the EMBL outstation the Bixropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bain P.A., Yoo M., Clarke T., Hammond S.H., Payne A.H.;
"Multiple forms of mouse 3 beta-hydroxysteroid dehydrogenase/delta 5-
delta 4 isomerase and differential expression in gonads, adrenal
glands, liver, and kidneys of both sexes.",
Proc. Natl. Acad. Sci. U.S.A. 88:8870-8874(1991).
-!-FONCTION: 3beta-HSD is a bifunctional enzyme, that catalyzes the
cxidative conversion of delta(5)-ene-3-beta-hydroxy steroid, and
the oxidative conversion of ketosteroids. The 3beta-HSD enzymatic
system plays a crucial role in the biosynthesis of all classes of
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: 3-beta-hydroxy-delta(5)-steroid + NAD(+) = 3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oxo-delta(5)-steroid + NADH.
-!- CATALYTIC ACTIVITY: A 3-oxo-delta(5)-steroid = a 3-oxo-delta(4)-
                                                                                                                                                                                                                                                                   01-MAY'1992 (Rel. 22, Created)
16-007-2001 (Rel. 20, Last sequence update)
16-007-2001 (Rel. 40, Last amortation update)
3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type II
15 aBeta-HyD II) [Includes: 3-beta-hydroxy-delta(5)-steroid dehydrogenase (BC 1.1.1.145) (3-beta-hydroxy-5-ene steroid dehydrogenase) (Progesterone reductase); Steroid delta-isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: Steroid biosynthesis.
-!- SUBCELLULAR LOCATION: Endoplasmic reticulum and mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro, IPR002225; 3Beta HSD.
Pfam, PF01073; 3Beta HSD; I.
Steroidogenesis; Oxidoreductase; NAD; Isomerase; Mitochondrion;
                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                 5.3.3.1) (Delta-5-3-ketosteroid isomerase)] (Fragment)
1.8%; Score 6; DB 1; Length 264;
100.0%; Pred. No. 3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 1; Length 265; 100.0%; Pred. No. 3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multigene family; Multifunctional enzyme; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C8074C0C20ABA917 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    membrane-bound protein.
--- TISSUE SPECIFICITY: Liver and kidney.
--- SIMILARITY: Belongs to the lbeta-HSD family.
                                                                                                                                                                                                                                 265 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M75886; -; NOT ANNOTATED_CDS.
MGD; MGI:96234; Hsd3D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92020952; PubMed=1924345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 AA; 29875 MW;
                       Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hormonal steroids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                        118 SSGLLV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                   75 SSGLLV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BALB/c;
                                                                                                                                                                                                                               3BH2 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON TER
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      HSD3B2
                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                  ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the Busopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Methyl-coenzyme M reductase II gamma subunit (EC 2.8.4.1) (Coenzyme-B
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEGUENCE FROM N.A.

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

WEDLINE=96337999; PubMed=86808087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlawage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Shith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coenzyme F430 is a yellow nickel porphinoid (By similarity).
-!- PATHWAY: Methanogenesis; last step.
-!- SUBUNIT: Hexamer of two alpha, two beta, and two gamma chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio) ethanesulfonic acid) with 7-mercaptoheptanoylthreonine phosphate to methane and an heterodisulfide (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanogenesis; Transferase; Multigene family; Complete proteome.
SEQUENCE 266 AA; 30764 MW; 51E7B3C7F984157A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-(7-mercaptoheptanoy1)threonine 3-0-phosphate (coenzyme B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-S-COB + methane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 1; Length 266;
100.0%; Pred. No. 38+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                         (MCR II gamma)
                                                                                                                                                                                                                                                                                                                                                           Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02240; MCR gamma; 1.
PIRSF; PIRSF000264; Meth_COM_rd_gama; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR009024; MCR fer like, InterPro; IPR003178; MCR_gamma.
                                                                                                                                                                                                                                                                           sulfoethylthiotransferase gamma)
MRTG OR MTRG OR MJ0082.
                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD005845; MCR gamma; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U67465; AAB98062.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                   Methanococcus jannaschii.
                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B64310; B64310.
265 KSPNIQ 270
                                       137 KSPNIQ 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; MJ0082;
                                                                                                                                            MCRZ METUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                  060387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                     d
```

16 EIVKIL 21

à

ó

0; Gaps

6; Conservative

Matches

67 DKSPNI 72

셤

38 EIVKIL 43

```
MEDLINE=97394467; PubMed=9252185;

MEDLINE=97394467; PubMed=9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Nelsohmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
MCKenney K., FirzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Cotton M.D., Weidman J.M., Pujil C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                        [Contains:
                                                                                                                                               Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                        complete genome sequence of the gastric pathogen Helicobacter
                                                                                        Phosphatidylserine decarboxylase proenzyme (EC 4.1.1.65) (Contair
Phosphatidylserine decarboxylase alpha chain; Phosphatidylserine
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 388:539-547(1997).
-!- CATALYTIC ACTIVITY: Phosphatidyl-L-serine =
phosphatidylethanolamine + CO(2).
-!- CORACTOR: Pyruvoyl group (By similarity).
-!- SIMILARITY: Belongs to the phosphatidylserine decarboxylase family. Subfamily 1.
                                        10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                  decarboxylase beta chain]
               STANDARD;
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                            NCBI_TaxID=210;
                                                                                                                                  PSD OR HP1357
                                                                                                                                                                                                                                                                                                                                                                                            Venter J.C.;
               PSD HELPY
                                                                                                                                                                                                                                                                                                                                                                                                                        pylori
PSD_HELPY
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN (BY SIMILARITY).
PHOSPHATIDYLSERINE DECARBOXYLASE ALPHA
CHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          biosynthesis; Lyase; Decarboxylase; Pyruvate; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHATIDYLSERINE DECARBOXYLASE BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLEAVAGE (NONHYDROLYTIC) (BY SIMI
CONVERTED TO A PYRUVOYL GROUP (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8CE79AC4126E8A4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY)
                                                                                                                                                                                                                                                                                                             HAMAP; MF 00662; -; 1.
Interpro; IPR003817; PS Dcarbxylase.
Interpro; IPR005221; PS decarb.
                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02666; PS Dcarbxylase; 1.
TIGRFAMS; TIGR00163; PS decarb: 1
                                                                                                                                                                                                                                EMBL; AE000636; AAD08399.1; -.
PIR; E64689; E64689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 AA; 30201 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236
236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phospholipid
                                                                                                                                                                                                                                                                                           TIGR; HP13
                                                                                                                                                                                                                                                                                                                  HAMAP; MF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation — the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptohyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                May B.J., Zhang Q., Li L.L., Pauetian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pateturella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001)
-I. CATALYTIC ACTIVITY: Myo-inositol 1-phosphate + H(2)0 = myo-inositol 4-phosphate.
-I. COPACTOR: Magnesium (By similarity).
-I. COPACTOR: Magnesium (By similarity).
-I. SIMILARITY: Belongs to the inositol monophosphatase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last annotation update)
Inositol-1-monophosphatase (EC 3.1.3.25) (IMPase) (Inositol-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143C_ARATH STANDARD; PRT; 268 AA.
Q9CSW6; Q9PFD3;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
14-33-3-like protein GF14 icta (General regulatory factor 12).
GRF12 OR ATIG26480 OR TIX7.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 1; Length 267;
100.0%; Pred. No. 3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000766; Inositol P.
Pfam; PF00459; inositol P; 1.
ProDom; PD023420; Inositol P; 1.
PROSITE; PS00629; IMP 1; 1.
PROSITE; PS00630; IMP 2; 1.
Hydrolase; Magnesium; Complete proteome.
SEQUENCE 267 AA; 29470 MW; E7070FAE3BA589CA CRC64;
                                                                                                                                                                41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE006067; AAK02399.1; -.
HSSP; P29218; 11MF.
                                                                                                                                  (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                             STANDARD:
                                                                                                                                                                                                                                                                         (I-1-Pase).
                                                                                                                                                                                                                                                                                                                                           Pasteurella multocida.
                                                                                                                                                                (Rel. 41, (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 DKASEE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 DKASEE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=747;
                                                                                                                                                                                                                                                                     phosphatase) (1
SUHB OR PM0315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Pm70;
                                                                                                                                  28-FEB-2003
                                                                                                                                                                   28-FEB-2003
                                                             PASMU
                             SUHB PASMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143C ARATH
RESULT 165
                                                                                              SOW WHAN THE PROPERTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

ö

Alsterfjord M., Rosenquist M., Larsson C., Sommarin M.;

SEQUENCE FROM N.A.

;

Gaps

.; 0

1.8%; Score 6; DB 1; Length 267; 100.0%; Pred. No. 3e+02; rative 0; Mismatches 0; Indels

```
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Witters L.
     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                            STRAINGLY. Columbia;

MEDLINE=21016719; PubMed=11130712;

MEDLINE=21016719; PubMed=11130712;

MILE O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Milte O., Alonso J., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Monto M.K., Conn L., Conway A.B., Corway A.R., Creasy T.H., Dewar K.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fuji C.Y.,

A cill J.E., Goldsmith A.D., Hass B., Hansen N.F., Hughes B., Hulzar L.,

Hunter J.L., Johnson-Hopson C., Khan S., Khaykin B.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

Miltscher J., Miranda M., Nguyen M., Nearman W.C., Osborne B.I.,

Miltscher J., Miranda M., Nguyen M., Neoney T., Rowley D.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sum H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: Is associated with a DNA binding complex that binds to the G box, a well-characterized cis-acting DNA regulatory element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P80386; 061048; 01-FEB-1995 (Rel. 31, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 110-OCT-2003 (Rel. 42, Last annotation update) 5'-AMP-activated protein kinase, beta-1 subunit (AMPK beta-1 chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N -> VVIHFKMRTDQRAWKLNEI (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 1; Length 268; 100.0%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 3e+02;
0; Mismatches 0; Indels
"Novel 14-3-3 isoforms in Arabidopsis thaliana.", Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          914F394CEC07A2BC CRC64;
                                                                                                                                                                                                                                                                                                                                               found in plants genes (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00244; 14-3-3; 1.
PRINTS; PR00305; 1433ZETA.
ProDom; PD000600; 14-3-3; 1.
SMART; SM0101; 14-3-3; 1.
PROSITE; PS00796; 1433-1; 1.
PROSITE; PS00797; 1433-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF98570.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF335544; AAK11271.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 AA; 30545 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P29312; 1A38.
InterPro; IPR000308; 14-3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AMPKb) (40 kDa subunit).
                                                                                                                                                                                                                                                                                                           Nature 408:816-820(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; F86391; F86391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 LKGYEA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 LKGYEA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multigene family.
                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC013427;
                                                                                                                                                                                                                                                                                               thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAKB RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRKAB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 167
SCHEEN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lue buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 35-158 FROM N.A., AND SEQUENCE OF 35-71; 78-82 AND 89-158. STRAIN=Sprague-Dawley; TISSUB=Liver; MEDLINE=950500763; PubMed=7961907. Stapleton D., Gao G., Michell B.J., Widmer J., Mitchelhill K.I., Teh T., House C.M., Witters L.A., Kemp B.E.; "Mammalian S'-AMP-activated protein kinase non-catalytic subunits are homologs of proteins that interact with yeast Snf1 protein kinase."; J. Biol. Chem. 269:29346(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROCEEDING AMPK TERRONGELE FOR THE REGULATION OF PATTY ACID SYNTHESIS BY PHOSPHORYLATION OF ACETYL-COA CARBOXYLASE. ALSO REGULATES CHOLESTEROL SYNTHESIS OF A PHOSPHORYLATION AND REGULATES CHOLESTEROL SYNTHESIS OF A PHOSPHORYLATION AND RACTIVATION AND INACTIVATION OF HYDROXYRETHYLGILUTAXYL-COA REDUCTASE AND HORWONE-SENSITIVE LIPASE. THIS IS A REGULATORY SUBUNIT, MAY BE A POSITIVE RECULATOR OF AMPK ACTIVITY. IT MAY ALSO SERVE AS AN ADAPTER WOLECULE FOR THE CATALITY: IT MAY ALSO SERVE AS AN ADAPTER TESURE SPECIFICITY: Highly expressed in kidney, heart, white adipose tissue, lung and spleen.

-!- TISSUE SPECIFICITY: Highly expressed in kidney, heart, white adipose tissue, lung and spleen.
-!- FTM: Phosphorylated when associated with the catalytic subunit.
-!- STHILARLIFY: Belongs to the 5'-AMP-activated protein kinase beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Warden S.M., Richardson C., O'Donnell J. Jr., Stapleton D., Kemp B.E.,
, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SER.24; SER-107 AND SER-181.
MEDLINE=97450976; PubMed=9305909;
Mitchelhill K.I., Michell B.J., House C.M., Stapleton D., Dyck J., Gamble J., Ullrich C., Witters L.A., Kemp B.E.;
"Posttranslational modifications of the 5'-AMP-activated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Post-translational modifications of the beta-1 subunit of AMP-activated protein kinase affect enzyme activity and cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE, MYRISTOYLATION, AND PHOSPHORYLATION OF SER-23;
                                                                                                                                                                                                             STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDINE=9624074; PubMed=6621499;
Gao G., Fernandez C.S., Stapleton D., Auster A.S., Widmer J.,
Dyck J.R.B., Kemp B.E., Witters I.A.;
"Non-catalytic beta- and gamma subunit isoforms of the
"Nan-activated procein kinase.";
J. Baiol. Chem. 271:8675-8681(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96215327; PubMed=8626596; Woods A., Cheung P.C.F., Smith P.C., Davison M.D., Scott J., Beri R.K., Carling D.; "Characterization of AMP-activated protein kinase beta and gasubunits. Assembly of the heterotrimeric complex in vitro."; J. Biol. Chem. 271:10282-10290(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUTAGENESIS, MYRISTOYLATION, AND PHOSPHORYLATION OF SER-23;
SER-24; SER-107 AND SER-181.
MEDLINE-21092935; PubMed=11171104;
                                                                                                                                                                            AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 272:24475-24479(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354:275-283 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U42411; AAC52579.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kinase betal subunit.
                                                                                                                                                                            SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=Wistar;
                                              Mammalia, Eutheri
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     localization.";
Biochem. J. 354
```

```
SHAFFF
                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92333688; PubMed=1321287;
Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicholas J., Coles L.S., Newman C., Honess R.W.; "Regulation of the herpesvirus saimiri (HVS) delayed-early 110-kilodalton promoter by HVS immediate-early gene products and a homolog of the Epstein-Barr virus R trans activator.";
         InterPro; IPR006828; AMPKBI.
Pfam; PF04739; AMPKBI; 1.
Fatty acid biosynthesis; Phosphorylation; Myristate; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicholas J., Cameron K.R., Coleman H., Newman C., Honess R.W., "Analysis of nucleotide sequence of the rightmost 43 kbp of herpesvirus saimiri (HVS) L-DNA: general conservation of genetic organization between HVS and Epstein-Barr virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                            .
0
                                                                                                          G -> E (IN REF. 1).
M -> I (IN REF. 3; AA SEQUENCE).
6245087E57E581E1 CRC64;
                                                                                                                                                      DB 1; Length 269;
                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Primary structure of the herpesvirus saimiri genome.";
                                                               (AUTO-).
                                                                                    PHOSPHORYLATION (AUTO-). PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                     N-myristoyl glycine.
PHOSPHORYLATION (AUT
PHOSPHORYLATION (AUT
                                                                                                                                                                Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
                                                                                                                                                                                                                                                                             269 AA.
                                                                                                                                                                           0; Mismatches
                                                                                                                                                      1.8%; Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92230228; PubMed=1314457;
                                                                                                                                                                                                                                                                                                                                                       Herpesvirus saimiri (strain 11).
                                                        23
24
107
181
25
55
51
30263 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Virol. 62:2457-2466(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virol. 66:5047-5058(1992).
                                                                                                                                                               100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X64346; CAA45674.1; -. EMBL; M86409; AAA46128.1; -. EMBL; M60850; AAA46160.1; -.
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                            STANDARD:
                                                                                                                                                                                                                                                                                                                              ne 51 glycoprotein.
OR EDRF2.
                                                              23
24
107
181
25
51
269 AA;
                                                                                                                                                                                                248 YISKPE 253
                                                                                                                                                                                                                   191 YISKPE 196
                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein.
                                                                                                                                                                           9
                                                                                                                                                                                                                                                                         VG51_HSVSA
Q01036;
                                                                                                                    CONFLICT
                                         MET
                                                                                                         CONFLICT
                                                                                                                                                     Query Match
                                                               MOD_RES
MOD_RES
                                                                                     MOD_RES
                                                                                               RES
                                                                                                                                                                                                                                                               VG51_HSVSA
                                                                                                                                                                           Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWHIL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Frichmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The minimal gene complement of Mycoplasma genitalium.";
Science 270:337-403(1995).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL LIPOPROTEIN MG440.

N-palmitoyl cysteine (Potential).

S-diacylglycerol cysteine (Potential).

6038B2290981F4C8 CRC64;
                                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                     1.8%; Score 6; DB 1; Length 269;
100.0%; Pred. No. 3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 1; Length 274; 100.0%; Pred. No. 3.16+02; ative 0; Mismatches 0; Indels
58 N-LINKED (GLCNAC. ...) (POTE)
74 N-LINKED (GLCNAC. ...) (POTE)
78 N-LINKED (GLCNAC. ...) (POTE)
137 N-LINKED (GLCNAC. ...) (POTE)
161 N-LINKED (GLCNAC. ...) (POTE)
170 N-LINKED (GLCNAC. ...) (POTE)
191 N-LINKED (GLCNAC. ...) (POTE)
191 N-LINKED (GLCNAC. ...) (POTE)
191 N-LINKED (GLCNAC. ...) (POTE)
191 A. 29574 MM; A6038FDE46A8652C CRC64;
                                                                                                                                                                                                                                                                       3e+02;
3e+02;
... 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the MG439 / MG440 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein, Lipoprotein, Membrane, Signal,
Complete proteome, Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 35, Last sequence update) (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical lipoprotein MG440 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001595; Lipoprotein 3.
InterPro; IPR00437; Prok lipoprot_S.
Edm; PF00938; Lipoprotein 3; 1.
ProDom; PD003276; Lipoprotein 3; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U39726; AAC72460.1; ALT_INIT.
TIGR; MG440; -,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE-96026346; PubMed=7569993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 26 N
26 26 S
274 AA; 30777 MW;
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                       286 KTQPIV 291
                                                                                                                                                                                                                                                                                                                                                                                                                            226 KTQPIV 231
                                                                                                                                                                                                   269 AA;
                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y440 MYCGE
P47678;
                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                   CARBOHYD
                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                           Query Match
        CARBOHYD
                                                             CARBOHYD
                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 169
Y440 MYCGE
                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
```

```
NCBI TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPN646 OR MP196.
   NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y44A MYCPN
P75151;
                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                     Y44A_MYCPN
                                                                                                                                                                                                                                                                                                                                        Matches
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL LIPOPROTEIN MG440 HOMOLOG 2.
                                                                                                                                                                                                                                                                          "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 24:4420-4449(1996).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 274 HYPOTHETICAL LIPOPROTEIN MG440 HOMOLOG
25 25 N-palmitoyl cysteine (Potential).
25 25 S-diacylglycerol cysteine (Potential).
274 AA; 30675 MW; EA3F5A3AD0046F32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Hypothetical lipoprotein MG440 homolog 2 precursor (E09_orf302).
MPN643 OR MP199.
                                                                                                                                                               Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                    Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 1; Length 274; 100.0%; Pred. No. 3.1e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom, PD003276, Lipoprotein 3; 1.
PROSITE, PS00013; PROKAR LIPOPROTEIN; 1.
Hypothetical protein; Lipoprotein; Membrane; Signal;
                                                                                                                                                                                                                                                                                                                           (Potential).
-!- SIMILARITY: Belongs to the MG439 / MG440 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-001-2001 (Rel. 40, Created)
16-001-2001 (Rel. 40, Last sequence update)
16-001-2001 (Rel. 40, Last annotation update)
Hypothetical protein yfdQ.
YFDQ OR B2360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000020; AAB95847.1; ALT INIT.
InterPro; IPR001595; Lipoprotein 3.
InterPro; IPR000437; Prok_lipoprot_S.
                                                                                                                                                                                                                           STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00938; Lipoprotein 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                 STANDARD;
27 ILEKQD 32
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 ILEKOD 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILEKOD 94
                      ILEKOD 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                         NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                Herrmann R.;
                                                                                                                                                                                                                                                                                         pneumoniae.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YFDQ_ECOLI
                                                                                 Y44B MYCPN
                      90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OCCUPATION
                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                            STRAIN=X12 / MG1655,
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical lipoprotein MG440 homolog 1 precursor (E09_orf277)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 1; Length 274;
100.0%; Pred. No. 3.1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000324; AAC75419.1; -.
PIR; E65009; E65009.
Ecodeme; EG14139; yfdQ.
Hypothetical protein; Complete proteome.
SEQUENCE 274 AA; 30442 MW; 3480CA08A045AB7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the MG439 / MG440 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S73522; S73522.
InterPro; IPR011595; Lipoprotein 3.
InterPro; IPR00437; Prok lipoprot_S.
Pfam; PF00938; Lipoprotein 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000020; AAB95844.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 LKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 LKKTAP 118
SEQUENCE FROM N.A.
```

PD003276; Lipoprotein_3; 1

```
STAAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             078449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 175
                             RESULT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YC80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YC80
                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                     POTENTIAL.
HYPOTHETICAL LIPOPROTEIN MG440 HOMOLOG 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAINE-21359325, PubMed=11466286; MED-1787;

MEDLINE-21359325, PubMed=11466286; MED-1787;

MEDLINE-21359325, PubMed=11466286; MED-1787;

MEDLINE-21359325, PubMed=11466286; MED-1787;

Gibson R., Idee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838 (2001).

-I. CYTALYTIC ACTIVITY: ATP + (R)-pantoate + beta-alanine = AMP +
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pantoate--beta-alanine ligase (EC 6.3.2.1) (Pantothenate synthetase)
                                                                  26 27 BYPUTHDILLUM CONTROLL (Potential).
26 26 N-palmitoyl oysteine (Potential).
26 26 3.1097 MW; Al7DC45BED6D3065 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiadese;
                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: Pantothenate biosynthesis; last step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 1; Length 281; 00.0%; Pred. No. 3.2e+02;
                                                                                                                                           Length 277;
                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 AA; 31543 MW; C42FC71AC2070409 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02569; Pantoate ligame; 1.
TIGRFAMs; TIGR00018; panC; 1.
Pantothenate biosynthesis; Ligame; Complete proteome.
          PROSITE, PSO0013; PROKAR LIPOPROTEIN, 1.
Hypothetical protein; Lipoprotein; Membrane; Signal;
Complete proteome; Palmitate.
                                                                                                                                        Score 6; DB 1; Ler
Pred. No. 3.1e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Matcn
Best Local Similarity 100.0%; Pred. No. 3.4
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003721; Pantoate ligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diphosphate + (R)-pantothenate.
                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE007789; AAK80857.1; ~.
PIR; F97258; F97258.
                                                                                                                                         1.8%; 5
                                                                                                                                                                                                                                                                                                                                                                                   (Pantoate activating enzyme).
                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                STANDARD;
                                                        25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF 00158; -; 1.
                                                                                                                                                                                              27 ILEKQD 32
                                                                                                                                                                                                                           90 ILEKOD 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                PANC OR CAC2915
                                                                                                                                                                                                                                                                                                PANC CLOAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                            097F38;
                                                      SIGNAL
                                                                                  LIPID
                                                                     CHAIN
                                                                                                 LIPID
                                                                                                                                                                                                                                                                                 PANC_CLOAB
                                                                                                                                                                                                                                                                                                엄
```

ò

Gaps

; 0

0; Indels

à g

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                     Projan S.J., Moghazeh S., Novick R.P.; "Nucleotide sequence of pS194, a streptomycin-resistance plasmid from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus.";
Nucleic Acids Res. 16:2179-2187(1988).
-!- FUNCTION: THIS PROTEIN IS REQUIRED FOR STREPTOMYCIN RESISTANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Douglas S.E., Penny S.L.; "The plastid genome of the cryptophyte alga, Guillardia theta: complete sequence and conserved synteny groups confirm its common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.8%; Score 6; DB 1; Length 282; Best Local Similarity 100.0%; Pred. No. 3.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR007530; Adenyl transf.
Pfam, PF04439; Adenyl transf; 1.
Antibiotic resistance; Plasmid.
SEQUENCE 282 AA; 33961 MW; 0C6A770634E5F58B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia
                                                                                                                                                                                                  Bacteria, Firmicutes; Bacillales; Staphylococcus
NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-ULI-1999 (Rel. 38, Last annotation update)
Hypothetical 33.2 kDa protein ycf80.
                                      (Rel. 12, Created)
(Rel. 12, Last sequence update)
(Rel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ancestry with red algae.";
J. Mol. Evol. 48:236-244(1999).
-!- SIMILARITY: Belongs to the ycf80 family.
282 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guillardia theta (Cryptomonas phi)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99128221; PubMed=9929392;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=88189810; PubMed=3357770;
                                                                                                                     Streptomycin resistance protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X06627; CAA29839.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                    Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S00938; S00938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 FNNILR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 FNNILR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=55529;
                                                                                                                                                                                             Plasmid pS194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast,
                                           01-OCT-1989
01-OCT-1989
                                                                                            01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GUITH
```

```
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., Mimer G., Goyal A., Pitce P., Noelling J., Reeve J.N., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fourth step.
-!- SIMILARITY: Belongs to the shikimate dehydrogenase family.
-!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A PROBABLE FRAMESHIFT
WAS CORRECTED AT POSITION 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997)
-!- CATALYTIC ACTIVITY: Shikimate + NADP(+) = 5-debydroshikimate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 6; DB 1; Length 282;
100.0%; Pred. No. 3.2e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP; MF_00222; -; 1.
InterPro; IPR006152; Shikimate.
InterPro; PR006151; Shikimate_DH.
Pfam; PF0148; Shikimate_DH; 1.
TIGRFAMs; TIGR00507; aroE; 1.
Aromatic amino acid blosynthesis; Oxidoreductase; NADP;
                                                                                                                                                                                                        EMBL, AF041468, AAC35638.1, -.
Hypothetical protein, Chloroplast.
SEQUENCE 282 AA, 33221 MW, 0D84447DCADA943A CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 AA; 30484 MW; 3293E04F92FC0B89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 40, Last sequence update) (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shikimate 5-dehydrogenase (EC 1.1.1.25)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000811; AAB84748.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIADLO 215
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 LIADLQ 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome SEQUENCE 283 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Delta H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR MTH242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AROE METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210
                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AROE METTH
   50000008%8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HANDER RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVED TO THE RESERVE
```

1.8%; Score 6; DB 1; Length 283;

Query Match

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-ATCC 19089 / CB15,

MEDLINE-21173698; PubMed=11259647;

MEDLINE-21173699; PubMed=11259647;

Miscrman W.C., Felddlyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Fotocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

Salzberg S.L., Venter J.C., Shaplro L., Fraser C.M.,

"Complete genome sequence of Caulobacter crescentus.",

"Complete genome sequence of Caulobacter crescentus.",

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Shikimate + NADP(+) = 5-dehydroshikimate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fourth step.
-!- SIMILARITY: Belongs to the shikimate dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 1; Length 285; 100.0%; Pred. No. 3.2e+02; tive 0; Mismatches 0; Indels
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; ME_00222; -; 1.
InterProf, TRR006151; Shikimate DH.
Pfam; PF01489; Shikimate DH; 1.
Aromatic amino acid biosynthesis; Oxidoreductase; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 AA; 29014 MW; 91174F9C770C14FE CRC64;
                      ..
  ; Pred. No. 3.2e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Shikimate 5-dehydrogenase (EC 1.1.1.25).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE005675; AAK21991.1; -. PIR; C87249; C87249.
                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
    100.0%;
                    6; Conservative
                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                              Caulobacter crescentus.
                                                        251 KPENLK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 LKLIGE 234
Best Local Similarity
Matches 6; Conserv
                                                                                              44 KPENLK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 LKLLGE 284
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
SEQUENCE 285 AA;
                                                                                                                                                                                                                                                                                                              AROE OR CC0003.
                                                                                                                                                                                             CAUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUS1 SCHPO
P78955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                       RESULT 177
                                                                                                                                                                         AROE_CAUCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUS1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4444
```

|||||| 57 TIFEDY 62

```
Mood V., Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Brown B., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gonlins M., Connor R., Davis P., Huchell C., Jagels K., James K., Jones L., Jones M., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornes M., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., Stevens K., Taylor K., Taylor R., Sanches S., Stevens K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McDonald S., McCombie W.R., Paulsen I., Potashkin J., McCombie W.R., Paulsen I., Potashkin J., McCombie W.R., Paulsen I., Potashkin J., McCombie W.R., Paulsen I., Potashkin J., McCombie S., Nare P., McDonald S., McDonald S., McCombie W.R., Paulsen I., Botashkin J., McCombie S., McDonald S., McDonald S., McCombie S., McDonald S., McCombie S., McDonald S., McCombie S., McDonald S., McCombie S., McDonald S., McCombie S., McCombie S., McCombie S., McCombie S., McDonald S., McCombie S., McCombie S., McCombie S., McCombie S., McCombie S., McCombie S., McCombie S., McCombie S., McCombie S., McCombie S., McCombie S., McCombie S., McCombie S., McCombie S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: Essential in controlling the S-M checkpoint that couples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitosis to the completion of DNA replication. It is also required for the response to DNA damage. Mutants defective in husl have a nucleus that is cleaved by the septum or the septum divides the
                                                                                                                                                                                                                                                             MEDLINE=97324587; PubMed=9180692;
Kostrub C.F., Al-Khodairy F., Ghazizadeh H., Carr A.M., Bnoch T.;
"Molecular analysis of hus1+, a fission yeast gene required for S-M
and DNA damage checkpoints.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       287 AA; 32713 MW; 283CE8F538DEFB78 CRC64;
                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell into a nucleate and anucleate compartment.
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                            Gen. Genet. 254:389-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GeneDB SPombe; SPAC20G4.04c; -.
InterPro; IPR007150; Hus1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitosis; DNA damage; DNA repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y09438; CAA70588.1; -.
EMBL; Z98600; CAB11254.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF04005; Hus1; 1
                              Protein hus1.
HUS1 OR SPAC20G4.04C.
                                                                                                                                                           Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; T43396; T43396.
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                    NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE COMPLETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishiyama M., Horinouchi S., Beppu T.; "Characterization of an operon encoding succinyl-CoA synthetase and malate dehydrogenase from Thermus flavus AT-62 and its expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Gen. Genet. 226:1-9(1991).
-!- CATALYTIC ACTIVITY: ATP + succinate + CoA = ADP + succinyl-CoA
                                                                                                                                                                                                                                                       MEDLINE-89041573; PubMed=1186449;
Nicholls D.J., Sundaram T.K., Atkinson T., Minton N.P.;
"Nucleotide sequence of the succinyl-CoA synthetase alpha-subunit
                                                                                                                                              Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=B / NCIB 11247;
MEDLINE=90375010; PubMed=2204576;
Nicholls D.J., Sundaram T.K., Atkinson T., Minton N.P.;
"Cloning and nucleotide sequences of the mdh and sucD genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the succinate/malate CoA ligase alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: Tricarboxylic acid cycle.
SUBUNIT: Tetramer of two alpha and two beta chains.
MISCELLANBOUS: THE ALPHA SUBUNIT BINDS ATP AND CATALYZES
PHOSPHORYL TRANFER TO ONE OF ITS HISTIDINE REGIDUES. THE CC
ACTIVE SITE IS PROBABLY LOCATED IN THE REGION OF ALPHA-BETA
                               01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Succinyl-CoA synthetase alpha chain (EC 6.2.1.5) (SCS-alpha).
288 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02629; CoA binding; 1.
Pfam; PF00549; ligame-CoA; 1.
Pfam; PF01799; SCOASYNTHASE.
TIGREPAMS; TIGR01019; SUCCOAJIDha; 1.
PROSITE; PS01216; SUCCINYL_COA_LIG_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (St
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 16:9858-9858(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=ATCC 33923 / DSM 674 / AT-62;
MEDLINE=91238680; PubMed=2034208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermus aquaticus B.";
FEMS Microbiol. Lett. 58:7-14(1990).
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003781; CoA binding.
InterPro; IPR005810; CoA lig alpha.
InterPro; IPR005811; CoA ligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M35832; AAA27504.2; -.
EMBL; X56033; CAA38507.1; -.
EMBL; X54073; CAA38007.1; -.
HSSP; P07459; 1SCU.
                                                                                                                                                                                                                                                                                                                 from Thermus aquaticus B.
STANDARD;
                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=B / NCIB 11247;
                                                                                                                            Thermus thermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subunit family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli."
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                 NCBI_TaxID=274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphate.
                                                                                                         SUCD OR SCSA.
THETH
                                                                                                                                                                 rhermus
                 P09143;
```

Conservative

Best Local Similarity Matches 6; Conserv

Query Match

.. 0

Gaps

..

1.8%; Score 6; DB 1; Length 287; 100.0%; Pred. No. 3.2e+02; Live 0; Mismatches 0; Indels

```
REALINE-22508454; PubMed=12620739;

REDIINE-22508454; PubMed=12620739;

RA MEDLINE-22508454; PubMed=12620739;

RA Maxino K., Oshima K., Kurokava K., Yokoyama K., Uda T., Tagomori K.,

RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Ilda T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism

RI distinct from that of V. cholerae.";

RI Lancet 361:743-749(2003).

C. - FUNCTION: Redox regulated molecular chaperone. Protects both

thermally unfolding and oxidatively damaged proteins from

irreversible aggregation. Plays an important role in the bacterial

CC thermally unfolding and oxidative stress (By similarity).

CC -- PTM: Under oxidizing conditions two disulfide bonds are formed

CC involving the reactive cysteines. Under reducing conditions zinc

important to the reactive cysteines and the protein is inactive (By
                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                           Gaps
PROSITE; PS00399; SUCCINYL COA LIG 2; 1.
Ligase; Tricarboxylic acid cycle; ATP-binding; Phosphorylation.
ACT SITE 246 246 TELE-PHOSPHOHISTIDINE INTERMEDIATE
                                                                                                     (BY SIMILARITY).

EET -> HLP (IN REF. 1; AAA27504).

TY -> RH (IN REF. 1; AAA27504).

IGT -> RRL (IN REF. 1; AAA27504).
                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                  243A68469E78AF68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
33 kDa chaperonin (Heat shock protein 33 homolog) (HSP33)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chaperone; Redox-active center; Zinc; Complete proteome.
DISULED 229 231 REDOX-ACTIVE (BY SIMILARITY)
DISULEID 262 265 REDOX-ACTIVE (BY SIMILARITY)
SEQUENCE 291 AA; 32284 MW; 2A646DB76356099B CRC64;
                                                                                                                                                                                                                                                                                                     Length 288;
                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                 DB 1; Len
                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 1
100.0%; Pred. No. 3.2v
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Belongs to the HSP33 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 1
100.0%; Pred. No. 3.3
tive 0; Mismatches
                                                                                                                                                                                                                           29822 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AP005073; BAC58393.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF 00117; -; 1.
InterPro; IPR000397; Hsp33.
Pfam; PF01430; HSP33; 1.
                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio parahaemolyticus.
                                                                                                                                     132
                                                                                                                                                                                               185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                        288 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 186 TFKDLL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 TEKDLL 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSLO_VIBPA
ID HSLO_VIBPA
                                                                                                                                                            CONFLICT
                                                                                                                            CONFLICT
                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSTO
                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NA FIT FIT SO SET THE SO SET THE SO SET THE SO SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE SET THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-- FWOTION: Redox regulated molecular chaperone. Protects both thermally unfolding and oxidatively damaged proteins from irreversible aggregation. Plays an important role in the bacterial defense system toward oxidatively stress (By similarity).
-- SUBCELLULAR LOCATION: Cytoplssmic (By similarity).
-- PTM: Under oxidizing conditions two disulfide bonds are formed involving the reactive cysteines. Under reducing conditions zinc is bound to the reactive cysteines and the protein is inactive (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHFB HUMAN STANDARD, PRT; 292 AA.
69UILB; Q9YEA2;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
PHD finger protein 11 (BRCA1-C terminus associated protein) (NY-REN-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., Choy H.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
                                                                                                                                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
33 KDa chaperonin (Heat shock protein 33 homolog) (HSP33).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chaperone; Redox-active center; Zinc; Complete proteome.
DISULPID 229 231 REDOX-ACTIVE (BY SIMILARITY)
DISULPID 262 265 REDOX-ACTIVE (BY SIMILARITY)
SEQUENCE 291 AA; 32631 MW; 1448E5FFE59E85C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.8%; Score 6; DB 1; Ler
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SIMILARITY: Belongs to the HSP33 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE016799; AA009383.1; -.
HAMAP; MF 00117; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF 00117; -; 1.
InterPro; IPR000397; Hsp33.
Pfam; PF01430; HSP33; 1.
                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                     Vibrionaceae; Vibrio.
230 KLLGEL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                     42 KLIGEL 47
                                                                                                                                                                                                                                                                 Vibrio vulnificus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 KLLGEL 235
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 KLLGEL 47
                                                                                                                                                                                                                                               HSLO OR WI0880.
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CMCP6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigen).
PHF11 OR BCAP.
                                                                                                                            HSLO VIBVU
QBDDS7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHFB_HUMAN
                                                                                                                            ò
```

.; 0

Gaps

;

DB 1; Length 291, 3.3e+02; 0; Indela

6; Conservative

Matches

```
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
    NCBI_TaxID=9606;
                                                                                                               Name=1
```

A MEDIINE=2238857; PubMed=12477932;

RA Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moorer T., Max S.I., Wang J., Hsieh F.,

RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Pahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R. Generation and initial analysis of more than 15,000 full-length

RI Drown Marl A., Prono M. T. R. D., Polichon M.A.,

R. T. Maman and mouse CDNA sequences.",

R. T. Mann and mouse CDNA sequences.", This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way MEDINES-2660539; PubMed=12754510;
Zhang Y., Leaves N.I., Anderson G.G., Ponting C.P., Broxholme J.,
Roll R., Edser P., Bhattacharyya S., Dunham A., Adcock I.M.,
Polleyn L., Barnes P.J., Harper J.I., Abecasis G., Cardon L.,
White M., Burnon J., Matthews L., Mott R., Ross M., Cox R.,
Moffatt M.F., Cookson W.O.C.M.;
"Positional cloning of a quantitative trait locus on chromosome 13q14
that influences immunoglobulin B levels and asthma.";
Nat. Genet. 34:181-186(2003).
-!- SUBUNIT: Interacts with BRCA1.
-!- ALTERNATIVE PRODUCTS: TISSUE=Renal cell carcinoma;
MEDLINE=99438124; PubMed=10508479;
Scanlan M.J., Gordan J.D., Williamson B., Stockert E., Bander N.H.,
Jongeneel C.V., Gure A.O., Jager D., Jager E., Knuth A., Chen Y.-T.,
old L.J.; "Antigens recognized by autologous antibody in patients with renal-Kato H., Seki N., Seto M., Ishida M., "A BRCA1-C terminus associated protein BCAP is encoded at B-CLL POLYMORPHISM: Variation in PHF11 seem to be associated with propensity to clinical asthma.
SIMILARITY: Contains 1 PHD-type zinc finger.
CAUTION: Ref.1. sequence differs from that shown due to frameshifts in positions 187 and 214. ISOI4-Q9UILB-1; Sequence-Displayed; IISSUE SPECIFICITY: Expressed in all normal tissues tested, including lung, testis, small intestine, breast, liver and Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). ALTERNATIVE SPLICING, AND ASSOCIATION WITH ASTHMA. J. Cancer 83:456-464(1999). deleted region in 13q14.", SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. carcinoma.

```
Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEDLINE-21357209; PubMed=11463916;
NEDLINE-21357209; PubMed=11463916;
NEDLINE-21357209; PubMed=11463916;
Nettin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
Peterson S., Heidelberg J., DeBON R.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
MoDonald L.A., Feldblyum T.V., Angiuoll S., Dickinson T., Hickey E.K.,
Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 293:498-506(2001).
-!- FUNCTION: Responsible for synthesis of pseudouridine from uracil-55 in the psi GC loop of transfer RNAs (By similarity).
-!- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the pseudouridine synthase truB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               097033;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last sequence of transpace)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٠,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 1; Length 292; 100.0%; Pred. No. 3.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae.
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                               modified and this statement is not removed.
                                 entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                          EMBL; AF155105; AAD42871.1; ALT_FRAME.
EMBL; AB011031; BAA32101.1; ALT_INIT.
EMBL; BC017212; AAH17212.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE007421; AAK75319.1; -. PIR; F95140; F95140.
                                                                                                                                                                                                                                                                               InterPro, IPR001965; Znf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Best Accessive
Conservative
                                                                                                                                                                                                                          Genew; HGNC:17024; PHF11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -phosphate + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 LYSSGL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 LYSSGL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Subfamily 1.
                                                                                                                                                                                                                                                        MIM; 607796; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRUB STRPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRUB_STRPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE AND THE STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   엄
```

ò

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21429245; PubMed=11544234; Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., Hoskins J., Alborn W.E. Jr., Arnold J., Fuller W., Geringer C., Gilmour R. G., Grass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Noris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., 2006, C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.
                                                                                                                                                                                                                                                                                                                                                              10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
tRNA pseudouridine synthase B (EC 4.2.1.70) (tRNA pseudouridine 55
synthase) (Psi55 synthase) (Pseudouridylate synthase) (Uracil
                                                                                                                                                                                                    ;
0
                                                                                                                                                              DB 1; Length 292; .. 3.3e+02; ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                            38 38 BY SIMILARITY.
292 AA; 32271 MW; B7A192469C4BC168 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 38 BY SIMILARITY.
292 AA; 32256 MW; 2716D45FFC2E145E CRC64;
                                                                                                                                                                                                                                                                                                                                          292 AA.
                                                                                                                                                            1.8%; Score 6; DB 1
100.0%; Pred. No. 3.3
tive 0; Mismatches
             HAMAP; MF 01080; -; 1.
InterPro; IPR004510; TruB.
InterPro; IPR005501; TruB.
Ffam; PF01509; TruB N; 1.
TIGRFAMF; TIGR0431; TruB; 1.
tRNA processing; Lyase; Complete proteome.
ACT_SITE 38 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            trna processing; Lyase; Complete proteome.
ACT SITE 38 38 BY SIMILARITY.
SEQUENCE 292 AA: 32256 MW. 271574555000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE008482; AAK99895.1; -. PIR; C98008; C98008.
HAMAP; MF 01080; -; 1.
INLETPRO; IPR004510; TruB.
INLETPRO; IPR002501; TruB.
PEam, PF01509; TruB.N; 1.
TIGRPAMS; TIGR00431; TruB; 1.
                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                        STANDARD:
                                                                                                                                                                                                                                                      275 LAILEK 280
                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                          25 LAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=171101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                OR SPR1092.
 TIGR; SP1212;
                                                                                                                                                                                                                                                                                                                                     STRR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                     hydrolyase)
                                                                                                                           SEQUENCE
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                      QBCWR2;
                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                       TRUB
à
                                                                                                                                                                                                                                                   g
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Emropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta 1307:331-338(1996).
-1- FUNCTION: Sulfation of estrone and estradiol. May control the level of the estrogen receptor by sulfurylating free estradiol (By
                                             Gaps
                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bstrogen sulfotransferase, isoform 1 (EC 2.8.2.4) (EST-1)
(Sulfotransferase, estrogen-preferring) (Estrone sulfotransferase).
                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + estrone = adenosine 3',5'-bisphosphate + estrone 3-sulfate.
-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the sulfotransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAPS BINDING SITE (POTENTIAL).
          DB 1; Length 292; 3.3e+02;
                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 1; Length 295;
100.0%; Pred. No. 3.3e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rikke B.A., Roy A.K., "Structural relationships among members of the mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 AA; 35509 MW; 696A12FDA923A12E CRC64;
   1.8%; Score 6; DB 1
100.0%; Pred. No. 3.3
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000863; Sulfotransferase.
Pfam; PF00685; Sulfotransfer; 1.
ProDom; PD001218; Sulfotransferase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Fischer 344; TISSUE=Liver;
MEDLINE=96305357; PubMed=8688469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sulfotransferase gene family."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase, Steroid-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U50204; AAB07680.1; -.
HSSP; P49891; 1AQU.
Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                    275 LAILEK 280
                                                                   25 LAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 KLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 KLIEFL 211
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                    STEI OR SULTIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity)
                                                                                                                                                                                    SUO1 RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUO2_RAT
ID SUO2_RAT
AC P52845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           당점점
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                              Rikke B.A., Roy A.K.,
"Structural relationships among members of the mammalian
sulfortansferase gene family."
Biochim. Biophys. Acta 1307:331-338(1996).
-!- FUNCTION: Sulfation of estrone and estradiol. May control the
level of the estrogen receptor by sulfurylating free estradiol (By
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nactus Adyseptus (Adv.).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
30-MAY-2000 (Rel. 39, Last annotation update)
Estrogen sulfotransferase, isoform 2 (EC 2.8.2.4) (EST-2)
(Sulfotransferase, estrogen-preferring) (Estrone sulfotransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Estrone sulfotransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE=92261615; PubMed=1374839; Demyan W.F., Song C.S., Kim D.S., Her S., Gallwitz W., Rao T.R., Slonczynska M., Chatterjee B., Roy A.K.; "Estrogen sulfortansferase of the rat liver: complementary DNA cloning and age- and sex-specific regulation of messenger RNA."; Mol. Endocrinol. 6:589-597(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + estrone = adenosine 3',5'-bisphosphate + estrone 3-sulfate. -!- SUBUNIT: Homodimer (By similarity). -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity). -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity). -!- SIMILARITY: Belongs to the sulfotransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                259 265 PAPS BINDING SITE (POTENTIAL) 295 AA; 35364 MW; 149B5C9D46039AAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
15-WAR-2004 (Rel. 43, Last amortation update)
Estrogen sulfotransferase, isoform 3 (EC 2.8.2.4) (BST-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 1; Length 295;
100.0%; Pred. No. 3.3e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 258-265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Sulfotransferase, estrogen-preferring) Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000663; Sulfotransferase.
Pfam; PF00685; Sulfotransfer; 1.
ProDom; PD001218; Sulfotransferase; 1.
Transferase; Steroid-binding:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                    STRAIN=Fischer 344; TISSUE=Liver;
MEDLINE=96305357; PubMed=8688469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U50205; AAB07681.1; -.
HSSP; P49891; 1AQU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 KLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 KLIEFL 211
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUO3 RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P49889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
   SOUND DAY NAME OF THE PROPERTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY OF THE PARTY
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                   1. Steroid Biochem. Mol. Biol. 52:35-44(1995).

1. Steroid Biochem. Mol. Biol. 52:35-44(1995).

1. FUNCTION: Sulfation of estrone and estradiol. May control the level of the estrogen receptor by sulfate + estrone = denosine 3',5'-bisphosphate + estrone 3-sulfate.

2. SUBGUIT: Homodimer (By similarity).

3. SUBGRILIT: Homodimer (By similarity).

3. SUBGRILIT: Homodimer (By similarity).

4. SUBGRILITS LOCATION: Cytoplasmic.

4. DEVELOWENTAL STAGE: Expressed only in the liver of young adult animals (100 days old) and is absent in the prepubertal male (27 days old), senescent male (800 days old) and female liver.

5. INDUCTION: Induced by androgens and suppressed by estrogens. The expression is under the influence of pituitary growth hormone and thyroid hormone. Is regulated by progesterone in the uterus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Sulfotransferase, estrogen-preferring) (Estrone sulfotransferase).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last amontation update)
Estrogen sulfotransferase, isoform 6 (EC 2.8.2.4) (EST-6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                   Falany J.L., Krasnykh V., Mikheeva G., Falany C.N.; "Isolation and expression of an isoform of rat estrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Falany J.L., Krasnykh V., Mikheeva G., Falany C.N., "Isolation and expression of an isoform of rat estrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 P -> Q (IN REF. 2).
238 T -> I (IN REF. 2).
295 L -> P (IN REF. 2).
35415 WW; A77807A21DD2E7EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 6; I
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A41930; A41930.
HSSP; P49891; 1AQU.
InterPro; IPR000863; Sulfotransferase.
                                                         TISSUE=Liver;
MEDLINE=95161323; PubMed=7857871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Liver;
MEDLINE=95161323; PubMed=7857871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M86758; AAA41128.1; -. EMBL; S76489; AAB33441.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 KLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 KLIEFL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                   sulfotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
238
295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUC RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
SANTA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA RANKA
```

```
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TURN
HELIX
TURN
TURN
STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TURN
STRAND
HELLX
TURN
HELLX
HELLX
TURN
STRAND
HELLX
TURN
TURN
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
TURN
HELLX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TURN
                                                                                                                                                                                                                                                                                                                                                                                                  HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TURN
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
         J. Steroid Biochem. Mol. Biol. 52:35-44(1995).

-!- FUNCTION: Sulfation of estrone and estradiol. May control the level of the estrogen receptor by sulfurylating free estradiol.

-!- CATALYTIC ACTIVITY: 3' - phosphoadenylyIsulfate + estrone = adenosine 3', 5' - bisphosphate + estrone 3 - sulfate.

-!- SUBUNIT: Homodimer (By similarity).
-!- SUBCELULIAR LOCATION: Cytoplasmic.
-!- DEVELOPMENTAL STAGE: Expressed in males rats, but not in females.
-!- INDUCTION: Induced by androgens and suppressed by estrogens.
Expression is under the influence of pituitary growth hormone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS), AND REVISION TO 113.
STRAIN-CSTBALKKSJ-DB/DB; TISSUB=Testis;
MEDLINE=98025056; Dubmed=9360604;
MEDLINE=98025056; Dubmed=9360604;
"Crystal Structure of estrogen sulphotransferase.";
Nat. Struct. Biol. 4:904-908[1997].
Alt. Struct. Biol. 4:904-908[1997].
-i- FUNCTION: Sulfation of estradiol and estrone. May control the level of the estrogen receptor by sulfurylating free estradiol.
-i- CATALYIC ACTIVITY: 3'-phosphoadenylylsulfate + estrone =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                  EMBL; S76430,
HSSP: P49891; 1AQU.
HSSP: P49891; 1AQU.
InterPro. PR00685; Sulfotransferase.
Pfam; PF00685; Sulfotransfer; 1.
ProDom; PD001218; Sulfotransferase; 1.
Transferase; Steroid-binding; Multigene family.
Transferase; Steroid-binding; Multigene family.
259 265 265
PFBC BINDING SITE (POTENTIAL).
27302 MW; PFBD5861AFDC9805 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95269690; PubMed=7750469;
Song W.-C., Moore R., McLachlan J.A., Negishi M.;
Song Warcular characterization of a testis-specific estrogen
sulfotransferase and aberrant liver expression in obese and
diabetogenic C57BL/KsJ-db/db mice.";
Endocrinology 136:2477-2484(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 1; Length 295;
100.0%; Pred. No. 3.3e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                               -!- SIMILARITY: Belongs to the sulfotransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
15-UUL-1999 (Rel. 38 Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Estrogen sulfotransferase, testis isoform (EC 2.8.2.4)
(Sulfotransferase, estrogen-preferring).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/KSJ-DB/DB; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                               thyroid hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 KLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 KLIEFL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUOT MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
CC -- SINDRICH Roughlate 17.5 'Siphosphate a feature 3 -- sulfate.

CC -- SINDRICH Roughlate (TP) sinilarity)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR LOCATION: Cytopanam (C)
-- SINDRICH ROUGHLAR CYTOPANAM (C)
-- SINDRICH ROUGHLAR CYTOPANAM (C)
-- SINDRICH ROUGHLAR CYTOPANAM (C)
-- SINDRICH ROUGHLAR CYTOPANAM (C)
-- SINDRICH ROUGHLAR CYTOPANAM (C)
-- SINDRICH ROUGHLAR CYTOPANAM (C)
-- SINDRICH ROUGHLAR CYTOPANAM (C)
-- SINDRICH ROUGHLAR CYTOPANAM (C)
-- SINDRICH ROUGHLAR CYTOPANAM (C)
-- SINDRICH ROUGHLAR CYTOPANAM (C)
-- SINDRICH ROUGHLAR CYTOPANAM (C)
-- SINDRICH ROUGHLAR
```

```
Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justice Justic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       May B.J., Zhang Q., Li L.L., Pauetian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
"Complete Steepering and rejoining of the recombining DNA molecules. The xerc.xerb complex is essential to convert dimers of the bacterial chromosome into monomers to permit their segregation at cell division. It also contributes to the segregational stability of plasmids (By similarity).

-!- SUBUNIT: Forms a cyclic heterotetrameric complex composed of two molecules of xerC and two molecules of xerD (By similarity).

-!- SUBCLIDIAR LOCATION: Cytoplasmic (By similarity).

-!- SIMILARITY: Belongs to the "phage" integrase family. XerC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                           ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
                                                                                                                                                                                                                                                                                                             DB 1; Length 295;
                                                                                                                                                                                       286
35590 MW; 8E85AB47952BFB1C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.8%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No. 3.3
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21145866; PubMed=11248100;
       252
252
266
267
267
                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 KLIEFL 305
                                                                                                                                                                                                                          295 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 KLIEFL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
   248
250
263
267
270
285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Pm70;
                                                                                                                                                                                                                          SEQUENCE
STRAND
TURN
HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 190

XERC PASMU
ID XERC PASMU
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
DT 10-OCT
                                                                                                                                                HELIX
                                                                                                             TURN
                                                                                                                                                                                       TURN
SPEFFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                      Gaps
                                                                                                                                   ٠.
                                                                       1.8%; Score 6; DB 1; Length 295;
100.0%; Pred. No. 3.3e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                     295 AA; 34206 MW; 99FD70DF1E37BA1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0326; GTP10BG
TIGREAMS; TIGRO0436; era; 1.
TIGREAMS; TIGRO0650; MG442; 1.
TIGREAMS; TIGRO0231; Small GTP; 1.
PROSITE; PSE50823; KH TYPE 2; 1.
GTP-binding; RNA-binding; Complete proteome.
NP BIND 10 17 GTP (POTENTIAL).
NP BIND 20 279 KH TYPE-2.
                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTP (POTENTIAL).
GTP (POTENTIAL).
GTP (POTENTIAL).
KH TYPE-2.
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP, MF_00367; -; 1.
InterPro; IPR005662; Bra.
InterPro; IPR006589; GTP-bindding_dom.
InterPro; IPR006073; GTP1 OBG.
InterPro; IPR004087; KH_dom.
InterPro; IPR004019; KH_prok.
InterPro; IPR004041; KH_TYPE.
InterPro; IPR002917; MMR_HSRI.
InterPro; IPR002917; MMR_HSRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTP-binding protein era homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE010538; AAL94476.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00013; KH; 1.
Pfam; PF01926; MMR_HSR1; 1.
                                                                                                  Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                139 LYSSGL 144
                                                                                                                                                                               73 LYSSGL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=ATCC 25586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERA OR FN0270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusobacterium
                                                                                                                                                                                                                                                                                                                                                           ERA_FUSNN
                     SEQUENCE
                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                      OBRGM1;
                                                                                                                                                                                                                                                                                                                                     ERA_FUSNN
                                                                                                                                                                                                                          Q
                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                HELLER BREEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFERS BEFER
                                                                                                                                                                                                                                                      ö
```

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RT03_ACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 194
           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration the European Bioinformatics Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                  Gaps
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                             Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Agaricaceae; Agaricus.
NCBI_TaxID=5341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEE-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Porphobilinogen deaminase (EC 2.5.1.61) (PBG) (Hydroxymethylbilane synthase) (HMBS) (Pre-uroporphyrinogen synthase).
                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                               -!- PATHWAY: Deoxyribonucleotide biosynthesis.
-!- SUBUNIT: Homodimer (By similarity).
-!- SIMILARITY: Belongs to the thymidylate synthase family.
                           DB 1; Length 296;
                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 296; . 3.3e+02; ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD001180; Thymidylat synt; 1.
PROSITE; PS00091; THYMIDYLATE SYNTHAGE; 1.
Transferase; Methyltransferase; Nucleotide biosynthesis.
ACT SITE 171 171 BY SIMILARITY.
 296 AA; 33929 MW; BO5FB966695E3969 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y SIMILARITY.
BFB8A8989D4A952A CRC64;
                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Thymidylate synthase (EC 2.1.1.45) (TS) (TSase)
                      1.8%; Score 6; DB 1
100.0%; Pred. No. 3.3
Nismatches
                                                                                                                                             296 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Match 1.8%; Score 6; DB 1
Local Similarity 100.0%; Pred. No. 3.33
Hes 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000398; Thymidylat_synth. Pfam; PF00303; thymidylat_synt; 1.PRINTS; PR00108; THYMDSNTHASE.
                                                                                                                                                                                                                Agaricus bisporus (Common mushroom).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ401221; CAB96042.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             296 AA; 33679 MW;
                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                     Query Match
Best Local Similarity
                                                               18 VKILKD 23
                                                                                   77 VKILKD 82
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 LRECIR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 LRECIR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P04818; 1HW4
                                                                                                                                         IYSY AGABI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEM3 FUSNN
QBRFP5;
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                     Q9P4T7
                                                                                                                   T 192
AGABI
                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 193
HEM3_FUSNN
S
                                                                                                                                                 ò
                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
```

```
*** MEDLINE=21886394; PubMed=11889109; A MEDLINE=21886394; PubMed=11889109; A MEDLINE=21886394; PubMed=11889109; A MEDLINE=21886394; PubMed=1189109; A MEDLINE=21886394; PubMed=1189109; A Meditacharya A., Bartman A., Gardner W., Grechkin G., Zhu L., A Vanisva O., Chu L., Kogan Y., Chaga O., Golteman E., Bernal A., A Fonstein M., Kyrpides N., Overbeek R.; A Fonstein M., Kyrpides N., Overbeek R.; The Genome sequence and analysis of the oral bacterium Fusobacterium Fur Genome sequence and analysis of the oral bacterium Fusobacterium Fur Indicatum strain ATCC 25586 "."

I. Bacteriol. 184:2005-2018(2002). The monopyrrole PBG into the hydroxymethylbilane preuroprophyrinogen in several discrete steps.

C. -! FUNCTION: Tetrapolymerization of the monopyrrole PBG into the hydroxymethylbilane preuroprophyrinogen in several discrete steps.

C. -! CATALYTIC ACTIVITY: 4 porphobilinogen in several discrete steps.

C. -! CATALYTIC ACTIVITY: 4 porphobilinogen a dipyrromethane cofactor to which the porphobilinogen subunits are added (By similarity).

C. -! PATHWAY: Porphyrin blosynthesis by the C5 pathway; fourth step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD002745; Porphobil deam; 1.
TIGREAMS; TIGR00212; hemC; 1.
PROSITE; PS00533; PORPHOBILLINGEN DEAM; 1.
POTPHYTIN biosynthesis; Transferase; Complete protecome.
BINDING 242 242
PYRROMETHAND COPACTOR (BY SIMILARITY).
SEQUENCE 298 AA; 33098 MW; 13908A7D0AAS6984 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 1.8%; Score 6; DB 1; Length 298; Local Similarity 100.0%; Pred. No. 3.3e+02; les 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the HMBS family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Acanthamoebidae; Acanthamoeba.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AE010575, AAL94841.1; -.
HAWAP; MF 00260; -; 1.
INTERPRO; IPR000860; Porphobil deam.
Pfam: PF01379; Porphobil deam; Pf03900; Porphobil deam; PFNINTS; PR0151; PORPHBDWASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrial ribosomal protein S3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acanthamoeba castellanii (Amoeba).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 30010 / Neff;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                   25586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 GLLVTL 119
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                   NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 GLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5755;
                                                                     Fusobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RT03 ACACA
P46754;
```

. 0

```
subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=AX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G3P DICDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  094469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 196
             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and propositit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESERVATE = 56601 / Serogroup Iccerohaemorrhagiae / Serovar lai;

RA MEDLINE=22598143; PubMed=12712204;

RA MEDLINE=22598143; PubMed=12712204;

RA Jiang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,

RA Jiang Y.-X., Kung H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,

RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,

RA Jiang J.-X., Gu W.-Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,

RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,

RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,

RA Jiang J.-G., Zhao G.-P.

RA Jiang J.-G., Zhao G.-P.

RA Jiang J.-G., Zhao G.-P.

RA Jiang J.-W. Shao G.-P.

RA Jiang J.-W. Shao G.-P.

RA Jiang J.-W. Shao G.-P.

RA Jiang J.-W. Shao G.-P.

RA Jiang J.-W. Shao G.-P.

RA Jiang J.-W. Shi M.-H.-P.

RA Jiang J.-W. Jiang J.-W. Shi M.-H. Jiang W.-W., Shi M.-H., Yin H.-P.

RA Jiang J.-W. Jiang J.-W. Jiang J.-W. Shi M.-H., Yin H.-P.

RA Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang J.-W. Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                           -!- SUBCELLULAR LOCATION: Mitchondrial.
                      Burger G., Plante I., Lonergan K.M., Gray M.W.,
"The mitochondrial DNA of the amoeboid protozoon, Acanthamoeba
castellani: complete sequence, gene content and genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.8%; Score 6; DB 1; Length 298; Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29415935EE187DE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prostrucy renvolunts and problem Prolley, Ribosomal S3 C; 1. PRO0417; Ribosomal S3 N; 1. PROSITE, PS00548; RIBOSOMAL S3; FALSE NEG. Ribosomal protein; Mitochondrion. SEQUENCE 298 AA; 36060 MW; 29415935EE1
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR009019; KH prok.
InterPro; IPR001351; Ribosomal 33 C.
InterPro; IPR008282; Ribosomal_S3_N.
  MEDLINE=95147275; PubMed=7844823;
                                                                                    organization.";
J. Mol. Biol. 245:522-537(1995).
                                                                                                                                                                                                                                                                                                                                                                       EMBL; U12386; AAD11841.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tyrosine recombinase xerD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                              PIR; S53849; S53849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 LFMLLK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 LFMLLK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR LA2483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XERD LEPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7ZAM7;
ð
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSIENT COVALENT LINKAGE TO DNA DURING STRAND CLEAVAGE AND REJOINING (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-A.1.

MEDLINE-A.1.

ROGER A.J., Smith M.W., Doolittle R.F., Doolittle W.F.;

Roger A.J., Smith M.W., Doolittle R.F., Doolittle W.F.;

"Evidence for the Heterolobosea from phylogenetic analysis of genes
encoding glyceraledryde-3-phosphate dehydrogenase.";

J. Bukaryot. Microbiol. 43:475-485(1996).

-!- CATALYITC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
-!- PATHWAY Second phase of glycolygis;
-!- PATHWAY Second phase of glycolygis;
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUMILARITY: Belongs to the glyceraldehyde 3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-UTL-1999 [Rel. 38, Last Sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH)
                                                                                                                                                                                               R HIGHARD, ME 01807; -; 1.

R INTERPROJ IPRO02104; Phage_integrase.

R InterProj IPR002104; Phage_integrase.

R Ent. PR00289; Phage_integrase; 1.

R Pfan; PF00289; Phage_integrase; 1.

KW DNA recombination; DNA-binding; Complete protecome.

FT ACT_SITE 173 173 BY SIMILARITY.

FT ACT_SITE 244 BY SIMILARITY.

FT ACT_SITE 247 247 BY SIMILARITY.

FT ACT_SITE 247 247 BY SIMILARITY.

FT ACT_SITE 247 247 BY SIMILARITY.

FT ACT_SITE 247 BY SIMILARITY.

FT ACT_SITE 247 247 BY SIMILARITY.

FT ACT_SITE 247 277 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 6; DB 1; Length 298;
Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 AA; 35073 MW; F1578AA6F23FEB25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetczoa, Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 LYSSGL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 LYSSGL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=22426901; PubMed=12522265;

MEDLINE=22426901; PubMed=12522265;

Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,

Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,

Tamannes J., Viguera B., Latorre A., Valencia A., Moran F., Moya A.;

Reductive genome evolution in Buchnera aphidicola.";

Proc. Natl. Acad. Sci. U.S.A. 100:581-586(2003)

-! CATALYTIC ACTIVITY: 1-(5-phospho-D-ribosyl)-ATP + diphosphate =

ATP + 5-phospho-alpha-D-ribose 1-diphosphate.

-! PATHWAY: Histidine biosynthesis; first step. Very important in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
ACTIVATES THIOL GROUP DURING CATALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: Homohexamer (By similarity).
-!- SUBCELIVIAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the ATP phosphoribosyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buchnera aphidicola (subsp. Baizongia pistaciae).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                  GLYCERALDEHYDE 3-PHOSPHATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 6; DB 1; Length 299;
Pred. No. 3.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 AA; 32407 MW; B5948FA38F8606F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
HISG OR BBP093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.8%; Score 6; DB 1;
Best Local Similarity 100.0%; Pred. No. 3.3¢
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulation of histidine metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF 00079; -; 1.
InterPro; IPR001348; ATP_phspho_trans.
PF01634; HisG; 1.
TIGRFAMS; TIGR00070; hisG; 1.
                                                                                       DictyBase; DDB0185087; gpdA.
InterPro; IPR000173; GAP dhdrogenase.
InterPro; IPR006424; GAPDH-I.
                                                                                                                                                                      Pfan, PF00044; gpdh; 1.
Pfam, PF02800, gpdh, C; 1.
PKINTS; PR00079; G3PDHDRGNASE.
TIGREAMS; TIGR01534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE014016; AAO26828.1; -.
                               EMBL; U55243; AAC47285.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               138
                                                                                                                                                                                                                                                                                                                                                                                                                                                          165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 PLAKII 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 PLAKII 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Long subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=135842;
                                                                                                                                                                                                                                                                                                                                                                                               138
                                                                                                                                                                                                                                                                                                                                                                                                                                                          165
                                                                     P56649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIS1 BUCBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P59453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 197
H191_BUCBP
H191_BUCBP
H191_BUCBP
DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT 10-0CT-DT
ò
```

PROSITE, PS01316; ATP_PHORIBOSYLTR; 1.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                            10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
33 kDa chaperonin (Heat shock protein 33 homolog) (HSP33).
Histidine biosynthesis; Transferase; Glycosyltransferase;
                                                 1.8%; Score 6; DB 1; Length 299;
100.0%; Pred. No. 3.3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                              HSLO OR HSP33 OR TLL0808,
Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REDOX-ACTIVE (BY SIMILARITY)
REDOX-ACTIVE (BY SIMILARITY)
2F8239B543BF42A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 1; Length 299; 100.0%; Pred. No. 3:3e+02; ive 0; Mismatches 0; Indels
             Complete proteome.
SEQUENCE 299 AA; 33618 MW; 58A189F6879D71F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01430; HSp33; 1.
Chaperone; Redox-active center; Zinc; Complete proteome.
DISULFID 240 242 RENDY-accept.
                                                                                                                                                                                           299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
-!- SIMILARITY: Belongs to the HSP33 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP005371; BAC08359.1; -. HAMAP; MF 00117; -: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32066 MW;
                                   Query Match
Best Local Similarity 100.0..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP; MF_00117; -; 1.
InterPro; IPR000397; Hsp33.
                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
                                                                                                   188 KDLLTR 193
                                                                                                                           22 KDLLTR 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 LKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 LKLLGE 256
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=32046;
                                                                                                                                                                                       HSLO_SYNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
SEQUENCE
                                                                                                                                                                                                   28DKO1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                 셤
                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
RAMANA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MARATA MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=AV19 / DSM 6324 / JCM 9639;
STRAIN=21927647; PubMed=11930014;
Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
Malykh A.G., Koonin E.V., Kozyavkin S.A.;
"The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaeal methanogens.";
Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
-!- SIMILARITY: Belongs to the FTR family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Formylmethanofuran--tetrahydromethanopterin formyltransferase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
SEC14 cytosolic factor (Phosphatidylinositol/phosphatidylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 300;
.. 3.3e+02;
ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; irro: 1.
Pfam; PP01913; FTR; 1.
Pfam; PP02741; FTR; 1.
PTRSF; PIRSP06414; FTR; 1.
ProDom; PD007702; FTR; 1.
Transferase; Complete proteome.
Transferase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=90330560; PubMed=2198263;
Salama S.R., Cleves A.E., Malehorn D.E., Whitters E.A.,
Bankaitis V.A.;
                                                                                 300 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 1
100.0%; Pred. No. 3.3
tive 0; Mismatches
                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE010372; AAM02029.1; -- HAMAP; MF_00579; atypical; 1. InterPro; IPR002770; FTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanopyrus kandleri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 LRECIR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 LRECIR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=2320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanopyrus
                                                                      FTRL METKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SC14 KLULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SC14 KLULA
ID SC14 KLULA
DT 01-MARS
DT 01-MARS
DE SEC14.
ON SEC14.
ON KLUVV
OC BUKATY
OC SACCHA
OC NACHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
OC SACCHA
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                 DDT THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY OF THE BEAUTY O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                       J. Bacteriol, 172:4510-4521(1990).

-!- FUNCTION: Required for transport of secretory proteins from the Golgi complex. Catalyzes the transfer of phosphatidylinositol and phosphatidylcholine between membranes in vitro (By similarity).

-!- SUBCELULLAR LOCATION: Associated with the Golgi complex as a peripheral membrane protein (By similarity).

-!- SIMILARITY: Contains 1 CRAL-TRIO domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEIC ACIDS KES. 24:9420-4449(1996).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
"Cloning and characterization of Kluyveromyces lactis SEC14, a gene
                                       whose product stimulates Golgi secretory function in Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MPNSSS OR MP257.
Mycoplasma pneumoniae.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential).
-!- SIMILARITY: BELONGS TO THE MG067 / MG068 / MG395 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 1; Length 301;
100.0%; Pred. No. 3.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical lipoprotein MPNS85 precursor (D02_orf302).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 AA; 34529 MW; 8B8353752FF5FCE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transport; Protein transport; Golgi stack.
DOMAIN 270 CRAL-TRIO.
                                                                                                                                                                                                                                                                                                                                                                   PIR; A37766; A37766.
HSSP; P24280; IAUA.
INTERPRO; IRRO01251; CRAL TRIO C.
INTERPRO; IRRO01251; CRAL TRIO N.
INTERPRO; IRRO01071; RetBind/tocTrans.
Pfam; PF00650; CRAL TRIO; 1.
Pfam; PF00506; CRAL TRIO; 1.
PRINTS; PR00180; CRETINALDHBP.
SWART; SM00516; SECI4; 1.
PROSITE; PS50191; CRAL TRIO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S73583; S73583.
InterPro; IPR002414; DUF30/31.
InterPro; PPR00437; Prok lipoprot_S.
Pfam; PF01732; DUF31; 1.
PRINTS; PR00840; Y06768FAMILY.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 24:4420-4449(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000025; AAB95905.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 DTIFED 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 DTIFED 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YF85 MYCPN
P75195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YF85_MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARTE BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BARRES BAR
```

RESULT 203

```
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98037514; PubMed-9371463; Smith D.R., Deloughery C., Lee H.-M., Dubois J., Smith D.R., Devocette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDangall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(197).
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
                                     POTENTIAL.

HYPOTHETICAL LIPOPROTEIN MPN585.

N-palmitoyl cysteine (Potential).

S-diacylglycerol cysteine (Potential).

OD2B90B2DC7FC78A CRC64;
                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
                                                                                                                                                    Length 302;
                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 1; Length 304;
100.0%; Pred. No. 3.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 0 BY SIMILARITY.

1 1 GATASE (BY SIMILARITY).

304 AA; 33779 MW; 02F652DE0FF6FCR9 CRC64;
Hypothetical protein, Lipoprotein, Membrane, Signal,
Complete proteome, Palmitate.
                                                                                                                                                                     3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutamine amidotransferase-like protein MTH191.
                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                   304 AA.
                                                                                                                                                             Local Similarity 100.0%; Pred. No. 3.4 les 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF00310; GATASE 2; 1.
PROSITE; PS00443; GATASE TYPE II; FALSE NEG.
Transferase; Glutamine amidotransferase; Com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                              1.8%; Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanobacterium thermoautotrophicum.
                                                      23 302 HY.
23 23 N-|
23 23 S-|
302 AA; 35102 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A69122; A69122.
HSSP; P00497; 1A00.
InterPro; IPR000583; GATase_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000806; AAB84697.1; -.
                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                       213 PLFSKS 218
                                                                                                                                                                                                                   5 PLFSKS 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Delta H;
                                                                                                                                                                                                                                                                                                                                               Y191 METTH
                                                                                                         SEQUENCE
                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              026293;
                                                      CHAIN
                                                                                                                                                                                                                                                                                                          RESULT 202
Y191_METTH
                                                                                                                                                                              Matches
   KW
FF
FF
SO
FF
                                                                                                                                                                                                                                                                                                                                            ਨੇ
                                                                                                                                                                                                                                                  d
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine/threonine protein phosphatase ppel (EC 3.1.3.16) (Phosphatase
                                                                                                                                                                  Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Hymenoptera, Apocrita, Aculeata, Apoidea,
                                                                                                                                                                                                                                                                                                      Crozier R.H., Crozier Y.C.; "The mitochondrial genome of the honeybee Apis mellifera: complete
                                                                                                                                                                                                                                                                                                                                      sequence and genome organization.";
Genetics 133:97-117(1993).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- SIMILARITY: Belongs to the complex I subunit 1 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
SEQUENCE 305 AA; 36838 MW; 01C4F46DFCF7A6E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=972 / HM123;
MEDLINE-93250325; PubMed=8387356;
Shimanuki M., Kinoshita N., Ohkura H., Yoshida T., Toda T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 305;
                                             01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last Bequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NADH-ubiquinone oxidoreductase chain 1 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungî; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 6; DB 1; Ler
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JTM-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00146; NADHdh; 1.
PROSITE; PS00667; COMPLEXI ND1 1; FALSE NEG.
PROSITE; PS00668; COMPLEXI ND1_2; FALSE_NEG.
                     305 AA.
                                                                                                                                  Apis mellifera ligustica (Common honeybee). Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Fred. No. 3.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPE1 OR ESP1 OR PPX1 OR SPCC1739.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001694; Resp_NADH_dhl.
                                                                                                                                                                                                                                                                                      MEDLINE=93114603; PubMed=8417993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L06178; AAB96810.1; -. PIR; S52972; S52972.
                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 ILFMLL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 ILFMLL 106
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                     NCBI TaxID=7469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=4896;
              NU1M APILI
P34847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPE1_SCHPO
P36614;
NUIM_APILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPE1_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 204
                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                쉼
```

·;

ö

Gaps

; 0

Conservative

9

Matches

276 ASEEVS 281

g

38 ASEEVS 43

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                      RX MDLINE=21848401; PubMed=11859360;

RA MEDLINE=21848401; PubMed=11859360;

RA MOOD V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Stewart A., Steover V., Gwilliam R., Rajandream M.A., Lyne B., Downan S., Chillingworth T., Churcher C.M., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., A Collins M., Connor R., Conin N., Hadalog J., Hodgson G., Gentles S., Goble A., Hamilin N., Harris D., Hidalog J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., R., Monds M., Sharther S., McDonald S., McHean J., R., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Ruther S., Saunders D., Seeger K., Sharp S., Allower K., Ruther S., Saunders D., Seeger K., Sharp S., Rutherford K., Ruther S., Saunders D., Seeger K., Sharp S., Ry Limer K., O'Neil S., Pagares R., Squares S., Stevens K., K., Taylor K., Taylor RG, Tivey A., Walsh S.V., Warren T., Whitehead S., Rebtton J., Simmonds M., Squares R., Scheefer M., Melbert H., Reinhardt R., Pohl T.M., RA Ber P., Zimmermann W., Wedler H., Reinhardt R., Pohl T.M., Raber P., Zimmermann W., Wedler H., Reinhardt R., Purnelle S., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Deans M., Rochet M., Caillardin C., Holzer B., Horst S.M., Daga R.R., Cruzado L., Jimenez J., Sanchez M., Holzer B., Benito J., Sanchez M., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Potsburg S.L., Spakovski G.V., Ussery D., Barrell B.G., Nurse P., The Granner Beguence of Schizosaccharomyces pombe.";

R. Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
-!- SUBUNIT: Interacts with sts5, ekcl and mis12.
-!- SUBUNIT: Interacts with sts5, ekcl and mis12.
-!- SUBCELIULAR LOCATION: Nuclear; associated with chromatin.
-!- SIMILARITY: Belongs to the PPP phosphatase family. PP-V subfamily.
-!- SIMILARITY: Belongs to the PPP phosphatase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation and characterization of the fission yeast protein phosphatase gene pper+ involved in cell shape control and mitosis."; Mol. Biol. Cell 4:303-313(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphate.
                                                                                                                         [2]
SEQUENCE FROM N.A.
MEDLINE=33250328; PubMed=8387358;
Matsumoto T., Beach D.;
Matsumoto T., Beach D.;
"Interaction of the pim1/spi1 mitotic checkpoint with a protein "Interaction of the pim1/spi1 mitotic checkpoint with a protein "Interaction of the pim1/spi1 mitotic checkpoint with a protein "Interaction of the pim1/spi1 mitotic checkpoint with a protein "Interaction of the pim1/spi1 mitotic checkpoint with a protein "Interaction of the pim1/spi1 mitotic checkpoint with a protein "Interaction of the pim1/spi1 mitotic checkpoint with a protein "Interaction of the pim1/spi1 mitotic checkpoint with a protein "Interaction of the pim1/spi1 mitotic checkpoint with a protein "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint with a protein "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "Interaction of the pim1/spi1 mitotic checkpoint" "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z18925; CAA79358.1; --
EMBL; AL031540; CAA20786.1; --
PIR; A47727; A47727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P08129; 1FJM.
GeneDB_SPombe; SPCC1739.12; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D13712; BAA02865.1; -. EMBL; Z18925; CAA79358.1; -.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Yanagida M.;
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Clostridia; Clostridiales; Heliobacteriaceae;
Heliobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                 10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
tRNA pseudouridine synthase B (EC 4.2.1.70) (tRNA pseudouridine synthase) (Pseudouridylate synthase) (Vacil
                                                                                                                                 IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON AND MANGANESE (BY SIMILARITY).
GENERAL ACID (BY SIMILARITY).
GO; GO:0007049; P:cell cycle; ISS.
GO; GO:0016043; P:cell organization and biogenesis; ISS.
InterPro; IPR004843; M-ppestrase.
InterPro; IPR004884; T_phtase_apaH.
Promo; PR006186; T_phtase_apaH.
PRINTS; PR00114; STPHPHTASE.
PROD15; PROD15; PPAG; 1.
SMART; SM00156; PPAG; 1.
PROSITE; PS00125; SER_THR_PHOSPHATASE; 1.
PROSITE; PR00125; SER_THR_PHOSPHATASE; 1.
                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                            Score 6; DB 1; Length 305;
Pred. No. 3.4e+02;
                                                                                                                                                                                             MANGANESE (BY SIMILARITY).
MANGANESE (BY SIMILARITY).
                                                                                                                                                                                                                     001980A1CC7646D7 CRC64;
                                                                                                                                                                                                                                         1.8%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                  307 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF 01080; -; 1.
InterPro; IPR004510; TruB.
InterPro; IPR002501; TruB.
Pfam; PF01509; TruB. N; 1.
TIGRFAMB; TIGR00431; TruB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AY142837; AAN87441.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                           10-0CT-2003 (Rel. 42, Created)
                                                                                                                                      51 IR
53 IR
79 IR
111 MA
112 MA
161 MA
235 MA
                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tRNA processing; Lyase.
ACT_SITE 45 45
                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydrolyase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heliobacillus mobilis.
                                                                                                                                                                           111
112
161
235
305 AA;
                                                                                                                                                                                                                                                                                                  126 LFMLLK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                         93 LFMLLK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=28064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Subfamily 1.
                                                                                                                               Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                      TRUB HELMO
                                                                                                                                                                                        ACT SITE
METAL
                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   28GB99;
                                                                                                                                                                METAL
                                                                                                                                                                                                                                                                                                                                                                         TRUB HELMO
                                                                                                                                                      METAL
                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                              METAL
                                                                                                                                                                                                                                                                                                                                                                                                ઠે
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97394467; PubMed=9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness B.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.B., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori (Campylobacter pylori).
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Exhibits a S-adenosyl-dependent methyltransferase activity (By \operatorname{Similarity}).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                    1.8%; Score 6; DB 1; Length 307;
100.0%; Pred. No. 3.4e+02;
                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase, Methyltransferase; Complete proteome.
SEQUENCE 308 AA; 34976 MW; 9C435C791E719FBB CRC64;
               307 AA; 34836 MW; 9AD3D85DAF098EEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.4e+02;
                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
S-adenosyl-methyltransferase mraW (EC 2.1.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No. 3.4.
                                                             100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the mraw family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF 01007; -; 1.
InterPro; IPR002903; Bac Metrnfrse.
Pfam, PR01795; Methyltransf 5; 1.
ProDom; PD004685; Bac Metrnfrse; 1.
IIGRFAMS; TIGR00006; TIGR00006; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000584; AAD07761.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=26695 / ATCC 700392;
                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pylori.";
Nature 388:539-547(1997).
                                                                     Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C64608; C64608.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 EFLSSF 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 EFLSSF 191
                                                                                                                               233 GELILD 238
                                                                                                                                                            166 GELILD 171
                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                    MRAW OR HP0707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IIGR; HP0707;
                                                                                                                                                                                                                                                          MRAW HELPY
                   SEQUENCE
                                                     Query Match
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:
                                                                                                                                                                                                                                                        à
                                                                                                                               à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         X EAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).

X FRAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).

A Niefind K., Hecht H.-U., Schomburg D.;

Incrobacillus confusus at 2.2-A resolution. An example of strong

T asymmetry between subunits.";

J Mol. Biol. 251:256-281(195).

- !- FUNCTION: Catalyzes the NADP dependent reversible and strencespecific interconversion between 2-ketcoarboxylic acids and 1-2-hydroxy-carboxylic acids.

- SUBUNIT: Homotertamer.

- I SUBUNIT: Homotertamer.

- MISCELLANEOUS: Can be applied in an industrial process for the production of L-amino acid.

- SUMILARITY: Belongs to the LDH family.
                                                                                                                                                                                          Lerch H.-P., Frank R., Collins J., "Cloning, sequencing and expression of the L-2-hydroxyisocaproate dehydrogenase-encoding gene of Lactobacillus confusus in Escherichia
                                                                                                                                                                                                                                                                                                     Collins J.,
                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-25.

Tsai H., Lerch H.-P., Kalwass H., Schuette H., Hoppe J., Collin (In) Neijssel O.M., van der Meer R.R., Luyben K.C.A.M. (eds.); Proceedings 4th European congress biotechnology, pp.2:228-231, Elsevier, Amsterdam (1987).
                          01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
1-2-hydroxysisocaproate dehydrogenase (EC 1.1.1.-) (L-HicDH).
Lactobacillus confusus.
                                                                                                   Bacteria; Firmicutes; Lactobacillales; Weissella.
309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROBILE, PSO0064; L.LDH; 1.
Oxidoreductase; NADP; 3D-structure.
INIT MET
                                                                                                                                                                 STRAIN=DSM 20196;
MEDLINE=90060838; PubMed=2684788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02866; ldh C; 1.
PRINTS; PR00086; LLDHDRGNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUR, JODIT4; JOLI14.
PDB; 1HYH; 15-OCT-95.
INTERPO; IPRO01537; L. LDH.
InterPro; IPRO01236; 1dh.
InterPro; IPRO0205; NAD_BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M31425; AAA88213.1; -. EMBL; A22409; CAA01601.1; -.
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 83:263-270(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00056; ldh;
Pfam; PF02866; ldh C
                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178
                                                                                                                   NCBI_TaxID=1583;
DHL2_LACCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT SITE
STRAND
HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HELIX
HELIX
STRAND
HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAND
              P14295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TURN
```

```
ö
the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
-!- FUNCTION: Catalyzes the NAD-dependent oxidative cleavage of
spermidine and the subsequent transfer of the butylamine moiety of
spermidine to the epsilon-amino group of a specific lysine residue
of the eIF-5A precursor protein to form the intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=JCM 10545 / 7;

MEDLINE=21456156; PubMed=11572479;

Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,

Aoki K.-I., Masuda S., Yanagii M., Nishimuza M., Yamagishi A.,

Oshima T., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 309;
                                                                                        Genew; HGNC:14743; OR4C6.

Genew; HGNC:14743; OR4C6.

Pitarerror; IPR00021; 7tm 1; 1.

PRINTS; PR000237; GPCRRHODOPSN.

PROSITE; PS00237; GPROTEIN RECEP F1 1; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.

EXTRACELLULAR (POTENTIAL)

DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                 2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                        4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                    6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C481E2356F227426 CRC64;
                                                                                                                                                                                                                                       1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                               3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable deoxyhypusine synthase (BC 2.5.1.46) (DHS).
                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
N-LINKED (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 6; DB 1; Les
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34557 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                        47
55
77
78
98
1118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYS OR ST1293.
Sulfolobus tokodaii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 GLLVTL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=111955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 GLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             1138
138
157
157
218
234
257
                                                                                                                                                                                                                                                                                                                                                                                                                                              95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SULTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sulfolobus
                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DHYS SUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DATABASE: AMME=Human Olfactory Receptor Data Exploratorium (HORDE);
WWW="http://bioinformatics.weizmann.ac.il/cgi-bin/HORDE/showGene.pl?key=symbol6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Substantin, Arita M., Futami K., Matsumoto S., Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumi S., Aburatani H., Asai K., Akiyama Y.; "Genome-wide discovery and analysis of human seven transmembrane helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 1; Length 309;
100.0%; Pred. No. 3.4e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor genes.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33049 MW; 267A9D0F9CEF66A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: Putative odorant receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100...
5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olfactory receptor 4C6.
                                                                                                                                        142
145
148
1164
1171
1176
1188
1191
1195
                                                                                                                                                                                                                                                                                                                                                                                                     256
260
271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 EKLLQS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 EKLLÓS 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 AA;
                                                                                                                                                     O4C6_HUMAN
ID O4C6_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8NH72;
         TURN
STRAND
HELIX
TURN
HELIX
TURN
STRAND
TURN
HELIX
HELIX
STRAND
TURN
HELIX
STRAND
TURN
HELIX
STRAND
STRAND
STRAND
TURN
HELIX
HELIX
HELIX
HELIX
HELIX
HELIX
HELIX
HELIX
HELIX
HELIX
HELIX
HELIX
HELIX
HELIX
HELIX
HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAND
```

à g 

```
g
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE THE REPORT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
A wayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
A wayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
A Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Dugnet M., Gasererland T.,
A Garrett R.A., Ragan M.A., Sensen C.W., Van der Cost J.;
I.The complete genome of the crenarchaeon Sulfolobus solfataricus P2.",
Proc. Natl. Acad. Sci. U.S.A. 98.7835-7840(2001).
I. Proxyacetone phosphate to form quinolinate (By similarity).
C. -- PATHWAY: NAD biosynthesis; aspartate to NaW; second step.
C. -- STHILAMILY: Belongs to the quinolinate synthetase A family.
C. -- STHILAMILY: Subbongs to the quinolinate synthetase A family.
                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
deoxyhypusine residue (By similarity).
-!- CATALYTIC ACTIVITY: [eIF5A-precursor]-lysine + spermidine |
-!- CEFFA-precursor]-deoxyhypusine + propane-1,3-diamine.
-!- COFACTOR: NAD (By similarity).
-!- PATHWAY: Hypusine biosynthesis; first step.
-!- SIMILARITY: Belongs to the deoxyhypusine synthase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01916; DS; 1.
Probom; PD007730; DS; 1.
Hypusine biosynthesis; Transferase; NAD; Complete proteome. SEQUENCE 311 AA; 38303 MW; OEF215.0E2550CDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 1; Length 311; 100.0%; Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Quinolinate synthetase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Preq. nc.
                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF 00153; -; 1.
InterPro; IPR002773; Deoxyhypus_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=AICC 35092 / DSM 1617 / P2;
MEDLINE=21332296; PubMed=11427726;
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP000985; BAB66337.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
1es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sulfolobus solfataricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 VKILKD 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TAXID=2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NADA OR SSO0998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NADA SULSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: Belongs to the C.elegans receptor-like protein srg
                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                    1.8%; Score 6; DB 1; Length 311;
100.0%; Pred. No. 3.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 311;
                                                                                                     TIGRFAMS; TIGR00550; nadA; 1.
Pyridine nucleotide biosynthesis; Complete proteome.
SEQUENCE 311 AA; 34884 MW; 93515D3B89F3ACD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D3DC0612C61DE1E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Serpentine receptor class gamma 6 (Srg-6 protein).
SRG-6 OR T12A2.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 6; DB 1; Let
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                  311 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multigene family.
EMBL; AE006719; AAK41269.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormPep; T12A2.13; CE07482.
InterPro; IPRO00609; Srg.
Pfam; PPC0118; Srg; 1.
PRINTS; PRO0699; TMPROTEINSRG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36702 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U13019; AAK84569.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity luv...
6; Conservative
                    PIR; F90251; F90251.

HAMAP; MF 00568; -; 1.

InterPro; IPR003473; NadA.

Pfam; PF02445; NadA; 1.
                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
168
220
255
286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T15559; T15559.
                                                                                                                                                                                                                                                                                 156 AKIILF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 ENLKLM 258
                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 ENLKLM 24
                                                                                                                                                                                                                                                                                                                          54 AKIILF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Latreille P
                                                                                                                                                                                                                                                                                                                                                                                                                                  CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 211
                                                                                                                                                                                                                                                                                                                                                                                                             SRG6_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                    SRG6
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
A Madupu W. T., Lindeberg M., Selengut J., Paulsen I.T.,
A Madupu W. S., Dadiperty S., Brinkac L., Beanan M.J., Haft D.H.,
A Madupu W. Davidsen T., Zafar N., Zhou L., Liu J., Yuan Q.,
A Nelson W.C., Davidsen T., Zafar N., Zhou L., Liu J., Yuan Q.,
A Wan Aken S.B., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R.,
A Jana Aken S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L.,
A White O., Fraser C.M., Collmer A.,
I'm complete genome sequence of the Arabidopsis and tomato pathogen
Pseudomonas syringae pv. tomato DC3000.",
Droc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
C. - FUNCTION: Fetrapolymerization of the monopyrrole BG into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydroxymethylbilane preuroporphyrinogen in several discrete steps.
-!-CATALYTIC ACTIVITY: 4 porphobilinogen + H(2)0 = hydroxymethylbilane + 4 NH(3).
-!-COPACTOR: Covalently binds a dipyrromethane cofactor to which the porphobilinogen subunits are added (By similarity).
-!-PATHWAY: Porphyrin biosynthesis by the C5 pathway; fourth step.
-!-SUBUNIT: Monomer (By similarity).
-!-SUBUNIT: Belongs to the HMBS family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; Proise,
Pfam; Projeo;
Pfam; Projeo;
Prophysis,
PROGIS;
PROSITE; PROGIS;
PROSITE; PROGIS;
PROSITE; PROGIS;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                        (Hydroxymethylbilane
                                                                                                                                                                                                                                                                                                                              Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 1; Length 313;
100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                          synthase) (HMBS) (Pre-uroporphyrinogen synthase)
                                                                                                      15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Porphobilinogen deaminase (EC 2.5.1.61) (PBG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MF_00260; -; 1.
InterPro; TPR000860; Porphobil deam.
Pfam; PF01379; Porphobil deam; Pfam; PF03900; Porphobil_deam; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=DC3000;
MEDLINE=22834015; PubMed=12928499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE016856; AAO53682.1; -.
                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        HEMC OR PSPT00128.
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=323;
HEM3 PSESM
ID HEM3 PSESM
AC Q88B91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL OUTSTAIRT. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
"Genome-wide discovery and analysis of human seven transmembrane helix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                             Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PERMY: PF00106; adh short; 1.
PRINYS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH SHORT; 1.
Hypothetical protein; Steroid biosynthesis; Oxidoreductase; NADP;
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 1; Length 314;
100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C261F9ED72EAC245 CRC64;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Putative steroid dehydrogenase C06B3.4 (EC 1.1.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NADP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                           (SDR) FAMILY. 17-BETA-HSD 3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                                       Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                         WormPep; C06B3.4; CE07961.
InterPro; IPR002198; ADH short.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 AA; 34605 MW;
                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z77652; CAB01114.1; -. PIR; T18980; T18980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olfactory receptor 5B17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92
                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 DYEKLL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 DYEKLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor genes."
Submitted (JUL-2
                                                                                                                     NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OSBH HUMAN
Q8NGF7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT SITE
SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                              C06B3.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORSB17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OSBH_HUMAN
   à
```

Gaps

ö

Conservative

9

Matches

77 GLLVTL 82 GLLVTL 38

à g

33

Best Local Similarity

314 AA.

STANDARD;

RESULT 213 DHBV_CAREL ID DHBV_CAEEL AC Q17703;

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=EGD-e / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
MEDLINE=21537279; PubMed=11679669;
Baquero F., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chercuani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Faihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=10403S;
Hanawa T., Kai M., Kamiya S., Yamamoto T.;
"Cloning, sequencing, and transcriptional analysis of the dnaK heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Ribosomal protein L11 methyltransferase (EC 2.1.1.-) (L11 Mtase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 314; 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                          Genew; HGNC:15267; OR5B17.
InterProf: IPR000276; GRCR_Rhodpsn..
Pfam; PF00017; 7tm 1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Olfaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 shock operon of Listeria monocytogenes.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    952366E31FFD7C52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 1
100.0%; Pred. No. 3.5
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC
                                                                                                                                                                                                                   EMBL; AB065849; BAC06067.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 N 3 N 3 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 3 2 N 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Listeria monocytogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 LLVTLI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 LLVTLI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRMA_LISMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LISMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SWIBL outstation the buspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G., Maddwan E., Maltournam A., Maata Viocente J., Noy E., Nedjari H., Nordaiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R., Varquez-Boland J.-A., Voss H., Wehland J., Cossart P., "Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY. 17-BETA-HSD 3 SUBFAMILY.
                                                                                                                                                                                                                            -!- FUNCTION: Methylates ribosomal protein L11 (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the methyltransferase superfamily. PrmA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gardner A.; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; Methyltransferase; Complete proteome.
SEQUENCE 314 AA; 34811 MW; E71F4AF1DDF437F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Putative steroid dehydrogenase F11A5.12 (EC 1.1.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 6; DB 1; Ler
Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; AG1258; AG1258.
PIR; T43740; T43740.
Listilist; LM001471; -.
HAMAP; MF_00735; -; 1.
InterPro; IPR004498; Ribosomal_PrmA.
InterPro; IPR00051; SAM_bind.
TIGRFAMS; TIGR00406; prmĀ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB023064; BAA82791.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAC99549.1; -,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z92830; CAB07363.1; -. PIR; T20756; T20756. WormPep; F11A5.12; CE15790.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 10v..
Per 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 LSTFDI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 LSTFDI 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL591979
                                                                                                                                                                                                                                                                                                                                     family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DHBX CAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 216
   KWW W DDW DDW DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW B DDW 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REDLINE=22388257; PubbMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moorer T., Mang J., Heiteh F.,

L. Bornstein M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.A.,

Richards S., Worley K.C., Hales S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

"Hourn and mouse conk sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Placenta;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Isogai T., Ota T., Nagai K., Sugano S., Aotenka S., Yoshikawa Y.,
Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
"NEDO human cDNA sequencing project."; Susaki N.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=20538421; PubMed=10978331;
Titus S.A., Moran R.G.;
"Retrovirally mediated complementation of the glyB phenotype. Cloning of a human gene encoding the carrier for entry of folates into mitochondria.";
                                                                                                                                                                                                                            Gaps
               Pfam; PF00106; adh short; 1.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH SHORT; 1.
Hypothetical protein; Steroid biosynthesis; Oxidoreductase; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                   DB 1; Length 315; 0. 3.5e+02;
                                                                                                                              BY SIMILARITY.
F4C9D3D3BEFA539A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                             NADP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                   METC HUMAN STANDARD, PRT; 315 AA. 09H2D1; 096JZ6; 096SU7; 28-FRB-2003 (Rel. 41, Created) COCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Mitochondrial folate transporter/carrier.
                                                                                                                                                                                            100.0%; Prec. ...
                                                                                                                                                                 1.8%; Score 6; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol. Chem. 275:36811-36817(2000).
InterPro; IPR002198; ADH_short.
                                                                                                                              202 B
34872 MW;
                                                                                                                                                                                                Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                315 AA;
                                                                                                                                                                                                                                                           212 DYEKLL 217
                                                                                                                                                                                                                                                                                            114 DYEKLL 119
                                                                           Hypothetter
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MFTC OR MFT
                                                                                                                            ACT SITE
SEQUENCE
                                                                                                                                                                                   Query Match
                                                                                                         NP BIND
ACT SITE
                                                                                                                                                                                                                                                                                                                                                    RESULT 217
MFTC_HUMAN
                                                                                                                                                                                                                      Matches
 SO F F F W KW
                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                          g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
-!- FUNCTION: Transport folate across the inner membranes of
                                                                                                                                -1- SIMILARITY: Belongs to the mitochondrial carrier family.
-!- SIMILARITY: Contains 3 Solcar repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> H (IN REF, 1).
-> L (IN REF, 2; BAB55368).
EED376828B4D1069 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       core 6; DB 1; Length 315;
Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AK027787; BAB55368.1; -
EMBL; BC021893; AA421893.1; -
GO; GO:0005743; C:mitochondral inner membrane; NAS.
GO; GO:0005743; C:mitochondral inner membrane; NAS.
GO; GO:0018517; F:folate transporter activity; NAS.
GO; GO:001584; P:folate transport; NAS.
InterPro; IPRO1993; Mitoch.carrier.
PROSITE; PS50920; SOLCAR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MFTC MACFA STANDARD; PRT; 315 AA. 095J75; 10-00T-2003 (Rel. 42, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Preq. w.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitochondrial folate transporter/carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Repeat; POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOLCAR 1.
SOLCAR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOLCAR
R -> H
F -> L
                                                                                                      -!- TISSUE SPECIFICITY: Ubiquitous.
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF283645; AAG37834.1; -.
EMBL; AK027531; BAB55180.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35407 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecinae, Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300
109
209
306
306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
118
222
117
306
315 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 TVEYIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 TVEYIS 229
                                                                                inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                           mitochondria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
SOURCE STATE THE TENT OF SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
```

```
RACK RACK TAN IN S
                                                                                                                                                                                                                                                                                                                                                                        g
                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-alanine--D-alanine ligase (EC 6.3.2.4) (D-alanylalanine synthetase)
0-Ala-D-Ala ligase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: D-alanine branch of peptidoglycan biosynthesis; second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BM4174;
MEDLINE=96270057; PubMed=8662022;
Bers S., Casadewall B., Charles M., Dutka-Malen S., Galimand M., Courvalin P.;
Courvalin P.;
"Bvolution of structure and substrate specificity in D-alanine:D-alanine ligases and related enzymes.";
J. Mol. Evol. 42:706-712(1996).
-:- FUNCTION: Cell wall formation (By similarity).
-:- CATALYTIC ACTIVITY: ATP + 2 D-alanine = ADP + phosphate + D-
                                                                                                                                                                                                                                                                                               Pfam; PF00153; mito carr; 3.
PRINTS; PR00784; MTUNCOUPLING.
PROSITE; PS50920; SOLCAR; 3.
Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 315; . 3.5e+02; ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
SOLCAR 1.
SOLCAR 2.
SOLCAR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 1
100.0%; Pred. No. 3.5
tive 0; Mismatches
-!- SIMILARITY: Contains 3 Solcar repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                 EMBL, AB062992; BAB60754.1; -
InterPro; IPR002030; Mit_uncoupling.
InterPro; IPR001993; Mitoch_carrier.
                                                                                                                                                                                                                 EMBL; AB060884; BAB46890.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35416 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
1es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus gallinarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                  300
109
209
306
                                                                                                                                                                                                                                                                                                                                                                                             106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 TVEYIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 TVEYIS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicu
NCBI_TaxID=1353;
                                                                                                                                                                                                                                                                                                                                                                                          89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDL_ENTGA
Q47823;
                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 219
DDL ENTGA
DDL ENTGA
AC Q47823;
DT 01-NOV-
DT 01-NOV-
DT 10-OCT-
DE D-Alani
DE D-Alani
DE D-Alani
CN Battero
OX NCBL TI
RP SEQUEN
RC STRAIN
RA BVETS |
RA COULVA
RT "BVOLIN
RA BVETS |
RA COULVA
RT "BVOLIN
RA BVETS |
RA COULVA
RT "BVOLIN
RA BVETS |
RA COULVA
CC STRAIN
RA GOULVA
CC - | - PU
CC - | - PU
CC - | - PA
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - | - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
CC - SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
  g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=VPI-5482 / ATCC 29148;
MEDLINE=22550858; PubMed=12663928;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003).
-!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- PATHWAY: Arginine biosynthesis, sixth step.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the ATCase/OTCase family.
-!- CAUTION: Lacks the conserved threonine residue in position 48, which is part of the carbamoylphosphate binding site; it is replaced by a leucine residue.
                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteroides thetaiotaomicron.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arginine biosynthesis, Transferase, Complete proteome.
SITE CARBAMOXLPHOSPHATE BINDING (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
CARBAMOYLPHOSPHATE BINDING (BY
                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 1; Length 316; 100.0%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBAMOYLPHOSPHATE BINDING
                                                                                                                                                                                                                                             316 AA; 35261 MW; 4FESCDFDD716ABFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last Sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ornithine carbamoyltransferase (EC 2.1.3.3) (OTCase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00185; OTCace; 1.
Pfam; PF02729; OTCace, N; 1.
PRINTS; PR00100; AOTCĀSE.
PROSITE; PS00097; CARBAMOYLTRANSFERASE; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318 AA.
                                                                                                                                                                                        Ligame, Cell wall, Peptidoglycan synthesis.

NON TER 316 316
SEQUENCE 316 AA, 35261 MW, 4FESCDFDD716;
                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. No. 3.5 tive 0; Mismatches
                       HSSP; P07862; 11CV.
HAWAP; MF 00047; -; 1.
InterPro; IPR000291; Dala lig_Van.
Pfam; PF01820; Dala ligas; 1.
PROSITE; PS00843; DALA DALA LIGASE 1; 1.
PROSITE; PS00844; DALA DALA LIGASE 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAWAP; MF 01109; atypical; 1.
InterPro; IPR006130; ABP/Orn COtranf.
InterPro; IPR006131; OTCace O.
InterPro; IPR006132; OTCace-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE016941; AA078822.1; -.
EMBL; U39789; AAB17903.1; -.
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.00,
-hog 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147
                                                                                                                                                                                                                                                                                                                                                                                                                            244 IMTKYI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 IMTKYI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         + L-citrulline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARGF OR BT3717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTC_BACTN
Q8A1E9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SITE
```

```
FFFFS
                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its meeb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=5601 (A Serrogroup Icterohaemorrhagiae / Serrovar lai;
MEDLINE=22598143; PubMed=12712204;
Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-P.,
Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Xiu J.-G., Zhao G.-P.;
                                                                                                                                                               Gaps
                     IMPORTANT FOR STRUCTURAL INTEGRITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                               ;
0
                                                      ORNITHINE BINDING (BY SIMILARITY)
88116898BD4282B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF 01808; -; 1.

R InterPro: IPR004107; Phage_integr_N.
R InterPro: IPR004107; Phage_integrase.

R Eam; PF02899; Phage_integrase.

R Ffam; PF02899; Phage_integrase.

RW DNA recombination; DNA integration; Complete proteome.

FT ACT_SITE 170 170 BY SIMILARITY.

FT ACT_SITE 194 BY SIMILARITY.

FT ACT_SITE 262 262 BY SIMILARITY.

FT ACT_SITE 262 265 BY SIMILARITY.
                                                                                                                    Query Match 1.8%; Score 6; DB 1; Length 318; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                     318 AA.
  SIMILARITY)
                                                                                  318 AA; 36382 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tyrosine recombinase xerC.
XERC OR LA2347.
                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leptospira interrogans
                       160
                                                                                                                                                                                                         169 FKYVEL 174
                                                                                                                                                                                                                                             28 FRÝVEĽ 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=173;
                       160
                                                                                                                                                                                                                                                                                                                                                     XERC LEPIN
                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    O7ZAM8;
                       SITE
                                                                                                                                                                                                                                                                                                                                                   THE TAKE HERE HERE COULD COULD COUNTY TO THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF THE TENT OF T
      FT FT S
```

```
RA KUNBLINE-POUGBOARDAY, EUDROGE-25484/;

RANGE F., OGBGRWARTA N., MOSSEET I., Albertini A.M., Alloni G.,

RA AZEVEGO V., BETECTO M.G., BEGBIELEB P., BOLOTIN A., BORCHERT S.,

RA AZEVEGO V., BETECTE I., Brans A., Braun M., Brighell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Broizot F., Deviner K.M., Dusterhoft A., Erlich S.D., Emmerson P.T.,

RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel. S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Hilbert H., Molsappel. S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Iazarevic V.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Undega B., Park S.H.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Undega B., Park S.H.,

RA Presecan E., Pujic P., Purnelle B., Ropoport G., Rey M., Reynolds S.,

RA Rieger M., Rivolta C., Rocha B., Roche M., Sadaie Y.,

RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,

RA Scokin A., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of the Bacillus subtilis genome containing the skin element and many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=168 / JH642;
MEDLINE=97124195; PubMed=8969508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
                                                                                                                                                                                                                                                                                          Gaps
                   TRANSIENT COVALENT LINKAGE TO DNA STRAND CLEAVAGE AND REJOINING (BY
                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRANT=168 / Juf642;
MEDLINE=9219086, PubMed=7704261;
Takemaru K.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi Y.;
Takemaru E.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi Y.;
"Complete nucleotide sequence of a skin element excised by DNA
rearrangement during sporulation in Bacillus subtilis.";
Microbiology 141:323-327(1995).
                                                                                                                                                                                                           Query Match 1.8%; Score 6; DB 1; Length 318; Best Local Similarity 100.0%; Pred. No. 3.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                         56F72FB4DE7C4C1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein yqbD.
                                                                                                  SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microbiology 142:3103-3111(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
                                                                                                                                         318 AA; 37429 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
288
                                                                                                                                                                                                                                                                                                                                                                                                                                               164 LYSSGL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    73 LYSSGL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sporulation genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YOBD OR BSU26150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kobayashi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YOBD BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=168;
ACT_SITE
ACT_SITE
                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P45920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COBD_BACSU
```

```
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                S-palmitoyl cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. No. 3.6e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1993 (Rel. 27, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 AA.
                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                      PIR; S43850; S43850.
MGD; MGI:96929; Mc3r.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Melanocortin-3 receptor (MC3-R)
                                                                                                                                                                                                                                                                                                                                                                                                               16 N-
28 N-
315 S-
35806 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%;
                                            EMBL; X74983; CAA52918.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                  63
75
100
1118
1140
160
1181
1181
                                                                                                                                                                                                                                                                                                                               245
268
277
301
323
                                                                                                                                                                                                                                                                                                                                                                                                                                             315 3
323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 KEILCG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 KEILCG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                LIPID
SEQUENCE
                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
                                                                                                                                                                                                    FRANSMEM
                                                                                                                                                                                                                                RANSMEM
                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                        FRANSMEM
                                                                                                                                                                                                                                                                                                                                              FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MC3R RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and a its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=94226597; PubMed=8172596;
MEDLINE=94226597; PubMed=8172596;
Desarmand F., Labbe O., Eggerickx D., Vassart G., Parmentier M.;
"Molecular cloning, functional expression and pharmacological
characterization of a mouse melanocortin receptor gene.";
Biochem. J. 299:367-373(1994).
-!- FUNCTION: Receptor for MSH (alpha, beta and gamma) and ACTH. This
receptor is mediated by G proteins which activate adenylate
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler B., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
                                                                                                                                        Medigue C., Moszer I., Viari A., Danchin A., "Analysis of a Bacillus subtilis genome fragment using a co-operative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- TISSUE SPECIFICITY: Brain. -
-i- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 1; Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Complete proteome. SEQUENCE 322 AA; 36247 MW; 9922F6E2EF6A000A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 AA
                                                                                                                                                                                  Gene 165:GC37-GC51(1995).
-1- SIMILARITY: STRONG, TO B.SUBTILIS XKDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 3.5
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                              MEDLINE=96084975; PubMed=7489895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Melanocortin-3 receptor (MC3-R).
                                                                                                                                                                                                                                                                                                                                        EMBL; D32216; BAA06937.1; -.
                                                                                                                                                                      computer system prototype.";
                                                                                                                                                                                                                                                                                                                                                     EMBL; D84432; BAAL2399.1; -. EMBL; Z99117; CAB14556.1; -. PIR; G69946; G69946. Subtlinst; BG11275; yqbD.
                                                                                   Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 KASEEV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 KASEEV 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                               IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
  ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Fischer; TISSUE-Hypothalamus; MEDLINE-9402273; PubMed=8415620; Robeins L.S., Mortrud M.T., Iow M.J., Simerly R.B., Cone R.D.; Montifox L.S., Mortrud M.T., Iow M.J., Simerly R.B., Cone R.D.; Technication of a receptor for gamma melanotropin and other proppinelanocortin peptides in the hypothalamus and limbic system."; Proc. Natl. Acad. Sci. U.S., 90:8856-8860(1993).

-!- FINCTION: Receptor for MSH (alpha, beta and gamma) and ACTH.
-!- SUBCELLUIAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TO (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 6; DB 1; Length 323;
PRINTS, PRO001; 7tm 1; 1.

PRINTS, PR00237; GFCRRHONDORSN
PROSITE, P800237; G PROTEIN RECEP F1 1; 1.

PROSITE; P800202; G PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Phosphorylation; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                  1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 (FOIENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F4B7B02FA4A87B7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
```

```
0,
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses, Retroid viruses, Retroviridae, Mammalian type C retroviruses.
NCBL_TaxID=11812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=84121298; PubMed=6320371;
Kan N.C., Flordellis C.S., Mark G.E., Duesberg P.H., Papas T.S.;
"A common onc gene sequence transduced by avian carcinoma virus MH2
and by murine sarcoma virus 3611.";
Science 223:813-816(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 (POTENTIAL).
CYDOLASMIC (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
S-palmitcyl cysteine (Potential).
W; P4E4985C75E70A36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 224:285-289(1984).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-RAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Primary structure of v-raf: relatedness to the src family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 323; 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Serine/threonine-protein kinase transforming protein raf
                                                                                                                                                                                                                                                       PROSITÉ; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
YTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 1
100.0%; Pred. No. 3.6
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                      Phosphorylation; Lipoprotein; Palmitate.
                                                                                                                                                  PIR; A48254; S36636.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=84172180; PubMed=6324342;
Mark G.E., Rapp U.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
10-OCT-2003 (Rel. 42, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35866 MW;
                                                                                                                                                                                                      Pfam; PF00001; 7tm 1; 1. —
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                          EMBL; X70667; CAA50005.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine sarcoma virus 3611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
186
210
245
268
277
301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323
2
16
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 KEILCG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50 KEILCG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EC 2.7.1.37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oncogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAF MSV36
P00532;
                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V-RAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HERER REPORTED TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMIL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
           SIMILARITY: Belongs to the Ser/Thr family of protein kinases. RAF
                                                                                                                                                                                                                                                                                                                    ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE ST; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
Polyprotein; Serine/threonine-protein kinase; Transferase; Oncogene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBUNIT: Exists either as a homo- or heterooligomer.
-1- SUBCELULAR LOCATION: MITOCHONDRIAL, EITHER AS A CONSTITUENT OF THE MATRIX, OR IN TENOUS ASSOCIATION WITH THE INTERNAL SIDE OF THE INNER MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bowman S., Ackerman S.H., Griffiths D.E., Tzagoloff A.;
Characterization of ATPL2, a yeast nuclear gene required for the
assembly of the mitochondrial Pl-ATPase.";
J. Biol. Chem. 266:7517-7523(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Obermaier B., Piravandi B., Rinke M., Domdey H., Submitted (SEP-1995) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3core 6; DB 1; Length 323;
Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52A5423A66E362F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1991 (Rel. 19, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP12 protein, mitochondrial precursor. ATP12 OR YJL180C OR J0486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 6;
                                                                                                                                                                                                                    HSSP, P12931, 1FMK.
INTERFO; IPR000719, Prot kinase.
INTERPO; IPR008271; Ser Ehr pkin AS.
InterPro; IPR001245, Tyr pkinase.
Pfam; PF00069; pkinase; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                       EMBL; K01691; AAA46579.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=91210261; PubMed=1826907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36883 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%;
                                                                                                                                                                                                                                                                                                    PRINTS; PR00109; TYRKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                  284
38
50
143
                                                                                                                                                                                                        PIR; A00638; TVMVF6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F1-F0 complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 KDNLAI 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 KDNLAI
                          subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATPT YEAST
P22135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                    BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
             the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
   the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1992 (Rel. 23, Last sequence update)
15-MRA-2004 (Rel. 43, Last annotation update)
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (Tagatose-bisphosphate aldolase) (D-tagatose-1,6-bisphosphate aldolase)
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       van Rooijen R.J., van Schalkwijk S., de Vos W.M.;
"Molecular cloning, characterization, and nucleotide sequence of
tagatose 6-phosphate pathway gene cluster of the lactose operon o

    J. Biol. Chem. 266:7176-7181(1991).
    -!- CATALYTIC ACTIVITY: D-tagatose 1,6-bisphosphate = glycerone phosphate + D-glycertaldehyde 3-phosphate.
    -!- PATHWAY: Tagatose 6-phosphate pathway of lactose catabolism.
    -!- SIMILARITY: Belongs to the aldolase lacD family.

                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactococcus lactis (subsp. lactis) (Streptococcus lactis)
                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Characterization of the lactose-specific enzymes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91093107; PubMed=2125052;
de Vos W.M., Boerrigter I., van Rooyen R.J., Reiche B.,
Hengstenberg W.;
                                                                                                                                                                                                                                                                                 MITOCHONDRION (POTENTIAL).
                                                                                                                                                                                                                                                                                               ATP12 PROTEIN.
S -> N (IN REF. 1).
0571C6C493E12CB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphotransferase system in Lactococcus lactis.";
J. Biol. Chem. 265:22554-22560(1990).
                                                                                                                                                                                                   SGD; S0003716; AFP12.
GO; GO:0003754; F:chaperone activity; IPI.
GO; GO:0006461; P:protein complex assembly; IMP.
Mitcochondrion; Transit peptide.
TRANSIT 132 MITOCHONDRION (POTE)
                                                                                                                                                                                                                                                                                                                                                                                                 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     326 AA.
                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.0%; Pred. No. 5.00
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                          Score 6; DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91201377; PubMed=1901863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1992 (Rel. 23, Created)
                                                                                                                                                                                                                                                                                                                                        325 AA; 36554 MW;
                                                                                                                           EMBL; M61773; AAA34442.1; -. EMBL; Z49455; CAA89475.1; -. PIR; S56963; S56963. GermOnline; 141792; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                 325
48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lactococcus lactis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 LAILEK 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 LAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pMG820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=MG1820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LACLA
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LACD 17
P26593
                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 227
à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                   .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
17agatcose 1,6-diphosphate aldolase (EC 4.1.2.40) (Tagatose-bisphosphate aldolase) (D-tagatose-1,6-bisphosphate aldolase).
1ACD OR SP1190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Peldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K., Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Praser C.M., "Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- CATALYTIC ACTIVITY: D-tagatose 1,6-bisphosphate = glycerone phosphate + D-glyceraldehyde 3-phosphate.
-:- PATHWAY: Tagatose 6-phosphate pathway of lactose catabolism.
-:- SIMILARITY: Belongs to the aldolase lacb family.
                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                 Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                     TIGREAMS; TIGRO1232; lacD; 1.
Lactose metabolism; Lyase; Plasmid.
SEQUENCE 326 AA; 36476 MW; 37F22F556F47941B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMS; TIGN01232; lacD; 1.
Lactose metabolism; Lyase; Complete proteome.
SEQUENCE 326 AA; 36372 MW; 298CC7E188C37EE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 1; Len
100.0%; Pred. No. 3.6e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATCC BAA-334 / TIGR4;
MEDLINE=21357209; PubMed=11463916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF 00734; -; 1.
INTERPRO; IPR007377; LacD.
INTERPRO; IPR005927; LacD_Gpos.
Pfam; PF04274; LacD; 1.
                                                                                       HAMAP, MF_00734; -; 1.
InterPro; IPR007377; LacD.
InterPro; IPR005927; LacD_Gpos.
Pfam; PF04274; LacD_i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE007420; AAK75299.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 293:498-506(2001).
EMBL; M60447; AAA25180.1;
                                      AAA25171.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                  EMBL; M65190; AAA2517
PIR; D39778; D39778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; B95138; B95138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 KVLVAD 200
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 KVLVAD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR: SP1190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRPN
                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LACD
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LACD (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A COURT NAME OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT OF COURT
```

```
d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                             ö
                                                                                                                                                                                         15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tagatcse 1,6-diphosphate aldolase (EC 4.1.2.40) (Tagatose-bisphosphate aldolase) (D-tagatose-1,6-bisphosphate aldolase)
                                                                                                                                                                                                                                                                                                                                                 Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLester K., Mundy C.W., Nicas T.I., Sur F. H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young leallido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R., Jr., Skatrud P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glass J.I.;
"Genome of the bacterium Streptococcus pneumoniae strain R6.";
"Genome of the bacterium Streptococcus pneumoniae strain R6.";
J. Bacteriol. 183:5709-5717(2001).
-I- CATALYMIC ACTIVITY: D-tagatose 1,6-bisphosphate = glycerone phosphate + D-glyceraldehyde 3-phosphate.
-I- PATHWAY: Tagatose 6-phosphate pathway of lactose catabolism.
-I- SIMILARITY: Belongs to the aldolase lacD family.
                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
  DB 1; Length 326; 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 1; Length 326;
100.0%; Pred. No. 3.6e+02;
cive 0; Mismatches 0; Indels
                            0; Indels
                                                                                                                                                                                                                                                           Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF04274; LacD; 1.
TIGRFAMs; TIGR01232; LacD; 1.
Lactose metabolism; Lyase; Complete proteome.
SRQUENCE 326 AA; 36420 MW; 1F1F0F9CA844E9D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 AA.
                                                                                                                                                   326 AA.
1.8%; Score 6; DB 1
100.0%; Pred. No. 3.6
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=21429245; PubMed=11544234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; H98005; H98005.

HAMAP; MF_00734; -; 1.

InterPro; IPR07377; LacD.

InterPro; IPR05927; LacD_Gpos.
                                                                                                                                                                           15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequ
15-MAR-2004 (Rel. 43, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE008480; AAK99876.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
                            6; Conservative
                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                     195 KVLVAD 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 KVLVAD 200
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 KVLVAD 58
                                                                              53 KVLVAD 58
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=171101;
                                                                                                                                                                                                                                             LACD OR SPR1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 230
VSO9_ROTEO
ID VSO9_ROTEO
AC Q9IPD4;
                                                                                                                                                  STRR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                             Q8DPP2;
                                                                                                                                  LACD STRR6
ID LACD S
                                                                                                                        RESULT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                          Matches
                                                                                                                                                  셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=L2/434/Bu;
MEDLINE=99392470; PubMed=10463174;
Bannantine J.P., Rockey D.D.;
"Use of primate model system to identify Chlamydia trachomatis protein antigens recognized uniquely in the context of infection.";
Microbiology 145:2077-2085(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=D/UW-3/Cx;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Tsubokura K., Horiuchi H., Sato S., Oshima H., Imagawa H., Kamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 48 POTENTIAL.
69 69 N-LINKED (GLCNAC. .) (POTENTIAL).
145 145 N-LINKED (GLCNAC. .) (POTENTIAL).
326 AA; 37226 MW; 77D999E6562E2687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                        "Identification of the gene encoding VP7 of serotype G3 equine
                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydia.
16-OCT-2001 (Rel. 40, Created)
L6-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Glycoprotein VP7 (Serotype-specific antigen) (Outer shell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y067_CHLTR STANDARD; PRT; 326 AA.
098529; 084070;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Putative metal-binding lipoprotein CT067 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 6; DB 1; Ler
Pred. No. 3.6e+02;
                                                                                                                                                                              Equine rotavirus (serotype G3 / strain HO-5).
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coat protein, Transmembrane, Glycoprotein. TRANSMEM 32 48 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB046464; BAB03343.1; -.
InterPro; IPR001963; VP7.
Pfam; PF00434; VP7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000191; VP7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         NCBI_TaxID=148357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 PTEAVA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 PTEAVA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=813;
                                                                                                                      glycoprotein).
                                                                                                                                                                                                                                                                                                                                                                                                                          rotavirus.";
                                                                                                                                                                                                                                                                                                                                                            Matsuda H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHLTR
```

```
Pfam; PF00046; homeobox; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALX STRPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 233
ALX_STRPU
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                         (Prodable).
-!- SIMILARITY: Belongs to the bacterial solute-binding protein family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0690; ADHESNFAMILY.
Hypothetical protein; Transport; Metal-binding; Lipoprotein; Membrane;
             "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
Science 282:754-759(1998).
-!- FUNCTION: PART OF AN ATP-DRIVEN TRANSPORT SYSTEM
CT067/CT068/CT070 FOR A METAL. METAL-BINDING COMPONENT.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-palmitoyl cysteine (Probable).
S-diacylglycerol cysteine (Probable).
A -> V (IN SEROYAR L2).
5ASAA35AB6627D89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUTATIVE METAL-BINDING LIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 1; Length 326;
100.0%; Pred. No. 3.6e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thomas K.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: STRONG, TO S.POMBE AND YEAST SDS22.
-!- SIMILARITY: Contains 12 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-ERB-2003 (Rel. 41, Last annotation update)
Hypothetical protein T09AS.9 in chromosome III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF077010; AAC35948.1; ALT_INIT.
EMBL; AE001281; AAC67658.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .gnal; Complete proteome; Palmitate
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; E71561; E71561.
PHCI-2DPAGE; Q95529; -
InterPro; IPR006128; Lipoprotein 4.
InterPro; IPR006127; SBP_bac_9.
Pfam; PF01297; SBP_bac_9; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 22 N-
22 22 22 S-
190 190 A
326 AA; 37035 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 VEYISA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 VEYISA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                  Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YNZ9 CAEEL
P45969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thomas K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DDT TO DD
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Martinez P., Davidson E.H.;
"SpFrx-1, a sea urchin homeobox gene related to aristaless is expressed during embryogenesis.";
Submitted (MAY-1996) to the BMEL/GenBank/DDBJ databases.
-I- SUBCELLULAR LOCATION: Nuclear (By similarity).
-I- SIMILARITY: Belongs to the paired homeobox family. Bicoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  icore 6; DB 1; Length 220,
Pred. No. 3.68+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 le-Ocr-2001 (Rel. 40, Created)
16-Ocr-2001 (Rel. 40, Last sequence update)
10-Ocr-2003 (Rel. 42, Last annotation update)
Aristalese homeobox protein (ALX) (SpPrx-1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D4C5A5502FF0417B CRC64;
                                                                                                                                                                                                                                                                repeat; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 3.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: Contains 1 homeobox domain.
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                       LER 1.
LER 3.
LER 4.
LER 4.
LER 5.
LER 5.
LER 7.
LER 9.
LER 9.
LER 10.
LER 11.
                                                                                                                                                                                                                                                              Leucine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001356; Homeobox.
InterPro; IPR007104; Paired homeo.
                                                                                       WormPep; T09A5.9; CE01090.
InterPro; IPR001611; LRR.
InterPro; IPR007092; LRR_SDS22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37359 MW;
                                          EMBL; Z36753; CAA85336.1; -. PIR; T24722; T24722.
                                                                                                                                                                                                            PRINTS; PR00019; LEURICHRPT.
SMART; SM00446; LRRCap; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D85080; BAA19774.1; -.
                                                                                                                                                                  InterPro; IPR003603; LRRCap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                     Pfam; PF00560; LRR; 7
                                                                                                                                                                                                                                                           Hypothetical protein;
REPEAT 35 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 LSTFDI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 LSTFDI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                           58
81
103
128
147
172
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {RNA}(N).
SUBUNIT: Homodimer. The RNAP catalytic core consists of 2 alpha, 1 beta, 1 beta' and 1 omega subunit (By similarity).
DOMAIN: The N-terminal domain is essential for RNAP assembly and basal transcription, whereas the C-terminal domain is involved in interaction with transcriptional regulators and with upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : - FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-22297718; PubMed-12219091;
Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (RNAP alpha subunit) (Transcriptase alpha chain) (RNA polymerase alpha subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wigglesworthia glossinidia brevipalpis.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Wigglesworthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the RNA polymerase alpha chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome sequence of the endocellular obligate symbiont of tsetse
                                                                                                                                                                                                                                          0;
             SWART; SM00389; HOX; 1. PROSTITE; PS00027; HOMEDOX 1; 1. PROSTITE; PS00027; HOMEDOX 2; 1. HOMEDOX; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                     DB 1; Length 327;
                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SW00662; RPOLD; 1.
Transferase; Transcription; DNA-directed RNA polymerase;
Complete protecome.
                                                                                                                           321 325 POLY-PRO.
327 327
327 AA; 37146 MW; 0D387C5C72AECFD5 CRC64;
                                                                                                                                                                                                   1.8%; Score 6; DB 1; Ler
100.0%; Pred. No. 3.6e+02;
                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 3.00
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF 00059; -; 1.
InterPro; IPR009025; RBP11-like_RNApo.
InterPro; IPR01700; RNA_polA_bac_org.
Pfam; PF01000; RNA_polA_bac; 1.
ProDom; PD01119; RNA_polA_CTD; 1.
ProDom; PD01179; RNA_polA_bac_org; 1.
                                                                                                         HOMEOBOX.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter elements (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                flies, Wigglesworthia glossinidia.";
Nat. Genet. 32:402-407(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB063522; BAC24714.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-2003 (Rel. 42, Created)
ProDom; PD000010; Homeobox; 1.
                                                                                   Transcription regulation.
DNA BIND 212 271
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                         325
                                                                                                                                                                                                                                                                               134 EAPQIA 139
                                                                                                                                                                                                                                                                                                              6 EAPQIA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=36870;
                                                                                                                                                                                                                                                                                                                                                                                                          RPOA WIGBR
08D1Y8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aksoy S.;
                                                                                                                                                                SEQUENCE
                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                         RPOA WIGBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317-4331(2000).
-!- CARLAYITC ACTIVITY: ATP + D-glucose = ADP + D-glucose 6-phosphate.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBLIZARITY: BELONGS TO THE ROK (NAGC/XYLR) FAMILY.
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                          ALPHA C-TERMINAL DOMAIN (ALPHA-CTD) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C-125 / JCM 9153;
BIRDILINE-20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
ALPHA N-TERMINAL DOMAIN (ALPHA-NTD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase, Kinase, Glycolysis, ATP-binding, Complete proteome.
SEQUENCE 330 AA, 34496 MW, E5448D6CBD87456F CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 1; Length 330;
100.0%; Pred. No. 3.6e+02;
                                                                                                                                                                                         DB 1; Length 328; . 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                           9876CE4C9AF98C67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glucoknase (EC 2.7.1.2) (Glucose kinase).
GLCK OR GLK OR BH425.
Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                           SIMILARITY)
                                                                                            SIMILARITY)
                                                                                                                                                                                         Score 6; I
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00480; ROK; 1.
TIGRPAMS; TIGR00744; ROK_glcA_fam; 1.
PROSITE; PS01125; ROK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000600; ROK.
InterPro; IPR004654; ROK_glcA_fam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP001512; BAB05144.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G3P2 KLUMA STANDARD;
Q01077;
01-NOV-1997 (Rel. 35, Created)
                                                                                                                           328 AA; 36927 MW;
                                                                                                                                                                                         Query Match 1.8%; Best Local Similarity 100.0%; Matches 6; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.0
les 6; Conservative
                                                             328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A83828; A83828.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 ASDAFA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 ASDAFA 236
                                                                                                                                                                                                                                                                                                                            290 IVEIL 295
                                                                                                                                                                                                                                                                                                                                                                                             78 IVEILL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=86665;
                                                       247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLK_BACHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                           SEQUENCE
   DOMAIN
                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 236
G3P2 KLUMA
ID G3P2 K
AC Q01077
DT 01-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 235
                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              $\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\frac{1}{2}$$\fra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
```

```
SYW_UREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYW UREPA
        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Ewiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLYCERALDEHYDE 3-PHOSPHATE.
ACTIVATES THIOL GROUP DURING CATALYSIS.
FEDB08479F485F09 CRC64;
                                                                                                                                                                                                                                                     Fernandes P.A., Sena-Esteves M., Moradas-Ferreira P.,
"Characterization of the glyceraldehyde-3-phosphate dehydrogenase
gene family from Kluyveromyces marxianus - polymerase chain
reaction-single-strand conformation polymorphism as a tool for the
study of multigenic families.";
Yeast 11:725-733 (1955).
-!- CATALYIC ACTIVITY: D-glyceraldehyde 3-phosphate + phosphate +
NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
-!- PATHWAY: Second phase of glycolysis; first step.
-!- SUBUNIT: Homotetramer (By similarity).
-!- SUBUNITY: Belongs to the glyceraldehyde 3-phosphate.
                        28-FEB-2003 (Rel. 41, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase 2 (EC 1.2.1.12) (GAPDH 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
                                                                                    Kluyveromyces marxianus (Yeast) (Kluyveromyces fragilis).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
blactate dehydrogenase (EC 1.1.1.28) (D-LDH) (D-specific lbhdDOR TP0037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 331; 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Prea. ...
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; I
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000173; GAP dhdrogenase.
InterPro; IPR006424; GAPDH-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PP00044; gpdh; 1.
Pfam; PP02800; gpdh; 1.
Pfam; RN00704; GaPDHDRGMAE.
TIGREAM; TIGR01534; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD.
                                                                                                                                                                                                                 STRAIN=ATCC 10022;
MEDLINE=95397590; PubMed=7668042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 AA; 35539 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S80241; AAB35209.1; -. PIR; S57280; S57280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 PLAKII 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 PLAKII 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P06977; 1GAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149
                                                                                                                                                       NCBI_TaxID=4911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDHD TRE
083080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 237
LDHD TREPA
AC 083080
DT 15-MAR
DT 15-MAR
DE D-1act,
DE D-1act,
DE DHD ON
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT
CON NORT

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                    Praser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey B.K., Clayton R., Ketchum K.A., Sodergren B., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S. Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
27-FEB-2003 (Rel. 41, Last annotation update)
(Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAD (BY SIMILARITY).
SUBSTRATE BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: (R)-lactate + NAD(+) = pyruvate + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma
                                                                                                                                                                                                                                                           "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  773B01E6E2384E0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFam; PF00389; 2-Hacid DH; 1.

Pfam; PF02826; 2-Hacid DH C; 1.

PROSITE; PS0065; D_2 HYDROXYACID DH 1; 1.

PROSITE; PS00671; D_2 HYDROXYACID DH 2; 1.

PROSITE; PS00671; D_2 HYDROXYACID DH 2; 1.

PROSITE; PS00671; D_2 HYDROXYACID DH 3; 1.

Oxidoreductase; NAD; Complete profeome.

NP BIND

ACT_SITE

235

235

SUBSTRATE BINDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Prea. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; I
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Serovar 3;
MEDLINE=20500219; PubMed=11048724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR006139; 2-Hacid DH.
InterPro; IPR006140; 2-Hacid DH_C.
InterPro; IPR000205; NAD_BS.
STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE001189; AAC65033.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36873 MW;
                                                                                                                                                                                                                                                                                                                      Science 281:375-388(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D71373; D71373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       264 2
296 2
331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P30901; 2DLD.
TIGR; TP0037; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 LLKGYE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 LLKGYE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRPS OR UU175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            urealyticum.";
                                                                                                                                                                                                                                                                                                spirochete.";
```

```
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9UVC0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 240
G3P_PICCI
SOLUTION SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OC OS ME DE LES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ठ
                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932; Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Rlausner R.D., Colline S.S., Wagner L., Schaefer C.F., Batt M. Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Batt N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP, MF 00140; -; 1.

InterPro; IPR0012305; tRNA-synt_1b.

InterPro; IPR001421; tRNA-synt_1b.

InterPro; IPR001402306; TR FRNA-synt_1b.

Pfam; PF00579; tRNA-synt_1b; 1.

PRINTS; PR01039; TRNASYNTHTRP.

TIGRPAMS; TIGR00233; trp8; 1.

PROSTIR; PS00178; AA TRNA LIGASE I; 1.

Aminoscyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
15-OCT-2003 (Rel. 42, Last annotation update)
(Ficolin 1 precursor (Collagen/fibrinogen domain-containing protein 1)
(Ficolin-A) (Ficolin A) (M-Ficolin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                           -!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
-!- SUBUNIT: Homodiner (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fujimori Y., Harumiya S., Fukumoto Y., Miura Y., Yagasaki K., Tachikawa H., Fujimoto D.; "Molecular cloning and characterization of mouse ficolin-A."; Biochem. Biophys. Res. Commun. 244:796-800(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 1; Length 333;
LOO.0%; Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333 AA; 37755 MW; AE6646EB161797FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "KMSKS" REGION.
ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Matcn
Best Local Similarity 100.0%; Pred. No. 5.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "HIGH" REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BALB/c; TISSUE=Liver;
MEDLINE=98205801; PubMed=9535745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE002117; AAF30582.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
Nature 407:757-762(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18
204
203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P00953; 1D2R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 VADFLE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  284 VADFLE 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FCN1 OR FCNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FCN1 MOUSE
070165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FCN1 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
SO DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DEL DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DEL DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA DE LA DESTA D
```

```
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevcheko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Reneration and initial analysis of more than 15,000 full-length
human and mouse CDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(202).
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(202).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mach Multidence family.

InterPro; IPR008161; Collagen.
InterPro; IPR008161; Collagen.
InterPro; IPR00181; Fibrinogen_C.
Pfam; PF01391; Collagen; I.
ProDom; PP000007; Clg_hellx; 1.
ProDom; PP00186; PBG; I.
PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
Lectin; Collagen; Repeat; Glycoprotein; Signal; Multigene family.
SIGNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: HOMOPOLYMER. INTERACTS WITH ELASTIN (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: SECRETED. FOUND ON THE MONOCYTE SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12) (GAPDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LIVER AND SPLEEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 6; DB 1; Length 334;
Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the ficolin lectin family.
-!- SIMILARITY: Contains 1 collagenous domain.
-!- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 334 FICOLIN 1.
50 88 COLLAGEN-LIKE.
152 298 FIBRINOGEN C-TERMINAL.
261 261 N-LINKED (GLCNAC. . .) (PC
334 AA; 36298 MW, 9D30C05036AA04B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.8%; Score 6; DB 1;
Best Local Similarity 100.0%; Pred. No. 3.7%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB007813; BAA25126.1; -. EMBL; BC019180; AAH19180.1; -. PIR; JC5980; JC5980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pichia ciferrii (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1340905; Fcna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 KDLLTR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 KOLLTR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P02671; 1FZD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G3P PICCI
```

.; 0

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P52950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DBX1 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 242
      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-JAL. / DSM 2661 / ATCC 43067;
MEDLINE=9637999; PubMed=8680087;
MEDLINE=9637999; PubMed=8680087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYCERALDEHYDE 3-PHOSPHATE.
ACTIVATES THIOL GROUP DURING CATALYSIS.
                                                                              16-OCT-2001 (Rel. 40, Last sequence update)
SerBe-2003 (Rel. 41, Last annotation update)
Ketol-acid reductoiscomerase (EC 1.1.1.86) (Acetohydroxy-acid isomeroreductase) (Alpha-keto-beta-hydroxylacil reductoiscomerase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 1; Length 334;
100.0%; Pred. No. 3.7e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6C29C3BD06C79599 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILVC OR MJ1543.
Methanococcus jannaschii.
Archaea, Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000173; GAP dhdrogenase.
InterPro; IPR006424; GAPDH-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00044; gpdh; 1.
Pfam; PF02800; gpdh; 1.
Pfam; PR02800; gpdh C; 1.
PRINTS; PR00078; G3PDHPRGNASE.
TIGRFAMS; TIGR01554; GAPDH-I; 1.
PROSITE; PS00071; GAPDH; 1.
Glycolysis; Oxidoreductase; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF053300; AAF21710.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            334 AA; 36180 MW;
                                                                                                                                                                                                                                                                                                                                                                                dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100. es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 PLAKII 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 PLAKII 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 4GPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                              SEQUENCE FROM N.A.
NCBI_TaxID=36020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P00357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILVC METJA
058938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
NAME OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HD ACCOUNT OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE BOARD OF THE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP(+)
= s(8)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
= r(9)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
= r(9)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
-i- PATHWAY: Valine and isoleucine biosynthesis; second step.
-i- SIMILARITY: Belongs to the ketol-acid reductoisomerase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01450, IlvC; 1. _
TIGRFAMs; TIGR00465; ilvC; 1.
Oxidoreductase; Branched-chain amino acid biosynthesis; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 1; Length 334;
100.0%; Pred. No. 3.7e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 AA; 37300 MW; 9EC8DE89143B4002 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     earlier stages.
-!- SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAD; MF 00435; -; 1.
InterPro; IPR008927; 6DGDH_C like.
InterPro; IPR00506; AcH_ISOMICTSE.
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U67595; AAB99561.1; ALT_INIT.
TIGR; MJ1543; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95110746; PubMed=7811640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
Science 273:1058-1073(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homeobox protein DBX1.
DBX1 OR DBX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 AMKEIL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome. ACT_SITE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 AMKEIL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
```

```
Lectin, Collagen, Repeat, Glycoprotein, Signal, Multigene family.
    SHEFFFF
                                                                                                                                                                  ð
                                                                                                                                                                                         입
                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Sprague-Dauley;
Veshida Y., Tachikawa H., Fujimori Y., Miura Y., Yagasaki K.,
Veshida Y., Tachikawa H., Fujimori Y., Miura Y., Yagasaki K.,
Veshida Y., Tachikawa H., Fujimori Y., Miura Y., Yagasaki K.,
Veshida Y., Tachikawa B.,
Molecular cloning and characterization of rat ficolin-A.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: Involved in serum exerting lectin activity. Binds GloNAc-
--- SUBGNIT: HOMOPOLYMER. INTERACTS WITH ELASTIN (BY SIMILARITY).
--- SUBGNIT: HOMOPOLYMER. INTERACTS FOUND ON THE MONOCYTE SURFACE (BY SIMILARITY: Belongs to the ficolin lectin family.
--- SIMILARITY: Contains 1 collagenous domain.
--- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
                                                                                                                                                                                                                                                                                                                                                                                                                     16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Ficolin 1 precursor (Collagen/fibrinogen domain-containing protein 1)
(Ficolin-A) (Ficolin A) (M-Ficolin).
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                            .
                                                                                                                                                                           Homeobox; DNA-binding; Developmental protein; Nuclear protein. DNA_BIND 181 240 HOMEOBOX.
                                                                                                                                                                                                     319 331 ASP/GLU-RICH (HIGHLY ACIDIC)
335 AA; 36333 MW; 06312CD41F03F369 CRC64;
                                                                                                                                                                                                                                              Query Match
1.8%; Score 6; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                335 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00186; FBG; 1. -
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
                                       MGD; MGI:94867; Dbx1.
InterPro; IPR001356; Homeobox.
InterPro; IPR000047; HTH_lambrepressr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR008160; Collagen.
InterPro; IPR002181; Fibrinogen_C.
Pfam; PF01391; Collagen, 1.
Pfam; PF0147; fibrinogen_C; 1.
                                                                                        PRINTS; PRO0024; HOWEDBOX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
SNART; SM00389; HOX; 1.
PROSITE; PS00027; HOWEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB026057; BAA76940.2; -. HSSP; P02671; 1FZD.
              EMBL; S75837; AAB33013.1; -. HSSP; P23441; 1FTT.
                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                               PF00046; homeobox;
                                                                                                                                                                                                                                                                                                    247 KYISKP 252
                                                                                                                                                                                                                                                                                                                             204 KYISKP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=10116;
                                                                                                                                                                                         181
                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                FCN1 RAT
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE=22511545; PubMed=12622808;
Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O., Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C., Van der Cost J., Weissenbach J., Zivanovic Y., Forterre P.;
"An integrated analysis of the genome of the hyperthermophilic archaeorocus abyssi.";
Mol. Microbiol. 47:1495-1212(2003).
--- CATALYTIC ACTIVITY: ATP + (R)-mevalonate = ADP + (R)-5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphomevalonate.
--- CORACTOR: Magnesium (By similarity).
--- SUBUNIT: Homodimer (By similarity).
--- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
--- SIMILARITY: Belongs to the GHMP kinase family. Mevalonate kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R HAMAP; ME 00217; -: 1.

R InterPro; IPR006204; GHMP kinase.
R InterPro; IPR006204; GHMP kinase.
R InterPro; IPR006203; GHMP kinase.
R InterPro; IPR006205; Mev_gal kin.
R InterPro; IPR006205; Mev_gal kin.
R InterPro; IPR006206; Mev_gal kin.
R PRINTS; PR00959; Mev_gal kin.
R PRINTS; PR00959; Mev_gal kin.
R TIGRPAMS; TIGR0659; Mev_gal kin.; 1.
R TIGRPAMS; TIGR0659; Mev_gal kin.; 1.
R TIGRPAMS; TIGR0659; Mevalon kin.; 1.
R TIGRPAMS; TIGR0659; Mevalon kin.; 1.
R TIGRPAMS; TIGR0659; Mevalon kin.; 1.
R TIGRPAMS; TIGR0659; Mevalon kin.; 1.
R TIGRPAMS; TIGR0659; Mevalon kin.; 1.
R TIGRPAMS; TIGR0659; Mevalon kin.; 1.
R TIGRPAMS; TIGR0659; Mevalon kin.; 1.
R TIGRPAMS; TIGR0659; Mevalon kin.; 1.
ATP (POTENTALL).
C SEQUENCE 335 AA.; 35774 MW; ED0B06EDA186599C CRC64;
                                        COLLAGEN-LIKE.
FIBRINOGEN C-TERMINAL.
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                 Length 335;
                                                                                                                                                                                                                                  0; Indels
                                                                                                              -LINKED (GLUNAC. . .) (PO
1A7FC9568E76ED5D CRC64;
                                                                                                                                                                                 Score 6; DB 1; Ler
Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
MVK OR PYRAB05410 OR PAB0372.
                                                                                                                                                                                                                                        0; Mismatches
                       FICOLIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ248284; CAB49463.1; -.
                                                                                                                                                                              1.8%; £
                                                                                                                            36627 MW;
                                                                                                                                                    Query Match
Best Local Similarity 100.000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
22
335
88
298
271
                 23 3
50
152 2
271 2
335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR, H75172; H75172.
                                                                                                                                                                                                                                                                                               188 KDLLTR 193
                                                                                                                                                                                                                                                                                                                                                    127 KDLLTR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Orsay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIME PYRAB 09V1\overline{8}7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=GES
                                                                  DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                            SEQUENCE
                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 244
KIME_PYRAB
                       CHAIN
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. ILSOUE-LUNGS

WEDLINE-22380857; PubMed=12477932;

Radusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wickernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.M.,
Radhy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20167206; PubMed=10702296;
Perl A., Colombo E., Samoilova E., Butler M.C., Banki K.;
"Human transaldolase-associated repetitive elements are transcribed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning and chromosomal localization of a paralog and a mouse homolog of the human transaldolase gene.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97480738; PubMed=9339383; Banki K., Eddy R.L., Showe T.B., Halladay D.L., Bullrich F., Croce C.M., Jurecic V., Baldini A., Perl A.; "The human transaldolase gene (TALDO1) is located on chromosome 11 at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Banki K., Halladay D., Perl A., "Cloning and expression of the human gene for transaldolase. A novel highly repetitive element constitutes an integral part of the coding
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98192510; PubMed=9524206;
Kusuda J., Hirai M., Toyoda A., Tanuma R., Nomura-Kitabayashi A.,
Hashimoto K.;
                                                                       ..
1.8%; Score 6; DB 1; Length 335;
100.0%; Pred. No. 3.7e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                   TALL HUMAN STANDARD; PRT; 337 AA. P37837; O00751; O1-OCT-1994 (Rel. 30, Created) 30-MAY-2000 (Rel. 39, Last sequence update) Transaldolase (EC 2.2.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 275:7261-7272(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.",
J. Biol. Chem. 269:2847-2851(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94132057; PubMed=8300619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jenomics 45:233-238(1997).
                                Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 209:13-21(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA polymerase III."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                    156 AKIILF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                  11 AKILLF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p15.4-p15.5."
   Query Match
                                Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                              HERE BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERKER BERK
                                                                                                                                                                                                  a
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                    WARIANT TALDOI DEFICIENCY SER-171 DEL.
MEDILINE=21205587; PubMed=11283793;
Verhoeven N.M., Huck J.H.J., Roos B., Struys E.A., Salomons G.S.,
Verhoeven N.M., Huck J.H.J., Roos B., Struys E.A., Salomons G.S.,
"Transaldolase deficiency: liver cirrhosis associated with a new
inborn error in the pentose phosphate pathway.";
Am. J. Hum. Genet. 68:1086-1082 (2201).
-I- FUNCTION: Transaldolase is important for the balance of
metabolites in the pentose-phosphate pathway.
-I- CATALYTIC ACTIVITY: Sedohaptulose 7-phosphate + D-glyceraldehyde
3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                               -I- PATHWAY: Pentose phosphate pathway; nonoxidative part.
-I- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-I- DISEASE Defects in TALDOI are a cause of a deficiency that results in telangiectases of the skin, hepatosplenomegaly, and enlarged clitoris.
                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to the transaldolase family. Subfamily 1.
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 6; DB 1; Length 337; Pred. No. 3.7e+02; O; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTIG=VAR 011511.
209 213 LEDPG -> WKTW (IN REF. 1).
337 AA; 37540 MW; 8CB4992AEF364E64 CRC64;
                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0004801; F:transaldolase activity; TAS. GO; GO:0005975; P:carbohydrate metabolism; TAS. InterPro; IPR001585; Transaldolase_AB. InterPro; IPR004730; Transaldolase_AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAL1 MOUSE STANDARD, PRT; 337 AA. Q930<u>9</u>2; P70358; P70703; 01-NOV-1997 (Rel. 35, Created) 15-JUL-1998 (Rel. 36, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF010400, AAC52068.1, -.
EMBL, AF010398, AAC52068.1, JOINED.
EMBL, AF010399, AAC52068.1, JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF058913; AAF40478.1; -. EMBL; BC010103; AAH10103.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.8%; 8
Best Local Similarity 100.0%;
Matches 6; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L19437; AAB53943.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A49985, A49985.
BDB; IFOS; 13-UTL-00.
Genew; HGMC:11559; TALDO1.
GK; P37837; -.
MIM; 602063; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 KLLGEL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 KLLGEL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               606003; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAL1 MOUSE
ID TAL1 M
AC Q93092
DT 01-NOV
DT 15-JUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 246
   8
```

3.7e+02;

Best Local Similarity

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                A STAALMS-WANN; ILS-OUE-mammary 91-101;

RX MEDDINE=2238027; PubMed=12477932;

RA Klausher R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Datchenkov L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Scares M.B., Bonaldo M.F., Carannoi P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Carcia A.M., Gay L.J., Hulyk S.M.,

RA Nitlalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pakesley J., Helton E., Ketteman M., Green E.D., Dickson M.C.,

RA Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butserfield Y.S.N., Krzywinski M.I., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RY Generation and initial analysis of more than 15,000 full-length

RY Generation and initial analysis of more than 15,000 full-length

RY Generation and initial analysis of more than 15,000 full-length

RY Generation and initial analysis of more than 15,000 full-length

RY Generation and mouse cDNA sequences."

Proc. Natl Acad Sci. U.S.A. 99:16899-16903(2002).

-- FUNCTION: Transaldolase is important for the balance of metabolites in the pentose-phosphate pathway (By similarity).

-- C. - CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde

C. - CATALYTIC ACTIVITY: Belongs to the transaldolase family. Subfamily 1.

-- SUBCELLUAR LOCATION: Cytoplasmic (Probable).
                                                                                                                                                                                                                                                                                                      'Cloning and chromosomal localization of a paralog and a mouse homolog
                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                               MEDLINE=98192510; PubMed=9524206;
Kusuda J., Hirai M., Toyoda A., Tanuma R., Nomura-Kitabayashi A.,
Hashimoto K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOAD351FD778367F CRC64;
15-MDR-2004 (Rel. 43, Last annotation update)
Transaldolase (EC 2.2.1.2).
TALDO1 OR TALDO OR TAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P30148; IONR.
MGD; MGI:1274789; Taldol.
InterPro; IPR001585; Transaldolase.
InterPro; IPR004730; Transaldolase_AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMS; TIGRO0874; talaB; 1.
PROSITE; PSO0958; TRANSALDOLASE_2; 1.
PROSITE; PS01054; TRANSALDOLASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                                                                 human transaldolase gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, U67611; AAB83955.1; -.
EMBL, U63158; AAB08722.1; ALT SEQ.
EMBL, U63159; AAB08723.1; ALT SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00923; Transaldolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC004754; AAH04754.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37387 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase; Pentose shunt.
                                                                                                                                                                                                                                                                                                                                                    Gene 209:13-21(1998).
                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 AA;
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
```

Length 337;

DB 1;

Score 6;

1.8%;

Query Match

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                       ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 1; Length 337; 00.0%; Pred. No. 3.7e+02; ve 0; Mismatches 0; Indels
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 142 BY SIMILARITY.
337 AA; 37476 MW; E5436427605575F1 CRC64;
                                    ·.
                                                                                                                                                                                                                                                                                                     Q9EQSO;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Transaldolase (EC 2.2.1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein yxaG.
Hypothe Stage Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and Sequence and
                                                                                                                                                                                                                                                                            337 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 AA.
100.0%; Pred. .v..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transaldolase_AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF00923; Transaldolase; 1. TIGRRFAMS; TIGR00844; talAB; 1. PROSITE; PS01054; TRANSALDOLASE 1; 1. PROSITE; PS00958; TRANSALDOLASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR001585; Transaldolase.
Interpro; IPR004730; Transaldolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF069306; AAG43169.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase; Pentose shunt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                    6; Conservative
                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 KLLGEL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 KLLGEL 263
                                                                                          230 KLLGEL 235
                                                                                                                                       258 KLLGEL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P30148; 10NR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YXAG BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                            TALL RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P42106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 248
YXAG_BACSU
                                                                                                                                                                                                                            RESULT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                    Matches
                                                                                                                                          g
                                                                                                                                                                                                                                                                                                           ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSCHERT
                                                                                             ਨੇ
```

```
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for scamercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             RA KUNSTINES BY GARDARY 1. Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouilet S., Bruschi C.V., Cannerton I.F., Cummings N.J., Daniel R.A.,
RA Brouilet S., Deviner K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghims S.Y., Glaser P., Goffeau A., Golightly B.J., Grandd G.,
RA Hilbert H., Holsappel S., Hosen R., Haich U., Fr., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosen S., Hullo M.F., Itaya M., Jones L.,
RA Kotta B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Roone D., Pohl T.M., Portetelle D., Porvolik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rose M., Sadaie Y.,
RA Rieger M., Rivolta C., Rocha B., Roche B., Rey M., Raynolds S.,
Sato T., Scanlan E., Schleich S., Schroeter R., Schiener F.,
RA Sorokin A., Tanaka T., Tanaka T., Tarkanshi H., Takemaru K.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler B., Wedler H., Weitzenegger T.,
RY Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RY Yobhida K., Yohidava H.F., Zumstein Bacillus
RY The complete genome sequence of the Gram-positive bacterium Bacillus
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.,
RY Subtilis F.
                                                                                                                                                 Yoshida K.-I., Seki S., Pujimura M., Miwa Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujimura Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita Y., Fujita 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 6; DB 1; Length 337;
100.0%; Pred. No. 3.7e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Subtilist; EG11109; yxaG.
InterPro; IPR007113; Cupin sup.
Hypothetical protein; Complete proteome.
SEQUENCE 337 AA; 37584 MW; F9F13255C9D8C215A CRC64;
                                                                                         STRAIN=168 / BGSC1A1;
MEDLINE=96093926; PubMed=7584049;
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB005554; BAA21586.1; -.
EMBL; Z99124; CAB16035.1; -.
PIR; F70071; F70071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
NCBI TaxID=1423;
                                                                                                                                                                                                                                                                                                                                              STRAIN=168;
                                                        SEQUENCE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A3(2) / M145,
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby I., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Rabbinowitsch E., Sharp S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98422466; PubMed=9748446;
Grandvalet C., Rapoport G., Mazodier P.;
"hrch, encoding the repressor of the groEL genes in Streptomyces albus G, is associated with a second dnaJ gene.";
J. Bacteriol. 180:5129-5134(1998).
-!- FUNCTION: Negative regulator of class I heat shock genes (grpE-dark-dary and groELS operons). Prevents heat-shock induction of the dark-dary and groELS operons). Prevents heat-shock induction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                 Streptomyces albus G.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.8%; Score 6; DB 1; Length 338;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMAP; MF_00081; -; 1.
InterPro; IPR002571; HrcA.
Pfam; PF01628; HrcA; 1.
TIGRFAMS; TIGRS0331; hrcA; 1.
Transcription regulation; Repressor; Heat shock.
SEQUENCE 338 AA; 36976 MW; 81C15F9A92BA7A49 CRC64;
                                                                                                                                                                                                            Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomycineae; Streptomycetaceae; Streptomyces
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
36-FEB-2003 (Rel. 41, Last annotation update)
Heat-inducible transcription repressor hrcA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heat-inducible transcription repressor hrcA-HRCA OR SC02555 OR SCC77.22C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   these operons (By similarity). SIMILARITY: Belongs to the hrcA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF025656; AAC62528.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 LKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 LKLIGE 268
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                        NCBI_TaxID=1962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                 STRAIN=J1074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRCA STRCO
ID HRCA STRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9RDD6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 250
```

Gaps

; 0

6; Conservative

Matches

143 ASEEVS 148

g

38 ASEEVS 43

338 AA.

PRT;

STANDARD;

HRCA_STRAL ID HRCA_STRAL

RESULT 249

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                   -!- FUNCTION: Negative regulator of class I heat shock genes (grpg-dank-dank-dank) and groELS operons). Prevents heat-shock induction of these operons (By similarity).
-!- SIMILARITY: Belongs to the hrcA family.
                                                                                                                                                                                                                                                                                                                                                                                                 HAWAP; MF 00081, -; 1.
InterPro; IRR002571; HrcA.
Pfam; PF01628; HrcA; 1.
TIGRFAMS; TIGR00331; hrcA; 1.
Transcription regulation; Repressor; Heat shock; Complete proteome.
SEQUENCE 338 AA; 36575 MW; 12BD83F913E9F871 CRC64;
                   "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)."; Nature 417:141-147(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 6; DB 1; Length 338;
100.0%; Pred. No. 3.7e+02;
Artive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL939113; CAB66233.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.0ery Match
Best Local Similarity 100.0
Matches 6; Conservative
```

. .

Gaps

; 0

Search completed: April 12, 2004, 10:35:48 Job time : 29 secs

229 LKLIGE 234 1/1/1/ 263 LKLLGE 268

à qq

```
Q803v8 brachydanio
Q722a5 caenorhabdi
Q21643 caenorhabdi
Q21643 caenorhabdi
Q873k5 neurospora
Q84E19 vibrio vuln
Q8mz26 drosophila
Q95e33 drosophila
Q97u1 peeudomonas
Q97tu peeudomonas
Q9ptE neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08k312 mus musculu
07z4x0 homo sapien
08vdz8 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96fg1 homo sapien
Q8k038 mus musculu
                                                    April 12, 2004, 10:32:28; Search time 46 Seconds (without alignments) 2311.514 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                             1 MKKMPLFSKSHKNPAEIVKI.......FADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                             1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                         1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                            Post-processing: Listing first 300 summaries
                                    - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q21643
Q873K5
Q8DFL9
Q8MZ26
Q95S33
Q9W107
Q87TU1
Q9P8T6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q96FG1
Q8K038
Q8K312
Q7Z4X0
Q8VDZ8
Q803V8
Q7Z2A5
                                                                                                                                         Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                     sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mcan=!
                                                                                                                                                                                                                                                                                                                                                                                             _unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                      vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                sp_bacteriap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                  sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                        rvirus:*
                                                                                                                                                                                                                                                                                                                                                                                                                           sp archeap:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                             sp_virus:*
                                                                                          US-10-025-730-1
                                                                                                                                                                                                                                                              SPTREMBL 25:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22222
33461
33461
33461
33461
3473
3473
3473
3473
3473
3473
3473
                                                                                                                               OLIGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                000N44UUUUUUUU
                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
4400001111
44666744088888888888
                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                              Scoring table:
                                                                                                                                                                            Word size :
                                    OM protein
                                                                                                                                                                                                                                                              Database :
                                                                                                             Sequence:
                                                                                                                                                           Searched:
                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.
```

Q9v4r2 drosophila Q8sr14 encephalito Q8sr46 mus musculu Q8mzq1 drosophila Q810184 bacillus an Q810184 bacillus an Q810185 bacillus an Q810185 sulfolobus Q8137 sulfolobus Q8137 sulfolobus Q8131 mycobacteri Q8137 mycobacteri Q8137 mycobacteri Q8147 arabidopsis Q86pf7 trypanosoma Q899k1 clostridium Q999k1 clostridium Q999k1 clostridium Q999k1 clostridium Q999k1 clostridium Q999k1 clostridium Q999k1 clostridium Q999k1 clostridium Q999k1 clostridium Q999k1 clostridium Q999k1 clostridium Q990k1 clostridium Q9313 arabidopsis Q8xqg6 streptomyce Q8xqg6 streptomyce Q92dd5 peeudomonas Q92dd5 peeudomonas Q92dd5 peeudomonas Q92dd5 peeudomonas Q92dd pacteroides Q82d1 thiaria wul Q84xQ8 aminomonas Q92d1 thiaria wul Q84xQ8 aminomonas Q92d1 thiaria un Q86d1 sun musculu Q84xD8 musculu Q981k6 thizobium l Q981k6 thizobium l Q981k6 thizobium l Q981k6 thizobium l Q981k1 encephonyce Q98x16 whome sapien Q981k2 mus musculu Q98x20 mus musculu Q94x8 plutella xy Q84x10 corynebacte Q84x11 corynebacte Q84x11 corynebacte Q84x11 corynebacte	Q704f8 synechococc Q84xb8 linaria can Q84xb7 linaria vul Q84xb7 linaria vul Q8xbu7 mus musculu Q9x793 mycobacteri O52434 mycobacteri Q52630 clostridium Q8iyl6 homo sapien Q8D186 mus musculu Q97m91 clostridium Q8dpf4 streptococc Q99µf7 staphylococ Q74388 schizosach Q8y402 paramecium Q8x5k0 escherichia Q7za52 magnaporthe
	WWF7 W W W W W W W W W W W W W W W W W W
Q9V4R2 Q8RX14 Q8RX14 Q8VHE6 Q8VHZ0 Q81U84 Q81U84 Q81U84 Q81U84 Q81U87 Q82U87 Q89U81 Q89U81 Q89U81 Q88WG2 Q8WYD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8 Q8YKD8	0704FB 084RB 084RB 084RB 093479 097009 097009 0990F 74388 0885K
**************************************	
8011008880808080808080809090714490084860108888088880888888888888888888888	255555 2777 2777 2775 2775 2775 2775 27
44 044200000000000000000000000000000000	
®®®>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>	
11112222222222222222222222222222222222	277 74 4 7 7 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

0875w3 saccharomyc 08x12x activation 09xw3 oryza sativ 07vqi7 candidatus 090x45 rattus norv 0726q9 homo sapien 0862m3 macaca fasc 078xv4 brachydanio 0865m3 oryza sativ 0865m3 oryza sativ 0865m3 oryza sativ 0842j1 caedibacter 079xv2 drosophila 09xv2 drosophila 09xv2 drosophila 09xv2 drosophila 09xv2 drosophila 09xv2 drosophila 09xv3 drosophila 09xv3 drosophila 09xv3 drosophila 09xv3 drosophila 09xv3 drosophila 09xv3 drosophila 09xv3 drosophila 09xv3 drosophila 09xv3 drosophila 09xv3 drosophila 000781 leishmonia 001781 leishmonia 001781 leishmonia 001781 leishmonia 001781 leishmonia 001781 leishmonia 001781 leishmonia 001781 leishmonia 001781 leishmonia 001781 leishmonia 001781 leishmonia 001781 arabidopsis 094xs arabidopsis 094xs drosophila 09xv3 drosophila 09xv3 drosophila 09xv3 drosophila 09xv3 drosophila 09xv3 drosophila 09xv3 drosophila 09xv3 tetrahymena 08xv2 tetrahymena 08xv2 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena 08xv3 tetrahymena	007686 listeria se 0875w4 saccharomyc 09fses oryza sativ 088al5 pseudomonas 09a9p9 caulobacter 08tab3 homo sapien 027764 plasmodium
0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	7 2.1 902 2 7 2.1 906 3 7 2.1 1053 1 7 2.1 1053 1 7 2.1 1055 1 7 2.1 1094 4
087260 lactococcus 092778 lactococcus 095700 sulfolobus 006995 bacilius su 084bb3 erwinia chr 074237 candida ten 081151 oryza sativ 09797 sulfolobus 077407 secherichia 0893x8 escherichia 0893x8 escherichia 0893x8 escherichia 0893x8 escherichia 0893x8 escherichia 0893x8 escherichia 0893x8 escherichia 0893x8 serratia ma 084b92 kiebstella 093516 salmonella 093516 salmonella 093516 salmonella 093516 salmonella 093546 salmonella 093546 salmonella 093546 salmonella 093546 salmonella 093546 salmonella 093546 salmonella 093546 salmonella 093546 salmonella 093546 salmonella 09746 salmonella 09749 arabidopsis 087099 vibrio chol 080991 vibrio vuln 080991 precedlagus 080901 arabidopsis 090798 arabidopsis 090798 arabidopsis 090793 arabidopsis 090793 corpcolagus 080901 arabidopsis 090793 arabidopsis 090793 arabidopsis 090793 corpcolagus 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 080901 arabidopsis 08001 arabidopsis 08001 arabidopsis 08001 arabidopsis 08001 arabidopsis 08001 arabidopsis 08001 arabidopsis 08001 arabidopsis 08001 arabidopsis 08001 arabidopsis 08001 arabidopsis 08001 arabidopsis 08001 arabidopsis 08001 arabidopsis 08001 arabidopsis 08001 arabidopsis 08001 arabidopsis 08001 arabidopsis 08001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis 09001 arabidopsis	ictyosteli ibrio angu orachydani arabidopsi escherichi oryza sati
90	56 7 2.1 443 5 57 7 2.1 444 2 58 7 2.1 444 10 60 7 2.1 446 10 61 7 2.1 453 10 62 7 2.1 453 10

Q803p9 brachydanio Q8637 dictyosteli Q86925 aura virus Q62644 rattus norv Q5fta4 arabidopsis Q86326 dictyosteli Q86hy0 dictyosteli

Q8bn38 mus musculu Q98102 arabidopsis Q8t2g2 dictyosteli Q9he72 neurospora

08jhv7 brachydanio 09vmj7 drosophila 086iv6 dictyosteli

Q934V6	ALIG
16	
76	
4 rd 0 80	
ο ω	
300	

```
Q9Z2X9
Q9UB29
                                                 Q9UB28
Q7VI08
Q9T2M1
                                                         Õ75320
Q825B0
                                                                      068176
087599
098766
099W61
095109
081RF4
042008
          Q62644
Q9FTA4
Q86J26
Q86HY0
                    Q8BN38
Q9SL02
                            Q9HE72
Q8JHV7
Q9VMJ7
                                    Q861V6
Q8B5N2
                                                                 057372
Q89TJ8
                                                                                           Q8UZ87
Q8QXX5
Q8UZ91
Q8KEV0
                                                                                                         Q812T5
Q812T5
Q57171
Q87608
Q97RN1
                                                                                                                      Q89CS6
Q836L5
Q81GQ5
Q8TUF6
Q9GJR4
                                                                                                                                   Q8PZ57
Q87613
Q87601
Q99H01
Q8GY14
                                                                                                                                                Q87610
Q87595
Q87603
                                                                                                                                                             Q8X1Z9
Q9LG43
Q9YTN6
       086925
                                                                                                                                                        QBCYZ5
5555
11170
111899
111899
111899
111899
111899
111899
111899
111899
111899
111899
111899
111899
111899
111899
111899
111899
111899
111899
111899
111899
111899
11189
```

## SIMENTS

Q35503 paracentrot Q8x1z9 talaromyces Q91g43 oryza sativ G9ytn6 ateline her Q25358 helicobacte Q934v6 salmonella

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                           105
                                                                                                                                                                                                                                                                                                                                                                                                                                        213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FHVFKVFVASPHKTQPIVEILLKNQPKLIEFLSSFQKERTDDBQFADEKNYLIKQIRDLK 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FHVFKVFVASPHKTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 EKLLQSENYVTKRQSLKLLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEA
                                                                                                                                                                                                                                                                                                                                                                               94 KKDVTQIFNNILRRQIGTRSPTVEYISAHPHILFMLLKGYBAPQIALRCGIMLRECIRHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLITRHKVLVADFLEQNYDTIFEDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKLLQSENYVTKRQSLKLLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEA
                                                                                                                                                                                                                                                                                                                                                                                                KKDVTQIFNNILRRQIGTRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE
                                                                                                                                                                                                                                                                                                                                                                                                                                      154 PLAKIILFSNOFRDFFKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDY
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54; DB 11; Length 103;
Pred. No. 1e-47;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                    72.4%; Score 244; DB 4; Length 289;
                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (JUL.2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034159; AAH34159.1; -.
InterPro; IFR04892; Mo25.
Pfam; PF03204; Mo25; 1.
                                                                                                                                                                                          EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                        l protein.
289 Aa; 33738 MW; F57B9EFCF6ABF2D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11291 MW; EA86A9F6E9E426E0 CRC64;
            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0%; pred. No. 3.1e-245;
Matches 244; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.0%; Scor.
100.0%; Pred. No. r.
'.. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similar to RIKEN cDNA 1500031K13 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                           Straubberg R.;
Submitted (JUL-2001) to the EW
EMBL; BC010993; AAH10993.1; -.
Interpro; IPR008939; ARM.
Interpro; IPR004992; Mo25.
Pfam; PF03204; Mo25; 1,
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
            01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                       Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTAP 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S:
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214
                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8K038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8K038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
QBK03B
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                      ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ठ
```

087599 chimpanzee 087599 chimpanzee 099766 lactococcus 099401 ms sp. dbx 099199 streptomyce 081174 bacillus an 091500 arabidopsis 091500 garabidopsis 0801877 garlic late 0801877 garlic late 0801879 garlic late 080189 garlic late 081819 bacillus an 081215 bacillus an

Q8751 Interpretation (2077) Series concepts (2077) Series concepts (2077) Series concepts (2077) Series concepts (2077) Series concepts (2077) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076) Series (2076)

Q8b5n2 oropouche v O96216 plasmodium Q922x9 rattus norv Q9bb29 caenorhabdi Q9ub28 caenorhabdi Q7vi08 helicobacte

Q825b0 streptomyce Q8rtd3 escherichia 057372 brachydanio Q89tj8 bradyrhizob 068176 lactococcus

O9t2ml nicotiana t 075320 homo sapien

57

4 MPLFSKSHKNPAEIVKILKONLAILEKQDKKTDKASEEVSKSLQAMKEILCGTN

à

IID DATCOS OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCOOC OCCO

```
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.0
nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                            MO25 protein.
CAB39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7Z2A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q803V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q722A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q803V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
DD BE REP REP DE SON DE REP REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE REP DE RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
1 MPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTN 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.8%; Score 23; DB 11; Length 205; 100.0%; Pred. No. 3.5e-15; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 6.8%; Score 23; DB 4; Length 341; Similarity 100.0%; Pred. No. 5.5e-15; 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Zhao S.Y.;

"Cloning of a new human cDNA homologous to MO25 gene.";

Submitted (MAR-1399) to the EMBL/GenBank/DDBJ databases.

EMBL, AR134480; AAP37257.1;

SEQUENCE 341 AA, 39774 MW; D3A60160F7AR7ARN CPC44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC029053; AAH29053.1; -.
MGD; MG1:107438; Cab39.
InterPro; IPR008938; ARW.
InterPro; IPR004892; MO25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 205 AA; 24582 MW; 015261A02F808169 CRC64;
                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to calcium binding protein, 39 kDa (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341 AA
                                                                                                                                                                                                                                                           205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 IMTKYISKPENLKLMMNLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 IMTKYISKPENLKLMMNLLRDKS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 IMTKYISKPENLKLMMNLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 IMTKYISKPENLKLMMNLLRDKS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF03204; Mo25; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MO25-like protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Sim-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8VDZ8
Q8VDZ8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q724X0
                                                                                                                                                                                                                                                      08K312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
2724X0
AC 0724X
AC 0724X
DT 01-00
DT 01-00
DT 01-00
DE HOMO
OC BURD
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
OC MARM
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
                                                                                                                                                                       RESULT 3
Q8K312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08VDZ8
ID 08
AC 08
DT 01
```

à

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RÓ2E12.2.
Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
usa muscurus (mouse).
Eukaryota, Merazoa: Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.8%; Score 23; DB 11; Length 341; Best Local Similarity 100.0%; Pred. No. 5.5e-15; Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                          Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC020041; AAH20041.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC044172; AAH44172.1; -.
InterPro; IPR004893; ARM.
InterPro; IPR004892; Mo25.
Pfam; PF03204; Mo25, 1.
SEQUENCE 343 AA; 39820 MW; F10450DA0446268A CRC64;
                                                                                                                                                                                                                                        MGD; MGI:107438; Cab39.
InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
Pfam; PF03204; Mo25; 1.
SEQUENCE 341 AA; 39843 MW; E7FECA529D6FE811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-UUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein R02E12.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.0%; Score 17; DB 13; L
100.0%; Pred. No. 9.7e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similar to MO25 protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 377 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 IMTKYISKPENLKLMMLLRDKS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 IMTKYISKPENLKLMMNLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 SENYVTKROSLKLLGEL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 SENYVTKROSLKLIGEL 237
```

·.

```
B2314.090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSDFL9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OBDFL9
                                                                                                                                                                                                                                                                                                                                                          Q873K5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                   RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8DFL9
                                                                                                                                                                                                                                                                                                                                      Q873K5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBL_TaxID=6239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                               "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.2%; Score 14; DB 5; Length 377;
100.0%; Pred. No. 1.4e-05;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U53337; AAA96186.2; -.
PIR; T16650; T16650.
PIR; T16651; T16651.
WormPep; R02E12.2a; CE28410.
                                                                                                                                                                                                                               "The sequence of C. elegans cosmid R02E12."; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL: 05337; AAP40522.1; -.
Hypothetical protein.
SEQUENCE 377 AA: 43470 MW; 8F9B8AA070216176 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The sequence of C. elegans cosmid R02E12.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                      Waterston R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                   STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2001 (TrEMBLrel. 18,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 LRRQIGTRSPTVEY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 LRRQIGTRSPTVEY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                       STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEOUENCE FROM N.A.
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leimbach D.;
                                                                                                                                                                                                             Leimbach D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson R.;
                                                             Wilson R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         021643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
Q21643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECREATE SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF SET OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., Choy H.E.;
                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                         4.2%; Score 14; DB 5; Length 636;
100.0%; Pred. No. 2.2e-05;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 2.7%; Score 9; DB 3; Length 370; Local Similarity 100.0%; Pred. No. 2.2; les 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016797; AAO08729.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           German Neurospora genome project;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX284746; CAD70300.1; -
                         InterPro; IPR004892; Mo25.
Pfam, PF03204; Mo25; 1.
Hypothetical protein.
SEQUENCE 636 AA; 72282 MW; 85D5853E9F0E3193 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUT-2003 (TrEMBLrel. 25, Last annotation update)
Probable protein required for conidiophore development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF03204; Mo25; 1.
SEQUENCE 370 AA; 42812 MW; 2E82CG3BD06DBB9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  370 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequ
01-JUN-2003 (TrEMBLrel. 24, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                        105 LRRQIGTRSPTVEY 118
                                                                                                                                                                                                                                                                                                                            378 LRRQIGTRSPTVEY 391
                                                                                                                                                       Query Match 4.2%;
Best Local Similarity 100.04
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR008938; ARM. InterPro; IPR004892; Mo25.
InterPro; IPR008938; ARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                274 FHVFKVFVA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 FHVFKVFVA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Predicted permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio vulnificus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CMCP6;
```

```
OOC CARRAN AND BEING AND BEING AND BEING AND BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEING BEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATE PROPERTIES OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chawez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG16912.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                        DB 16; Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 339;
                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRTAMS; TIGRO0234; tyrs; 1.
PROSITE; PS00178; AA TRNA LIGASE I; 1.
SEGUTENCE 339 AA; 37776 MW; DF58AF0E4601FD3D CRC64;
                                Pfam; PF01925; DUF81; 1.
Complete proteome.
SEQUENCE 251 AA; 26763 MW; B023D2C45EC6D0C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AY113395, AAM29400.1; -
FlyBase; FBGn0035064; CG16912.
GO; GG:0005524; F:ATP binding; IEA.
GO; GG:0004831; F:tyrosine-tRNA ligase activity; IEA.
GO; GO:0006437; P:tyrosine-tRNA aninoacylation; IEA.
InterPro; IPR002105; tRNA-synt Ib.
InterPro; IPR002105; TRNA-synt I.
FRAM: PF00579; TRNA-synt Ib.
PRINTS; PR01040; TRNA-synt Ib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
GM10508p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                           2.4%; Scor.
100.0%; Pred. No. 10.
0; Mismatches
                                                                                                                                                                                                                                     18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.4%; Score 8; DB 5
100.0%; Pred. No. 23;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Guery Local Similarity 100...
Best Local Similarity 100...
InterPro; IPR002781; DUF81.
                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                             156 SSGLLVTL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 ADLQLIDF 173
                                                                                                                                                                                                                                                                                                                                           75 SSGLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADLOLIDE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patel S., Ph
Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RE07958p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             095833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O8MZ26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG16912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBMZ26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    095833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
78872
AC 08M22
AC 08M22
DT 01-0C
DT 01-0C
DT 01-0C
DT 01-0C
OC DT 01-0C
OC CEPAY
OC EPAY
OC EPAY
OC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC EPAY
CC C EPAY
CC EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C EPAY
CC C C EPAY
CC C C EPAY
CC C C EPAY
CC C C EPAY
CC C C EPAY
CC C C EP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20095533
1D AC Q9
DDT Q01
DDT Q01
DDT Q01
GN CG
GN CG
OC BU
S K DR
                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                    ð
```

```
MEDINE=20196006, PubMed=10731132;

MEDINE=20196006, PubMed=10731132;

MEDINE=20196006, PubMed=10731132;

Manatides P.G., Scherer S.E., Holt R.M., Hoskins R.A., Galle R.F.,

Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Galle R.F.,

Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Galle R.F.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej K.G., Champe M., Pfeiffer B.D.,

An K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Besaley E.M.,

Ballew R.M., Basu A., Baxendale J., Brotaken P., Bolshakov S.,

Ballew R.M., Buson P.V., Berman B.P., Bhandari D., Bolshakov S.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Abrick R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Acherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

A Cherry J.M., Cawley S., Dahlke C., Perraz C., Ferriera S., Fleischmann W.,

A Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Brothin K.J., Brougelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

Rosler C., Gabriellan A.E., Garg N.S., Gabbat W.M., Glasser K.,

Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Harris N.L., Harvey D., Heiman T.J., Wernison J.R., Ketchum K.A.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
                                                                                                             SEQUENCE FROM N.A.

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

A Champe M., Chavez C., Dorsett V., Farian D., Frise E.,

Gonzalez M., Chavez C., Miranda A., Mungall C.J.,

A Gonzalez M., Gavarin H., Li P., Liao G., Miranda A., Wangall C.J.,

Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,

A V. C., Lewis S.E., Rubin G.M., Celniker S.;

Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AY060975; AAL28523.1;

BEMBL, AY060975; AAL28523.1;

BEMBL, AY060975; AAL28523.1;

BEMBL, AY060975; FAMP binding; IEA.

GO; GO:000524; FAMP binding; IEA.

GO; GO:000524; FAMP binding; IEA.

GO; GO:000524; FAMP-Synt L.b.

BITCEPPO; IPRO02305; FRNA-Synt L.b.

BITCEPPO; IPRO02305; FRNA-Synt L.b.

BITCEPPO; IPRO02305; TRNA-Synt L.b.

BITCEPPO; IPRO02305; TRNA-Synt L.b.

BR PRINTS; PRO1040; TRNASYNTHTYR.

BY PRINTS; PRO1040; TRNASYNTHTYR.

BY PRINTS; PRO1040; TRNASYNTHTYR.

BY PRINTS; PRO1040; TRNASYNTHTYR.

SEQUENCE 442 AA; 49898 WW; 347257A9372FBBCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 8; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
2.4%; Score 8; DB 5;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464 AA.
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9W107;
01-MAY-2000 (TIEMBLER 13,
01-MAY-2000 (TIEMBLER 13,
01-OCT-2003 (TIEMBLER 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 ADLÓLIDF 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 ADLQLIDF 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CG16912 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9W107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
```

576 AA; 65151 MW; 871FC7A0E8316D47 CRC64;

SEQUENCE

```
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Mirphy D.M., Nelson D.L.,
Molson D.R., Nelson K.A., Nixon N., Pacleb J.M.,
Nelson D.R., Nelson K., Sunders R.D.C., Scheeler F., Shen H.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun B.,
Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
Nang Z.-Y., Wassarman D.A., Weinstrok R., Wang A.H., Wang X.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Abeng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Chee 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M., Dodson R., Deboy R., Durkin A., Kolonay J., Madupu R., Daugherty S., Barinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T., White O., Fraser C., Collmer A.; "Complete sequence of Fseudomonas syringae."; Submitted (MAR.2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Dolichyl-phosphate-mannose-protein mannosyltransferase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILID. TIGREDANS, TIGROSO34; LYIS; 1.
PROSITE; PSO0178; AA TRNA LIGASE I; 1.
SPOOTTE: 464 AA; 52574 MW; BIFFCBF164148C73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBGN0035064; CG16912.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004831; F:tyrosine-tRNA ligase activity; IEA.
GO; GO:0006437; P:tyrosyl-tRNA aminoacylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase; Glycosyltransferase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 8; DB 5;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match
Local Similarity 100.0%; Pred. No. 30;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002305; tRNA-synt 1b.
InterPro; IPR001412; tRNA-synt I.
InterPro; IPR001307; Tyr_tRNA-synt I.
Pfam; PF00579; tRNA-synt lb; 1.
PRINTS; PR01040; TRNASYNTHTYR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003465; AAF47271.1; -. HSSP; P00952; 4TS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 ADLOLIDF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 ADLQLIDF 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=DC3000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSPTO5588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q87TU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
0297701
DD 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 
         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                     MEDLINE=20561721; PubMed=11109485;
Girvitz T.L., Ouimet P.M., Kapoor M.;
"Heat shock protein 80 of Neurospora crassa: sequence analysis of the gene and expression during the asexual phase.";
Can. J. Microbiol. 46:981-991(2000).
BMBL; AR212996; ARF34607.1; ---
HSSP; P07900; 1YER.
GO, GO:0005524; F:ATP binding; IEA.
GO, GO:0007754; F:Chaperone activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromadorea; Rhabditida; Strongylida;
                                ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Stron
Trichostrongyloidea, Haemonchidae, Haemonchinae, Haemonchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Moredun;
Redmond D.L., Knox D.P.;
"Putative metallopeptidase, Mep2, isolated from Haemonchus
Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 695;
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contortus.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF080117; AAC28740.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3P90; 1.
78909 MW; 8EAB594ADBA2BC18 CRC64;
                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
                36;
                                                                                                                                                               695 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.4%; Score 8; DB 3;
00.0%; Pred. No. 42;
ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           747 AA
2.4%; Score 8; DB 1
100.0%; Pred. No. 36;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Putative zinc metallopeptidase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemonchus contortus (Barber pole worm).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR001404; Hsp90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS, PRO0775; HEATSHOCK90.
SMART; SMO0387; HATPARE C; 1.
PROSITE; PS00299; HSP90; 1.
SEQUENCE 695 AA; 78909 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02518; HATPase c; 1.
Pfam; PF00183; HSP90; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2003 (TrEMBLrel. 25,
                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                      Heat shock protein 80.
                                                                                    285 GLLVTLIA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 EPLAKIIL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 EPLAKIIL 175
                                                         77 GLLVTLIA 84
               Best Local Similarity
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     Neurospora crassa.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6289;
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                              Q9P8T6;
                                                                                                                                                             09P8T6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          076750
                                                                                                                                RESULT 15
Q9P8T6
                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 16
                                                                                    g
                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
RC STRAINBERKeley,

RX Addams M.D.,

Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RAMAMS M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RAMAMS M.D., Celniker S.E., Holt R.A., Evans R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Holt R.A., Evans R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.K.,

Brandon R.C., Rogers Y.-H.C., Blazej K.G., Change M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej K.G., Change M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrewe-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessley B.M.,

RA Ballew R.M., Basu D.A., Butler H., Cadieu B., Center R., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu B., Center R., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Hostin D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wernison J., A., Ketchum K.A.,

Rammel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Hostin D., Mattei B., McIntosh T.C., McIndoy W., McIphy L., Muzny D.M., Nelson D.L.,

RA Holson K.A., Moy M., Mirphy B., Mirphy L., Muzny D.M., Nelson D.L.,

RA Holson D.R., Nelson K.A., Nixon K., Nixon R., Palazolo M., Pittman G.S., Panl S., Pollard J., Puri V., Reine M., Reinert K., Remington K., Seunders R.D.C., Scheeler F., Shen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            ·:
0
GO; GO:0005622; C:intracellular; IEA.

RG; GO:0006237; F:merallular; IEA.

RG; GO:0004245; F:merallopeptiase activity; IEA.

RG; GO:0004245; F:neprilyelm activity; IEA.

RG; GO:0004245; F:neprilyelm activity; IEA.

RG; GO:0003700; F:transcription factor activity; IEA.

RG; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

RICEPTO; IPRO0005; HTHARG.

RICEPTO; IPRO0005; HTHARG.

RICEPTO; IPRO00978; Peptidase M13.

RICEPTO; IPRO08753; Peptidase M13.

REAL PFO1431; Peptidase M13. I.

REAL PFO5649; Peptidase M13. I.

REAL PFO5649; Peptidase M13. I.

REAL PFO3649; Peptidase M13. I.

REAL PFO3649; PEPTINSINSINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                               Length 747;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                 747 AA; 84782 MW; DFBEF8FD5608234B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.4%; Score 8; DB 5;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    923 AA
                                                                                                                                                                                                                                                                             PROSITE; PS00041; HTH ARAC FAMILY 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOR protein (RE49094p).
TOR OR CG1389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 EIVKILKD 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 EIVKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 17
Q9V4R2
    à
```

```
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhan S., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Myers E.W., Rubin G.M., Venter J.C.; Smith H.O., Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.,
                                                                                                                                                                                                                                                                                                                                EMBL; AZ03840; AAF59203.1; --
EMBL; AX071403; AAL49025.1; --
EMBL; AX071403; AAL49025.1; --
EMBL; AX071403; AAL49025.1; --
EMBL; AX071403; AAL49035.1; --
EMBL; AZ071403; AAL49037.1; --
EMBL; AZ071403; Lordon Emphrane; NAS.

GO; GO:00030381; P:eggshell pattern formation (sensu Insecta); IMP.

GO; GO:0007362; P:terminal region determination; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21576510; PubMed=11719806;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Encephalitozoon cuniculi.
Eukaryota, Fungi, Microsporidia, Unikaryonidae, Encephalitozoon.
Smith T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00060; FN3; 1.

SMART; SM00219; TYKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.

SEQUENCE 923 AA; 105200 MM; 746F46ElA4277ACF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                        (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.4%; Score 8; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 2410 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001245; Tyr Dkinase.
InterPro; IPR008266; Tyr Dkinase_AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003961; FN III.
InterPro; IPR000719; Prot_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Prot kinase; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 SSGLLVTL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75 SSGLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ubiquitin ligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6035;
                                                                                                                                                                                                   STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=GB-M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=GB-M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Зеповсоре;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8SR14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08SR14
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q94K21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q94K21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q81U84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q81U84
ID Q8
AC Q6
DT 01
DT 01
DT 01
OE Hy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             094K21
             DE REPRESENTATION OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=CS7BL/6xCBA/J;
Ibanez-Tallon I., Gorokhova S., Heintz N.;
"Loss of function of axonemal dynein Mdnah5 causes primary ciliary dyskinesia and hydrocephalus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M., Weissenbach J., Vivares C.P.; "Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 2.4%; Score 8; DB 11; Length 4621; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.4%; Score 8; DB 5; Length 2410;
100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                 Nature 414:450-453(2001).

EMBL; AL590449; CAD25857.1; -.

EMBL; AL590449; CAD25857.1; -.

EMBL; AL590449; CAD25857.1; -.

GO; GO:0005621; F:ubiquitin rycle; IEA.

GO; GO:0006512; P:ubiquitin cycle; IEA.

Ffam; PF00632; P:ubiquitin cycle; IEA.

Ffam; PF00632; P:ubiquitin cycle; IEA.

Ffam; PF00632; P:ubiquitin cycle; IEA.

Ffam; PF00632; PECT; 1.

SMART; SW00119; HECT; 1.

FROSITE; PS50237; HECT; 1.

EROSITE; PS50237; HECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4621 AA; 527491 MW; E4E044A2D4998298 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hum. Mol. Genet. 11:0-0(2002).

BMBL; AF466704; AAL69993.1; -
MGD; MGI:107718; Dnahcs.

GO; GO:0003878; C:axonemal dynein complex; IMP.
GO; GO:000375; F:axonemal motor activity; IMP.
GO; GO:0001539; P:ciliary/flagellar motility; IMP.
InterPro; IPR004273; Dynein heavy.
InterPro; IPR004273; Dynein heavy.
InterPro; IPR00169; SHprot_acsite.
Pfam; PF03088; Dynein heavy; 1.
SWART; SM00382; AAA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBMZQ7;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 4621 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00382; AAA; 3.
PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Cr
01-MAR-2002 (TrEMBLrel. 20, La
01-OCT-2003 (TrEMBLrel. 25, La
Axonemal dynain heavy chain 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1815 LIEFLSSF 1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 PTVEYISA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491 PTVEYISA 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 LIEFLSSF 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNAHCS OR DNAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBVHE6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8VHE6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8MZQ7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOUTH TO THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOUTH THE SOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OBMZQ7
ID O
AC DT
DT O
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

```
Lam B., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., 18hida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.K., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                          Azadan R.J., Danielson P.B., Fogleman J.C.,
"Isolation of a novel cytochrome P450 from Drosophila pachea.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF506532, AAMJ-400.1;
FlyBase; FBGN0062760; Dpac\Cyp4c3.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR001128; Cytochrome_P450.
NON TER.
1 SEQÜENCE 52 AA, 6072 MM; 9EDE3D761CEF7DD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 10; Length 66; 100.0%; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 AA; 7464 MW; D51D8E09207D8507 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 5;
100.0%; Pred. No. 51;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus anthracis (strain Ames).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q81U84;
01-JUN-2003 (TrEMBLrel. 24, C)
01-JUN-2003 (TrEMBLrel. 24, Ls
01-JUN-2003 (TrEMBLrel. 24, Ls
Hypothetical protein.
                           Cytochrome P450 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 LLGELIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 LLGELIL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 LLVTLIA 84
                                                                          Drosophila pachea.
                                                                                                                                                                               NCBI TaxID=103846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LLVTLIA 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown protein.
```

0

.. 0

```
01-JUN-2003 (TrEMBLrel.
                                                                                                                                                                                NCBI_TaxID=323;
                       01-JUN-2003
01-JUN-2003
                                                                                            PSPT00332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8J2Y6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                049831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08J2Y6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 26
Q49831
ID Q49833
AC Q49833
DT 01-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8J2Y6
    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                              MEDLINE=22608414; PubMed=12721629;
Read T.D., Peterson S.N., Tourasse N., Baillie D.W., Paulsen I.T.,
Read T.D., Peterson S.N., Tourasse N., Baillie D.W., Paulsen I.T.,
Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
Kolomay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
DeBOY R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.H.,
Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Hazen A., Cline R., Redmond C., Thwaite J.E., Nierman W.C.,
Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-22608415; PubMed=12721630;
MEDLINE-22608415; PubMed=12721630;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.;
                                                                                                                                                                                                                                                                                                                                                "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
Nature 423:81-86(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of Bacillus cereus and comparative analysis with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 93; . 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 16; Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Complete proteome. SEQUENCE 93 AA; 11272 MW; 131D15787B957F1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Complete proteome.
SEQUENCE 93 AA; 11095 MW; 82BDD67F88587CEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSM 31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
2.1%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus cereus (strain ATCC 14579 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 423:87-91(2003).
EMBL; AE017001; AAP07998.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE017027; AAP24987.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus anthracis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 IVKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 IVKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVKILKD 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 İVKİLKD 34
                       NCBI_TaxID=198094;
                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=226900;
                                                                                                                                                                                                                                                                                                                                                                                                                                          BA1000; -.
                                                                                                                                                                                                                                                                                                                               Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q88AQ4
Q88AQ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q81H15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q81H15
                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 23
1081H15
AC 081H11
AC 081H11
DT 01-JUU
DT 01-JUU
DT 01-JUU
DE HYDOT
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACIO
ON BACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q88AQ4
ID Q8
AC Q8
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                 STRAIN=DC3000;
Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Buell R., Joardar V., Van Aken S., Feldblyum T., Gwinn M.,
Bodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Brinhac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
White O., Fraser C., Collmer A.,
"Complete sequence of Pseudomonas syringae.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
IIGR: PSPT00332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ODSN.
Sulfolobus acidocaldarius.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                       Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-DSM639;
Schmidt C.L., Henninger T., Schaefer G.;
"A novel RNAse from the hyper-thermoacidophilic crenarchaeon Sulfolobus acidocaldarius.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; Score 7; DB 16; Length 95; 100.0%; Pred. No. 85; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 1; Length 99;
100.0%; Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF202955; AAO13707.1; -.
InterPro; IPR007138; ABM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypochetical protein; Complete proteome.
SEQUENCE 95 AA; 10614 MW; 131F36BC7DA74252 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 AA; 11763 MW; ECOD7CD66C464F94 CRC64;
(TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   049811;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                     Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF03992; ABM; 1
                                                                    Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 LLVTLIA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 LLVTLIA 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 EIVKILK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIVKILK 32
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2285;
```

```
Eukarvota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        086PF7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             086PF7
                                                                                                                                                                       042147
                                                                   Matches
                                                                                                                                                 RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 29
    8 E S
                                                                                                                                                                                 d
                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         R03C1.3 OR COG-1.
Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steward C.A.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; A715:1210, AAN72827.1;
EMBL; A22279; CAD52039.1;
WormPep; R03C1.3b; CE33290.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:00053700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22370693; PubMed=12482710;
Palmer R.E., Inoue T., Sherwood D.R., Jiang L.I., Sternberg P.W.;
"Caenorhabditis elegans cog-1 locus encodes GTX/Nkx6.1 homeodomain proteins and regulates multiple aspects of reproductive system
                                                                                                                                                                                                                            ö
                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                     DB 2; Length 103;
                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
COG-1B (C.elegans COG-1 protein) (Corresponding sequence
                                                                                                                               Robison K.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U00018; AAA17261.1; -.
PIR; S72925; S72925.
SEQUENCE 103 AA; 11211 MW; DID4D669AB82A50F CRC64;
                                                                                      Smith D.R.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                               106 AA.
                                                                                                                                                                                                   2.1%; Score 7; DB 2;
100.0%; Pred. No. 91;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001356; Homeobox.
InterPro; IPR00047; HTH lambrepressr.
Pfam; PR00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dev. Biol. 252:202-213(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                        Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00389; HOX; 1.
         B2168_C1_182,
Mycobacterium leprae.
                                                                                                                                                                                                                                                15 AEIVKIL 21
                                                                                                                                                                                                                                                                       87 AEIVKIL 93
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                      NCBI TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                               R03C1.3b)
                                                                                                                                                                                                                                                                                                       RESULT 27
                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                    g
```

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Auxin -responsive GH3 product (Fragment).

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II, Brassicales; Brassicaceae, Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
2.1%; Score 7; DB 10; Length 108;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.1%; Score 7; DB 5; Length 109; Best Local Similarity 100.0%; Pred. No. 96; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Philipps G., Gigot C.;
Submitted (OCT-1993)
EMBL, Z26804, CAA81417.1;
InterPro; IPR004993; GH3.
PF03321; GH3; 1.
                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Brener;
Andersean B., Bontempi E.J.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC137988; AAO44096.1; --
SEQUENCE 109 AA; 12625 MW; 366F63960B464239 CRC64;
PROSITE; PS00027; HOMBOBOX 1; 1.
PROSITE; PS50071; HOMBOBOX 2; 1.
SEQUENCE 106 AA; 12098 WW; EAFBD6B4678F3A20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER 1 1 1 1 1 NON TER 108 108 SEQUENCE 108 AA; 12003 MW; AOD4AOB5EF6E548A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                             2.1%; Score 7; DB 5;
100.0%; Pred. No. 94;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
TCC31.39.
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 EILLKNQ 298
                                                                                                                                                                                             67 AQLAQEL 73
                                                                                                                                                                                                                                             50 AQLAQEL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 EILLKONO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 MKEILCG 55
                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trypanosoma cruzi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5693;
```

```
Streptomyces avermitilis.
                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 KDNLAIL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 KDNLAIL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metabolites."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aureus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       082036
                                                  Q99WB7
     RESULT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 33
                                COOMB;
                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22457253; PubMed=12552129;
Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H., Becker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A., Gottschalk G., "The genome sequence of Clostridium tetani, the causative agent of
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Magai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramateu K.;
"Genome and virulence determinants of high virulence community-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium tetani.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.1%; Score 7; DB 16; Length 115; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 16; Length 116;
100.0%; Pred. No. 1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP004823; BAB94306.1; -. Hypothetical protein; Complete proteome. SEQUENCE 115 AA; 12926 MW; CBBD662267FA7F07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 AA; 13707 MW; 7FC5AAE44641CAE7 CRC64;
                                                                                                                                                                                          22, Last sequence update) 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tetanus disease.";
Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
EMBL; AE015936; AA034823.1; -.
                                                                                                                                                                                                                                                                                    Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 AA
                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                (TrEMBLrel. 22, (TrEMBLrel. 22,
                                                                                                                                                                                                                                       Hypothetical protein MW0441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359:1819-1827(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Massachusetts / E88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                         01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 KIILFSN 163
99 MKEILCG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 KDNLAIL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 KILLFSN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KUNLAIL 84
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=196620;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conserved protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acquired MRSA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lancet
                                                                                                                   Q8NY02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q899K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 31
10,0899X
AC 0899X
AC 0899X
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
셤
                                                                                                                   ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

```
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S., "Complete genome sequence and comparative analysis of the industrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SPECIES=S.aureus (strain Mb50), and S.aureus (strain N315);
MEDLINE=21311952; PubMed=11418146;
Kuxoda M., Ohta T., Uchlyama I., Baba T., Yuzawa H., Kobayashi I.,
Kuxoda M., Ohta T., Uchlyama I., Baba T., Yuzawa H., Kobayashi I.,
Kunamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba J.
Hattori M., Ogasawara N., Hayashi H., Hiramateu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

STRAIN=21477403; PubMed=11572948;

OMUTA S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,

Kikuchi H., Shiba T., Sakaki Y., Hattori M.;

"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bactéria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.1%; Score 7; DB 16; Length 122; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP003359; BAB56648.1; -.
EMBL; AP003130; BAB41674.1; -.
PIR; G89814; G89814.
FYPCHetical protein; Complete proteome.
SEQUENCE 122 AA; 13755 MW; 038F9597F059A195 CRC64;
                                                                                                                                       Staphylococcus aureus (strain Mus0 / ATCC 700699), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165; MEDLINE=22608306; PubMed=12692562;
01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SAV0486.
SAV0486 OR SA0444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q82QG6;
Q-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                    Staphylococcus aureus (strain N315).
Bacteria, Firmicutes, Bacillales, Staphylococcus.
NCBI_TaxID=158878, 158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative MerR-family transcriptional regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lancet 357:1225-1240(2001).
```

·.

```
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        023309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      023309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q88WG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 37
Q88WG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          023309
                 OX REPRESENT TO THE SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCOORDING THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEACT OF THE BEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
microorganism Streptomyces avermitilis.";
Mat. Biotechnol. 21:226-531(2003).

EMBL; AP005023; BAC68250.11;
GO; GO:0005522; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:000355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR00551; HTH_MerR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=2155285; PubMed=11759840; Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watacko T., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kibida Y., Kohara M., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Yasuda M., Tabata S.; "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.1%; Score 7; DB 16; Length 133; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anabaena sp. (strain PCC 7120).
Plasmid pCC7120alpha.
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anabaena sp. (strain PCC 7120).
Plasmid pCC7120gamma.
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0046821; C:extrachromosomal DNA; IEA.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 134 AA; 14913 MW; BOCIDA922114279A CRC64;
                                                                                                                                                                                                                                                                                                                           Complete proteome.
SEOUENCE 133 AA; 14887 MW; FCD73C03FC88BFCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match
2.1%; Score 7; DB 1
Local Similarity 100.0%; Pred. No. 1.1
les 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein All7360. ALL7360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein Alr8014.
                                                                                                                                                                                                                                                         PRINTS; PRO0040; HTHMERR.
SMART; SM00422; HTH MERR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 NLAILEK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; AH2522; AH2522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 VAQLAQE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 VAQLAQE 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBYKA2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8YKA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  089KA2
1D 08
AC 08
DT 01
DT 01
DE Hy
GN AI
OS AI
      RT
DR DR
DR DR
SQ SW S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Sperimatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids, eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terryn N., Kreis M., Kavanagh T., Entian K.D., Rieger M., James R., Puigdomenech P., Hatzopoulos P., Obermaier B., Duesterhoft A., Sones J., Palme J., Ansorge W., Delseny M., Bancroft I., Mewes H.W., Schueller C., Chalwatzis N.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                    Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kibida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";

EMBL; AP003603; BAB77344.1; -.

R PRS, AG2522, AG2522.

R PGO; GO:004681; C:extrachromosomal DNA; IEA.

PR GO: GO:004681; C:extrachromosomal DNA; IEA.

PR GO: GO:004681; C:extrachromosomal DNA; IEA.

PR GO: GO:004681; C:extrachromosomal DNA; IEA.

Plasmid; Hypothetical procein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 16; Length 134; 100.0%; Pred. No. 1.1e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 10; Length 135; 100.0%; Pred. No. 1.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; 27336; CAB10232.1; -.
EMBL; Al161539; CAB78495.1; -.
PIR; F71407; F71407.
Hypothetical protein.
SEQUENCE 135 AA; 15617 MW; A0675960CFC3B311 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q88WG2;
01-JUN-2003 (TrEMBLrel. 24, Created)
SEQUENCE FROM N.A.
MEDLINE=21595285; Pubmed=11759840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 NLAILEK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 QLibred 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 QLIDFEG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
```

```
STRAIN=6605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9AJD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q7XJG8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 40
Q7XJG8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9AJD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A D
             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Lib P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Lib P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.E., Yandradl M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Erottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Ade Pablos B., Delcher A., Dong Z., Mays A.D., Dew I., Dietez S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,
Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Adoloek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Ibegwam C.,
                                                                                                                                                                                                                                                                                                MEDLINE=22480296; PubMed=1256566;
Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
Kleerebezem M., Boekhorst J., van Kranenburg R., Sandbrink H.M.,
Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
De Vos W.M., Siezen R.J.;
"Complete genome sequence of Lactobacillus plantarum WCFS1.";
Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
EMBL; AL935256; Cab64107.1, -.
GO; GO:0016829; F:lyase activity; IEA.
InterPro; IPR006683; Thioestr_supf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 16; Length 137; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                          Lactobacillus plantarum.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lyase; Complete proteome.
SEQUENCE 137 AA; 15115 MW; 317140F95D1C9D13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=NCIMB 8826 / WCFS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF03061; 4HBT; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 LRRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 LRRQİĞT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                        *.4.1.-7.
FABZ2 OR LP 1677
                                                                                                                                                                                                        NCBI_TaxID=1590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CG5316 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9VDX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 38
109900X3
100-MX
20900X
AC 09900X
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01-MX
DT 01
     à
```

```
Williams B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLedd M.P., McPherson D.,
Liu X., Mattei B., McIntosh T.C., McLedd M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., MOY M., Murphy B., Murphy D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Musskern D.R., Pacleb J.M.,
Nelson D.R., Siden-Kiamos G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ranazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Shue B.C., Siden-Kiamos I., Weinstock G.M., Weisenbach J.,
Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weisenbach J.,
Miliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A. John S.M., Myers B.W., Rubin G.M., Venter J.C.;
Cibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
Cichence 28:2185-2195/2000)
REMBL, AE003726; AAF55667.1;
FIRMEL, AEDONATALO, TUDNOMATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, EDDNATALO,
FIRMEL, E
                                Ketchum K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taguchi F., Tanaka R., Kinoshita S., Ichinose Y., Imura Y., Andi S., Taguchi F., Shiraishi T., Yamada T.;
"HarpinPeta from Pseudomonas Pyringae pv. tabaci is defective and deficient in its expression and HR-inducing activity.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AB049570; BAB40655.1;
-.
InterPro; IPR005961; HrpZ.
Pfam; PF04877; HrpZ; 1.
SEQUENCE 140 AA; 14801 MW; 713A26C4FA7C08B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas syringae (pv. tabaci).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.1%; Score 7; DB 5; Length 139; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.1%; Score 7; DB 2; Length 140; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01230; HIT; 1.
SEQUENCE 139 AA; 16018 MW; 4641400E7B2B5BFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09AJD5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 ISKPENL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 ISKPENL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 AQLAQEL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 AQLAQEL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=322;
```

·.

```
01-0CT-2003 (TrEMBLEEL 25, 01-0CT-2003 (TrEMBLEEL 25, 01-0CT-2003 (TrEMBLEEL 25, 05JNBb0048E02.12.
                                                                                                                                                                                                            Science 294:849-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Theiler-like virus NGS910.
                                                                                                                                                                                                                                                                                                       Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                           102 NNILRRO 108
                                                                                                                                                                                                                                                                                                                                                                  99 NNILRRO 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 SLQAMKE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 SLOAMKE 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=204729;
       NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=NGS910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L* protein.
                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7XUY5;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Q80IV1;
                                                                                                                                                                                                                                                                                                                                                                                                                            Q80IV1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q7XUY5
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7XUY5
                                                                                                                                                                                                                                                                                                                                                                                                                  D80IV
       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                         Linaria vulgaris (Toadflax).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Lamiales; Plantaginaceae; Antirrhineae; Linaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Lamiales; Plantaginaceae; Antirrhineae; Linaria.
                                                                                                                   SEQUENCE FROM N.A.
Guebitz T., Caldwell A., Hudson A.;
"Rapid molecular evolution of CYCLOIDEA-like genes in Antirrhinum and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Guebitz T., Caldwell A., Hudson A.;
"Rapid molecular evolution of CYCLOIDEA-like genes in Antirrhinum and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                        Score 7; DB 10; Length 147;
Pred. No. 1.2e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria innocua.
Bacteria; Firmicutes; Bacillales; Disteriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                       147 147
147 AA; 16623 MW; 347F7C17D23EA393 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 151
151 AA; 16940 MW; DCE40F01B3BC631B CRC64;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DICHOTOMA-like (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Hypothetical protein lin1379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 10; Le
100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                 Query Match
2.1%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                 Mol. Biol. Evol. 0:0-0(2003).
EMBL; AY316702; AAP84108.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        its relatives.";
Mol. Biol. Evol. 0:0-0(2003).
EMBL; AY316701; AAP84107.1; -.
                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2003 (TrEMBLrel, 25, 01-0CT-2003 (TrEMBLrel, 25, 01-0CT-2003 (TrEMBLrel, 25, DICHOTOWA-like (Fragment).
                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                             129 QSENYVT 135
                                                                                                                                                                                                                                                                                        218 QSENYVT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 QSENYVT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 QSENYVT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                Linaria maroccana
                                                                                                                                                          its relatives.";
                                                                                                                                                                                         NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
SEQUENCE
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q92C12
                                                                                                                                                                                                                                                                                                                                                                         Q7XJG9
                                                                                                                                                                                                                                                                                                                                               RESULT 41
07XG9
AC Q7XGG
DT 01-0C
DT 01-0C
DE DICHO
OS ELWAT
OC SPETM
OC NCBI
RR SEQUE
RA HABI
RT HABI
RT HABI
ST NON T
SECURE
ST NON T
SECURE
ST NON T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 42
092012
1D 092013
AC 09201
DT 01-DE
DT 01-DE
DT 01-DE
DT Hypor
GN Linni3
OS Liste
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TIP 11262 / Serovar 6a;

MEDLINE-21537279; PubMed=11679669;

A claser P., Frangeul L., Buchtleser C., Rusnick C., Amend A.,

A Raquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

Charbit A., Chetcuani F., Couve B., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duchaud B., Durant L., Dussurget O.,

B Entian K.-D., Faihi H., Garcia-del Portillo F., Garrido P.,

A Bauter L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Jones L.-M., Xearst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Madueno E., Maitcurnam A., Mata Vicente J., Ng E., Nedjari H.,

Nordaick G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Sohlueter T., Simose N., Tierrez A.,

Nazquez-Boland J.-A., Vose H., Wehland J., Cossart P.;

Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Obsawa K., Watanabe Y., Miyata H., Sato H.;
"Genetic Analysis of a Theiler-Like Virus Isolated from Rats.";
Submitted (AUG-2002) to the EMBL/GenBank/DOBJ databases.
EMBL; AB090161; BACS8036.1;
SEQUENCE 156 AA; 18183 MW; 9D8DCEDCOA6ESDEO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 16; Length 154; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.1%; Score 7; DB 12; Length 156; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Complete proteome.
SEQUENCE 154 AA; 18073 MW; 5A95AB680C57F330 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL596168; CAC96610.1; -. PIR; AB1605; AB1605.
ListiList; LIN01379; -.
```

```
215 KLLQSEN 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             093157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     093187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      093187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCOCCOS ON THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE STANT OF THE ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H., Lu Y.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y.J., Hu H., Jia P.X., Olan Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y., Lu G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H., Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-VPI-5482 / ATCC 29148; MEDLINE=22550858; PubMed=12663928; Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K., Chiang H.C., Hooper L.V., Gordon J.I.; A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."; Science 299:2074-2076(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteroides thetaiotaomicron.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 2.1%; Score 7; DB 10; Length 157; Local Similarity 100.0%; Pred. No. 1.3e+02; Pred 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 16; Length 162; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein, Complete proteome.
SEQUENCE 162 AA; 18772 MW; B9C22B0528F0EF5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 AA; 17266 MW; DA8AC54057F26D3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Histidinol-phosphate aminotransferase (Fragment).
Aminomonas aminovorus.
Bacteria; Proteobacteria.
NCBI_TaxID=135579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Conserved hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE016926; AA075283.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 KERTDDE 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 DKASEEV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 KERTDDE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 DKASEEV 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                    NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8KY28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8ABD4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8KY28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8ABD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 45
08ABD
AC 08ABD
AC 08ABD
DT 01-JU
DT 01-JU
DT 01-JU
DE CONSE
GN BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BACTE
OC BA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8KY28
ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OS BET DE SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
```

```
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AP003362; BAB57480.1; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005224; F:ATP binding; IEA.

GO; GO:0004009; F:ATP-binding; IEA.

GO; GO:0004009; F:ATP-binding; IEA.

GO; GO:0004009; F:ATP-binding; IEA.

InterPro; IPR003439; ABC_transporter.

Propon; PD000006; ABC_transporter; 1.

PROSITE; PS00211; ABC_TRANSPORTER 1; 1.

PROSITE; PS50893; ABC_TRANSPORTER 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                   Taylor E.G., Smith N.L., Colby J., Black G.W., "The 3-hexulose-6-phosphate synthase-encoding gene of the obligate methylotroph Aminomonas aminovorus C2A1 is not present on a gene cluster encoding other enzymes of the ribulose monophosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 16; Length 165; 100.0%; Pred. No. 1.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 2; Length 164;
100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                            pathway.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 AA; 18835 MW; 7A488E4DB5A9C540 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 AA; 17791 MW; 2736F03BB5D1830E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus aureus (strain Mu50 / ATCC 700699).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Firmicutes, Bacillales, Staphylococcus, NCBI_TaxID=158878;
                                                                                                                                                                                                                         EMBL; AF294615; AAM88571.1; -...
GO; GO:0008483; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0009058; F:biosynthesis; IEA.
InterPro; IPR004839; Aminotrans I/II.
InterPro; IRR01917; Aminotrans II.
PROSITE; PS00599; AA_TRANSFER_CLASS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequ
(TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; Aminotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 10v...
T; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABC transporter homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 TLIADIO 87
SEQUENCE FROM N.A.
STRAIN=NCIMB 11268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 TLIADLO 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
SEQUENCE 165 AA;
```

```
24 LLVTLIA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome
SEQUENCE 180 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blr1340 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=USDA 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATPH OR OB2978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tabata S.;
                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                   Q89US1;
                                                                                                                                                                                                                                                                                                                                                                                            Q89US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8EM80
                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                               RESULT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 51
OBEM80
                                                                                                                                                                                                                                                                                                                                                                       289US1
           8 K B B B
                                                                                                                                                                                                                                                                                                                                                                                            ਨੇ
                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21396509; PubMed=11481432;
Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Daris R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
Sinorhizobium meliloti pSymA megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 392:353-358(1998).

-!- SIMILARITY: BELONGS TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL REGULATORS.

EMBL, ABO00682; AAC06593.1; -.

PIR; G70325; G70325.

G0; G0:0003700; F:transcription factor activity; IEA.

G0; G0:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16; Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE007234; AAK65097.1; -.
PIR; G95316; G95316.
G0; G0:0046821; C:extrachromosomal DNA; IEA.
Hypochetical protein; Plasmid; Complete proteome.
SEQUENCE 171 AA; 19006 MW; 23995EE398413CA0 CRC64;
                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNM-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein RA0439.
RA0439 OR SMA0809.
Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymA (megaplasmid 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Transcriptional regulator (TETR/ACRR family).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.4e+02;
                                                                                                                                        171 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. wv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; Score 7; I
100.0%; Pred. No.
                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1998 (TrEMBLrel. 07, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
Les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                     PRELIMINARY;
|||||||
63 KLLQSEN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 PTEAVAQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PTEAVAQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACRR3 OR AQ 281.
Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         066635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               066635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 49
066635
                                                                                         RESULT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                              0922177

0002

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

0003

000
                         원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22484999; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=HTE831 / DSM 14371 / JCM 11309;
MEDLINE=22250767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genomic sequence of nitrogen-fixing symbiotic bacterium Baddyrhicobium japonicum USDA110.";
DNA Res. 9:189-197(2002)
EMBL; AP005939; BAC46605.1; -.
                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٥;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                   Query Match 2.1%; Score 7; DB 16; Length 179; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 16; Length 180;
100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0; Indels
                                           PRINTS; PR00455; HTHTETR.
DNA-binding; Transcription regulation; Complete proteome.
SEQUENCE 179 AA; 20720 MW; 1E56B2FDA4B4C850 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
H(+)-transporting ATP synthase delta chain (EC 3.6.1.34)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 AA; 18714 MW; 60C7654EAE004943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                              180 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OSEMBO;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
InterPro; IPR001647; HTH_TetR.
Pfam; PF00440; tetR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 100..
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bradyrhizobium japonicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                        155 LAKIILF 161
                                                                                                                                                                                                                                                                                                           100 LAKILLF 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 LLVTLIA 84
```

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8N7X8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8YRB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08N7X8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28YRB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8N7XB
                   KAR REPERENT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND DR KETT AND D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC OC OS STAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=SV129;
MEDLINE=20016253; PubMed=10547268;
Silva A.M., Bottrel R.L.A., Reis L.F.L.;
"Identification and partial characterization of FRAG-6, a novel interferon-stimulated gene that is expressed in an IRF-1-independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
EMBL, AP004603; BAC14934.1; -.. GG; GO:0016787; F: Hydrolase activity; IEA. GG; GO:0016787; F: Hydrolase activity; IEA. GG; GO:0016592; P: Proton transport; IEA. GG; GO:0015929; P: Proton transport; IEA. RIMERPRO; IRRO00711; ATPSynt_OSCP. Pram; PF00213; OSCP; 1.. PRINTS; PR00125; ATPSEDELTA. RIGHTANS; PR01145; ATP SYNT delta; 1.. RPCSITE; PS00399; ATPASE_DELTA; 1.. RHYDrolase; Complete protecome. SEQUENCE 181 AA; 20306 MW; IEE81347B683D4AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
2.1%; Score 7; DB 16; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 11; Length 185; 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 185
185 AA; 21318 MW; 843031FA1EB3C54B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, Created) 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-RIMD 2210633 / Serotype 03:K6;
MEDLINE=22508454; Pubmed=12620739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine 11:813-821(1999).
EMBL, U76754; AAB92383.1; --
Hypothetical protein.
NON TER 185 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q87175;
01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio parahaemolyticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 LVADFLE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 LCGTNEK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 LVADFLE 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCGTNEK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       055132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          manner."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPA0731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 53
207175
AC 0087171
AC 0087171
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               055132
             OR KER DER OR SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \stackrel{>}{\circ}
```

```
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K., Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S., Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T., "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae.";
Lancet 361:743-749(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ40235.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=21595285; PubMed=11759840; Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., "Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Match 2.1%; Score 7; DB 16; Length 191; Local Similarity 100.0%; Pred. No. 1.5e+02; es 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBL_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                            Pfam; PF00691; OmpA; 1.
PRINTS; PR01021; OMPADOMAIN.
Hypothetical protein; Complete proteome.
SEQUENCE 187 AA; 20814 MW; F8A1476C6DE32B17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 AA; 22465 MW; AE36336359FC90DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Alx3529.
                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 16; Les
100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cyanobacterium Anabaena sp. strain PCC 7120.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 8:205-213(2001).

EMBL, AP003593, BAB75228.1; -.

HIR, AB2247, AB2247.

Hypothetical protein; Complete proteome.

SEQUENCE 191 AA; 22465 MW; AB3633635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                      EMBL; AP005086; BAC62074.1; -. InterPro; IPR006664; Bac_OmpA. InterPro; IPR006665; OmpA/MotB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 QSENYVT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 OSENYVT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 LIADLOL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 LIADLOL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606
```

ठ

```
Best Local Similarity 100.
Matches 7; Conservative
                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 LYSSGLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYSSGLL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mesorhizobium loti,
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pMLa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                Q8NBD8
Q8NBD8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0981K6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q981K6
RESULT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 58
                                        QSNBDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93186C
                                                                                                      A PACA REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT REPORT RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                            Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamanhita H., Matsuo K., Nakamura Y., Sekine M., Kimura K., Wanashita H., Sakine M., Sakine M., Sakine M., Sakine M., Sugano S., Nakamura K., Masubo Y., Nagai K., Isogai T., Nubo human cDNA sequencing project."; Submitted (UIL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AK097554; BAC05098.1; "InterPro; IRPO110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THIOLESTER FORMATION (BY SIMILARITY).

-1- SIMILARITY BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.

EMBL, BCO06827, AAH06827.1; -

GO, GO:0016874; F:ligase activity; IEA.

GO, GO:0004840; F:ubiquitin-protein ligase activity; IEA.

GO, GO:000512; P:ubiquitin-protein ligase activity; IEA.

InterPro; IPR006069; UBQ_conjugat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE = AMP + DIPHOSPHATE + PROTEIN N-UBIQUITYLLYSINE.
-!- PATHWAY: UBIQUITIN CONJUGATION; SECOND STEP.
-!- MISCELLANBOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypochetical ubiquitin-protein ligase (EC 6.3.2.19) (Ubiquitin-conjugating enzyme E2) (Ubiquitin carrier protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 4; Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 4; Length 199; 100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                               al protein.
197 AA; 21283 MW; 4E6807E266357A25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Ligase; Ubl conjugation pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 AA; 22836 MW; 0523FA017EBE8820 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. No. -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1.,
100.0%; Pred. No. -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONJUGAT 2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00179; UQ con; 1.
ProDom; PD000461; UBQ conjugat; 1.
PROSITE; PS50127; UBIQUITIN_CONJUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 ILEKODK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 ILEKQDK 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
Hes 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 NLAILEK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q96J08
Q96J08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 56
109640
10 AC 09640
DT 01-DE
DT 01-DE
DT 01-DE
DT 01-DE
DE (Fraging)
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mamma
OC Mam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
```

ð g

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Small intestine;

Anehori K. Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,

Anehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,

Anani H., Wattanabe S., Ishida S., Ono Y., Hotuta T., Wattanabe M.,

Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,

Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,

A Kimura K., Matsuko K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

Magatsuma M., Takahashi-Fujia A., Oshima A., Kawakami B.,

Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

T. Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AK096942; BAC04908.1;

EMBL; AK096942; BAccuase-like.

REN: PPEONTS: lactamase-B; 1.

Repair PPO0753; lactamase-B; 1.

Rypothetical protein.

SEQUENCE 199 AA; 22330 MW; 90A97FC36AlAD66A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Marsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.1%; Score 7; DB 16; Length 201; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 4; Length 199; 100.0%; Pred. No. 1.6e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid, Hypothetical protein, Complete proteome. SEQUENCE 201 AA; 23755 MW; 4E410B65A26DE7A1 CRC64;
                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein ml19335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 7:331-338(2000).
EMBL; AP003015; BAB54703.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium loti (Mesorhizobium loti),
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MAFF303099;
MEDLINE=21082930; Pubmed=11214968;
                                                                                                                                                                                       Hypothetical protein FLJ39623.
```

```
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228 SLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 SLKLLGE 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 RDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 RDLKKTA 115
                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                 NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NDIVA833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9D614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               018347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      018347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sera."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9D614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                018347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9D614
  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E E E E E E E E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Labibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y., A Habibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y., A Hottua T., Hizaoka S., Murakawa K., Takiguchi S., Kusano J., Matanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y., Sugiyama T., Irie R., Otsuki T., Sato H., Wakmatsu A., Ishii S., Kimura K., Matsuo K., Nakamura Y., Sato H., Wakmatsu A., Ishii S., R., Yamamoto J., Isono Y., Rawai-Hio Y., Satio K., Nishikawa T., Rahda K., Nakamura Y., Satio K., Nishikawa T., Kanda K., Nakamura Y., Satio K., Nishikawa T., Kanda K., Nakamura Y., Satio K., Nishikawa T., Kanda K., Nakamura Y., Satio K., Nishikawa T., Kanda K., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T., Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

C. C. TINCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER PROTEINS (BY SIMILARIYY).

C. C. CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE = AMP + PROTEINS (BY SIMILARIYY).

C. C. PATHWAY: BLOONTOATION (SECOND STER).

C. DATHWAY: BLOONTOATION (BY SIMILARIYY).

C. C. PATHWAY: BLOONTOATION (BY SIMILARIYY).

C. C. SIMILARIY: BREDONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.

DR GO: GO: 0004440; F: Ubiquitin conjugating enzyme activity; IEA.

GO: GO: 0004440; F: Ubiquitin nonjugating enzyme activity; IEA.

DR GO: GO: 0004440; F: Ubiquitin cycle; IEA.

DR HOFFM: PROFILE CONJUGAT.

DR GO: 00004440; F: Ubiquitin cycle; IEA.

DR HOFFM: PROFILE CONJUGAT.

DR HOO: GO: 00004440; F: Ubiquitin cycle; IEA.

DR HOFFM: PROFILE CONJUGAT.

DR HOFFM: PROFILE CONJUGAT.

DR HOFFM: DR HORD CONJUGAT.

DR HOFFM: DR HORD CONJUGAT.

DR HOFFM: DR HORD CONJUGAT.

DR HOFFM: DR HORD CONJUGAT.

DR HOFFM: DR HORD CONJUGAT.

DR HOFFM: DR HORD CONJUGAT.

DR HOFFM: DR HORD CONJUGAT.

DR HOFFM: DR HORD CONJUGAT.

DR HOFFM: DR HORD CONJUGAT.

DR HOFFM: DR HORD CONJUGAT.

DR HOFFM: DR HORD CONJUGAT.

DR HOFFM: DR HORD CONJUGAT.

DR HOFFM: DR HORD CONJUGAT.

DR HOFFM: DR HORD CONJUGAT.

DR HOFFM: DR HORD CONJUGAT.

DR HOFFM: DR HORD CONJUGAT.

DR HOFFM: DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ31826 (EC 6.3.2.19) (Ubiquitin-conjugating
enzyme E2) (Ubiquitin-protein ligase) (Ubiquitin carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probom; PR00179; UQ con; 1—Probom; PR00179; UQ con; 1—Probom; PD000461; UBQ conjugat; 1.
PROSITE; PS50127; UBIQUITIN_CONJUGAT 2; 1.
Hypotherical protein; Ligase; Ubl conjugation pathway.
SEQUENCE 217 AA; 24277 MW; 3C74AF937AE2BCCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.7e+02;
                                                                                                                                                                                                      217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 4
100.0%; Pred. No. 1.7
Live 0; Mismatches
                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, OSJUBA0067K08.19 protein.
                                                                                                                                                                                                                                                     (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                      235
                                                                  173 LKLLGEL 179
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 NLAILEK 27
                      LKLLGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OSJNBA0067K08.19
                                                                                                                                                                                                                                                     01-DEC-2001
01-DEC-2001
                   229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                       protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q7XQH7
Q7XQH7;
                                                                                                                                                                                                                               296MV4;
                                                                                                                                                                                                    096MV4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                               RESULT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7XQH7
                                                                                                                                                                                                 HID DEPTH OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF T
                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
```

```
Subsequence round with the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dirofilaria immitis (Cánine heartworm).
Eukaryota, Metazoa, Nematoda, Chromadorea, Spirurida, Filarioidea,
Onchocercidae, Dirofilaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tripp C.A., Wisnewski N.; "Dirofilaria immitis larval cDNA clone isolated with immune dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 10; Length 218; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 5; Length 221;
100.0%; Pred. No. 1.7e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEAM; PF00188; SCP; 1.
PRINTS; PR00837; VSTPXLIKE.
ProDom; PD000542; Allrgn, V5/Tpx1; 1.
SMART; SMO199; SCP; 1.
PROSITE; PS01010; SCP AG5 PR1 SC7 2; 1.
SEQUENCE 221 AA; 25158 MW; 5542B42B455046F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
2900024010Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venom allergen antigen 5-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF001100; AAB62535.1; -
GO; GO:0005576; C:extracellular; IEA.
InterPro; IPR001283; Allrgn_VS/Tpx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
```

. 0

·,

```
Pfam; PF00665; rve; 1.
                                            Complete proteome.
SEQUENCE 222 AA;
                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9BVX5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q82P19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9BVX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q82P19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9BVX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCOCCOS ON THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                 RA Arawa T., Hara A., Shipata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shipata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Alazawa K., Izawa M., Nishi K., Kiyosawa H., Komo S., Yamanaka I., Saito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Richel P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Baraki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Bromstein M.J., Bult C., Fletcher C., Fujita M., Gariholdi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyono P., Marchionni L., Mashima J., Mazzarelli J., Nombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whittaker C., Whittaker C., Wilming L., Marshiya Y., Kawaji H., Kohtsuki S., Ayashizaki Y., Yashida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22272406; PubMed=12384590; MEDLINE=22272406; PubMed=12384590; Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Vang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; Score 7; DB 11; Length 221; 100.0%; Pred. No. 1.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00753; laccamase B; 1.
SEQUENCE 221 AA; 24486 MW; 9A604DFBE6B64DFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          through comparison with genomes of Es
Nucleic Acids Res. 30:4432-4441(2002)
                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Hippocampus; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AKO13594; BAB28918.1; -.
MGD; MGI:1920102; 2900024010Rik.
InterPro; IPR001279; Blactmase-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae; Shigella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001)
2900024010RIK.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Putative transposase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYSSGLL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 LYSSGLL 79
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 083534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 63
Q83.5.4
AC Q83.5.4
AC Q83.5.4
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-JUJ
DT O1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
Sakaki Y., Hattori M., Omura S.;
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence and comparative analysis of the industrial microorganism Streptcomyces avermitilis.";
Nat. Biotechnol. 21:526-531 (2003).
EMBL; APO05025; BAC68824.1; -
Hypothetical protein; Complete protecome.
SEQUENCE 227 AA; 23392 MW; BD9D02BE1BF9D08A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical ubiquitin-protein ligase (EC 6.3.2.19) (Ubiquitin-conjugating enzyme E2) (Ubiquitin carrier protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL B165;
MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa U., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                  2.1%; Score 7; DB 16; Length 222; 100.0%; Pred. No. 1.8e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 16; Length 227; 100.0%; Pred. No. 1.8e+02; tive 0; Mismatches 0; Indels
222 AA; 24899 MW; 5E42A1062243F9EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Query Match
Best Local Similarity 100...
Best Local Similarity 7; Conservative
                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
                                                                                                                                                                       145 MLRECIR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Fragment).
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 EÁVÁGLÁ 217
                                                                             Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 EAVAQLA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003
```

```
Matches
                                RESULT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q87RH6
                                                                                                       ACCOS SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SELECT SEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                       C -1- CATALYTIC ACTIVITY: ATP , UBLOUITIN + PROTEIN LYSINE = AMP + DIPHOSPHATE + PROTEIN N-UBLOUITIN. PROTEIN LYSINE = AMP + DIPHOSPHATE + PROTEIN N-UBLOUITING; SECOND STEE.

-1- PATHWAY: UBLOUGH CONUTGATION; SECOND STEE.

-1- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBLOUITIN-
THIOLESTER FORMATION (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE UBLOUITIN-CONUTGATING ENZYME FAMILY.

EMBL; BC000648; AH00848 a.j.

GO; GO:000448; Fubliquitin conjugating enzyme activity; IEA.

GO; GO:0004812; Fubliquitin-protein ligase activity; IEA.

GO; GO:0006812; Publiquitin-protein ligase activity; IEA.

GO; GO:0006812; Publiquitin-protein ligase activity; IEA.

RD; GO:0006813; D:0-Conj. 1.

R ProDom; P0001961; UBQ.conjugat;

R ProDom; P0001461; UBQ.conjugat; 1.
                                                                 Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER
- PROTEINS (BY SIMILARITY).
- PROTEINS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.,
Submitted (MAY-2002) to the BMBL/GenBank/DDBJ databases.
BMBL, BCG30044; AAH3004.2; -..
GO; GO:00044; AAH30012018Rik.
GO; GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.
GO; GO:0004840; F:ubiquitin cycle; IEA.
InterPro; IPR000609; UBQ_conjugat.
Fram; PF00179; UQ_con; 1.
PR0SITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 230; 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 11; Length 231
100.0%; Pred. No. 1.8e+02;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE, PS50127; UBIQUITIN CONJUGAT 2; 1.
Hypothetical protein; Ligase; Ubl conjugation pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 230 AA; 25882 MW; 97C13304B8E1D6E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 AA; 26011 MW; BDFCB7D7F5D51F1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2002 (TrEMBLrel. 22, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 2.1%; Score 7; DB 4 Best Local Similarity 100.0%; Pred. No. 1.8 Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN cDNA 2310012M18 gene (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 NLAILEK 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 NLAILEK 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
[1]
SEQUENCE FROM N.A.
                                               TISSUE=Cervix;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2310012M18RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8K2T0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·.
                                                                                                                                                                                                                                                                                                                                                       Hashimoto Y., Hayakawa T., Ueno Y., Fujita T., Sano Y., Matsumoto T., "Sequence analysis of the Plutella xylostella granulovirus genome.";
Virology 275:358-372(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=RIMD 2210633 / Serotype 03:K6;
MEDLINE=22508454; PubMed=12620739;
MakDinnE=22508454; PubMed=12620739;
MakDinnE=22508464; PubMed=12620739;
MakDino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Tijima Y., Najima M., Nakano M., Yamashita A., Kubota Y.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahasemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
Lancet 361:743-749(2003).
EMBL; AP005075; BAC55081.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                       deDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibrio parahaemolyticus.
Batceria, Proteobacteria, Gammaproteobacteria, Vibrionales,
Vibrionaceae, Vibrio.
NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 12; Length 251; 100.0%; Pred. No. 1.9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 16; Length 251; 100.0%; Pred. No. 1.9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Virôlogy 275:358-372(2000).
EMBL; AF270937; AAG27353.1; -.
Interpro; IPR007983; Bendo LEF-1.
Fram; PP05149; Bendo LEF-1; 1.
SEQUENCE 251 AA; 29931 MW; 167FB1736F7B9FB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 AA; 26482 MW; 2FE09CD409388D45 CRC64;
                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
       251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                               MEDLINE=20455581; PubMed=10998336;
                                                                                                                                                                               Plutella xylostella granulovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002781; DUF81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100..
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01925; DUF81; 1.
Complete proteome.
SEQUENCE 251 AA. 2640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 NLLRDKS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 SGLLVTL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 SGLLVTL 82
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                               NCBI_TaxID=98383;
                                                                                                                          PXORF55 peptide.
                                                                                                                                                                                                          Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q87RH6;
  09DVX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q87RH6
```

RESULT 69

```
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCOCCOOR REPAREMENT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; Manlysis of the mouse transcriptome based on functional annotation of 60,770 full-length oDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Tongue;
MEDLINE=20499374; PubMed=11042159;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatava N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and Subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CSTBL/60; TISSUE=Tongue;
Arakawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai C.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahabhi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muzamatsu M., Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/61; TISSUE-Tongue;
MEDLINE-20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazawa M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Masuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
                                                                                  01-MAR-2003 (TENNBLEE) 23, Last sequence update)
01-OCT-2003 (TENNBLEE) 25, Last amotation update)
01-OCT-2003 (TENNBLEE) 25, Last amotation update)
01-OCT-2003 (TENNBLEE) 25, Last amotation update)
01-OCT-2003 (TENNBLEE) 25, Last amotation update)
02.310012M18RIK.
Mus musculus (Mouse).

Bukaryota; Metazoa; Ohordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CS7BL/6J; TISSUE-Tongue;
MEDLINE=99279253; PubMed=10349636;
Carninol P., Hayashizaki Y.;
Chigh-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                   253 AA
                                                               (TrEMBLrel. 17, Created)
                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CS7BL/6J; TISSUE=Tongue;
MEDLINE-22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Tongue;
MEDLINE-21085660; PubMed=11217851;
RIKEN FANTOM CONSOTTIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001).
                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                               -JUN-2001
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CETAIN=YS-114 / AJ 12310 / DSM 44549 / JCM 11189;
CETRAIN=YS-114 / AJ 12310 / DSM 44549 / JCM 11189;
CETRAIN=YS-114 / AJ 12310 / DSM 44549 / JCM 11189;
CETRAIN=YS-114 / AJ 12310 / DSM 44549 / JCM 11189;
CETRAIN=YS-114 / AJ 12310 / DSM 44549 / JCM 11189;
CETRAIN=YS-114 / AJ 12310 / DSM 44549 / JCM 11189;
CETRAIN=YS-124 / JCM ASSHIMM J., HIND Y., Kikuchi H., Nakamura Y.,
CETRAIN=YS-124 / JCM ASSHIMM J., IICH T., Yamagishi A., Nishio Y.,
CETRAIN=YS-124 / JCM ASSHIMM J., IICH T., Yamagishi A., Nishio Y.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN=YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM ASSHIMM J.,
CETRAIN-YS-124 / JCM A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; Score 7; DB 16; Length 253;
100.0%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
2.1%; Score 7; DB 11; Length 253
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2e+02;
                                                                                                                                                                                                               Pfam; PF00179; UQ_con; I.
ProDom; PD000461; UBC_conjugat; 1.
SMART; SM00212; UBCC; UBC, UBC, UBCO; UBCO; UBCO; UBCO; UBCO; UBCO; UBCO; UBCO; SEQUENCE 253 AA; 28487 WW; 8FB9519FP26585CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 AA; 27807 MW; 51AB97E3BFBC0CB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similar to NICR-5 protein homolog. 3010021M21RIK.
10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium efficiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putative transposase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 YEKLLQS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 YEKLLOS 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 NLAILEK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
Genome Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8BVX5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8FS91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBBVX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 71
```

ó

```
67 AQLAQEL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Linaria canadensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNW2110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      084RB8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7U4F8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q7U4F8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q84RB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07U4F8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q84RB8
                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCOC ON SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVING SERVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                    the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dev. Biol. 252:202-213(2002).

Dev. Biol. 252:202-213(2002).

EMBL; RESZP3; CARGES66.2; --

EMBL; AY151209; AAN72826.1; --

PIR; T23866; T23866.

HSSP; PI4653; 1B7.

WormPep; R03C1.33, CE25964.

GO; GO:0003504; C:nucleus; IEA.

GO; GO:0003505; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Palmer R.E., Inoue T., Sherwood D.R., Jiang L.I., Sternberg P.W.; "Caenorhabditis elegans cog-1 locus encodes GTX/Nkx6.1 homeodomain proteins and regulates multiple aspects of reproductive system
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                  Nature 420:563-573 (2002).

BMBL; AK076148; BAC36218.1; -.

MGD; MGI:1924088; 3010021M21Rik.

GG; GG:0004440; F:ubiquitin conjugating enzyme activity; IEA.

GG; GG:0006512; F:ubiquitin cycle; IEA.

InterPro; IPR000608; UBQ_conjugat.

Pfcm, PP00179; UQ_con; 1.

SMART; SM00212; UBC.

SMART; CR00121; UBC.

SEQUENCE 255 AA; 28916 MW; 2F5077B3FAC2D6DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11; Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steward C.A.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Scc.
v 100.0%; Pred. No. 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=22370693; Pubmed=12482710;
                                                                                           SEQUENCE FROM N.A.
STRAIN-CSTBL/6J, TISSUE=Head;
MEDLINE=22354683; PubMed=12466851;
The PANTOM CONSORTIUM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN'1998 (TrEMBLrel. 05, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R03C1.3 protein (COG-1A).
R03C1.3 OR COG-1.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 NLAILEK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        017978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            017978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 72
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=22569055; PubMed=12679544;
Hileman L.C., Baum D.A.;
"Why Do Paralogs Persist? Molecular Evolution of CYCLOIDEA and Related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids, lamids, Lamiales, Plantaginaceae, Antirrhineae, Linaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22825697; PubMed=12917641;
Palenik B., Brahamaha B., Larimer F.W., Land M., Hauser L., Chain P., Lamerdin J., Regala W., Allen B.E., McCarren J., Paulsen I., Dufreene A., Partensky F., Webb E.S., Materbury J.;
"The genome of a motile marine Synechococcus.";
Nature 424:1037-1042(2003).
EMBL; BX569694; CE08625.1; -.
Complete protecome.
SEQUENCE 258 AA; 27641 MW; 419DDAF0E8894F3E CRC64;
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 16; Length 259; 100.0%; Pred. No. 2e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                   DNA-binding; Homeobox; NucTear protein.
SEQUENCE 256 AA; 28046 MW; E961B929941CC719 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hacteria, Cyanobacteria, Chroococcales, Synechococcus.
NCBI_TaxID=84588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative ABC transporter, multidrug efflux family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                             Query Match 2.1%; Score 7; DB 5; L
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0
              IPR000047; HTH lambrepressr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DICHOTOMA-like protein (Fragment).
                                                             PRINTS; PRO00024; HOMEOBOX.
PRINTS; PRO0031; HTHREPRESSR.
Probom; PD000010; Homeobox; 1.
SMART; SM01389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
InterPro; IPR001356; Homeobox,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                 InterPro; IPR000047; HTE
Pfam; PF00046; homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                        200 AQLAQEL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 LRRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 LRROIGT 102
```

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              053442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9X793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     053442
                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 78
053442
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 77
             ACA CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT O
                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamiids, Lamiales, Plantaginaceae, Antirrhineae, Linaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hileman L.C., Baum D.A.; "Wolecular Evolution of CYCLOIDEA and Related "Why Do Paralogs Persist? Molecular Evolution of CYCLOIDEA and Related
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                  2.1%; Score 7; DB 10; Length 264; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 2.1%; Score 7; DB 10; Length 267; Local Similarity 100.0%; Pred. No. 2.16+02; les 7; Conservative 0; Mismatches 0; Indels
Floral Symmetry Genes in Antirrhineae (Veronicaceae).";
Mol. Biol. Evol. 20:591-600(2003).
EMBL; AF512589; AAP03336.1; -.
Inter; PF03634; TCP.
Pfam; PF03634; TCP.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floral Symmetry Genes in Antirrhineae (Veronicaceae)."; Mol. Biol. Evol. 20:591-600(2003). EMBL, AF512290; AAP03337.1; ... InterPro; IPR005333; TCP.
                                                                                                                                  264 264
264 AA; 29428 MW; FEC08C31C452AB5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 AA; 29874 MW; 6DF6F2DBA2DA08CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, Created) 01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-CCT-2003 (TrEMBLrel. 25, Last annotation update) DICHOTOWA-like protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Dynamin-like 120 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                               267 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22569055; PubMed=12679544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Liver;
MEDLINE=22354683; PubMed=12466851;
The FANTOM CONSORTIUM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Linaria vulgaris (Toadflax)
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF03634; TCP; 1.
NON TER 1
                                                                                                                                                                                                                                                                                        218 QSENYVT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                             244 QSENYVT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 QSENYVT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 QSENYVT 253
                                                                                                                                                                                                                  Local Similarity
tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=43171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                           NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q84RB7;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q84RB7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8BKU7
                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 76
                                                                                                                                                                                                                                                                                                                                                                                                                 RT
DR
DR
DR
FT
SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,70 clul-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AKOSO383; BAC34224.1; -.
EMBL; AKOSO383; Carticolopian, IDA.
NGD; MCI 1921393; Carticolopian; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21128732; PubMed=11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Whugall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Squares S., Stevens K., Simon S., Simmonds M., Skelton J., Squares R.,
Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leproma, Mil952; -. GO, GO:0045300; F:acyl-[acyl-carrier protein] desaturase acti. GO; GO:0006631; P:fatty acid metabolism; IEA. InterPro; IPR005067; FA desat. FA prim; PF03405; FA desaturase 2; 1.
                                                                                                                                                                                                                                                                                                                                                       .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium leprae.
Bacteria, Actinobacteridae; Actinomycetales;
Corymebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 11; Length 272; 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 16; Length 275; 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                272 AA; 31438 MW; 9152E557CF9A21F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 AA; 31139 MW; 06C1B9F70B7DE46C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011[5001].
BEBL; AL049491; CAB39827.1; -
EMBL; AL583923; CAC30907.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DESA2 OR ML1952 OR MLCB1222.21.
                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acyl-[ACP] desaturase
                                                                                                                                                                                                                                                                                                                                                                                                         231 LLGELIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 LIGELIL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR, C87153; C87153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 ILKDNLA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 ILKDNLA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
                                                                                                                                                                                                   NON TER
SEQUENCE
```

```
TIGR; MT1126; -..
Tuberculist; Rv1094; -.
GO; GO:0045300; F:acyl-carrier protein] desaturase acti. . .; IEA.
GO; GO:0046531; P:fatty acid metabolism; IEA.
InterPro; IPR005067; FA_desat.
Pfam; PF03405; FA_desaturase_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CDC 1551 / Oshkosh,
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Hickey E.,
Feterson J., DeBoy R., Godson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Trekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., Mohean J., Moule S., Murphy L.,
Oliver S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                Stearoyl-acyl carrier protein desaturase (Acyl-(acyl-carrier-protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last nontation update)
Possible acyl-[acyl-carrier protein] desaturase DESA2 (Acyl-[ACP] desaturase) (Stearcyl-ACP desaturase) (BC 1.14.19.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.1%; Score 7; DB 16; Length 275; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL021897; CAA17210.1; -.
EMBL; AE006993; AAK45384.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 AA; 31359 MW; 448D136940150E99 CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 275 AA.
                                                                 desaturase, putative).
DESA2 OR RV1094 OR MTV017.47 OR MT1126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=AF2122/97;
MEDLINE=22709107; Pubmed=12788972;
                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; D70896; D70896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 ILKDNLA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 ILKDNLA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
                                                                                                                                                                                                                                             NCBI TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESA2 OR MB1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27U0P0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           040U1C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q7U0P0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDT READ BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECOND BY SECO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
Schreiber W., Durre P., "The glyceraldehyde-3-phosphate dehydrogenase of Clostridium acetobutylicum: isolation and purification of the enzyme, and sequencing and localization of the gap gene within a cluster of other glycolytic genes.";
                           Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R., Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.; "The complete genome sequence of Mycobacterium bovis.", Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).

EMBL; BX248337; CAD93985.1; ---
SEQUENCE 275 AA, 31359 MW, 448D136940150E99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
Camus J.-C., Medina N., Mansoor H.
                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 16; Length 275; 100.0%; Pred. No. 2.1e+02; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 2; Length 276; 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microbiology 145:1839-1847(1999).

EMBL; AF043386; AAC13159.1; -.
GO; GO:0030246; F:carbohydrate binding; IEA.
GO; GO:0030258; F:transcription regulator activity; IEA.
InterPro; IPR007324; Sugar-bind.
PF04198; Sugar-bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 276 AA; 30045 MW; 8B153308AECB11AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Similar to RIKEN cDNA 2900024010 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last seq 01-JUN-2003 (TrEMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99392446; PubMed=10463150;
Garnier T., Eiglmeier K.,
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 EIVKILK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 ILKDNLA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 ILKDNLA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 EIVKILK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium.
NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=DSM 792;
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   052630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8IY16
                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 80
052630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 81
Q81Y16
   DDT DDT READ BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND BY STAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

```
100 IFWNILR 106
                                                                                                                                                                                                                                                                                                                                                                                  APPC OR SPR1192.
                                                                                                                                                                                                                                                                                                           QBDPF4
QBDPF4;
                                                                                                                                                                                                                                                                                       RESULT 84
        à
                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                             2900024010RIK.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                   QBBL86;
U-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical metallo-beta-lactamase superfamily containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 7; DB 11; Length 279;
100.0%; Pred. No. 2.1e+02;
                                                                                  Length 279;
                                                                                                     0; Indels
         Strausberg R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                            EMBL; BC038220; AAH38230.1; -.
InterPro; IPR001279; Blactmase-like.
Pfam; PF00753; lactamase_B; 1.
SEQUENCE 279 AA; 3134I MW; 6343E17E62DC492D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 279 AA; 31206 MW; 83F882FF44580DF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2001 (TrEMBLrel. 18, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                              Query Match
2.1%; Score 7; DB 4; Ler
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AK046032; BAC32577.1; -. MGD; MGI:1920102; 2900024010Rik. InterPro; IPR001279; Blactmase-like. Pfam; PF00753; lactamase_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2001 (TrEMBLrel. 18, Created)
                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Brain;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Predicted methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
7; Conserve
                                                                                                                       73 LYSSGLL 79
                                                                                                                                         57 LYSSGLL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 LYSSGLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LYSSGLL 63
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1488;
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .16M760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAC0307
                                                                                                                                                                                           08BL86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q97M91
                                                                                                                                                                      RESULT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 83
                                                                                                                                                                                08BL86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RC
RA
DR
DR
SQ
SQ
                                                                                                                       ò
                                                                                                                                         g
                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

```
.
0
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., dibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing J. Benterium Clostridium accetobutylicum."; J. Bacteriol. 183:4823-4838 (2001).

E. MBL. ARCONST45: AAK78288.1; -
D. Bacteriol. 183:4823-4838 (2001).

E. MBL. ARCONST45: AAK78288.1; -
D. R. CO. GO. 0008168; F:nethyltransferase activity; IEA.

GO; GO. 0016740; F:transferase activity; IEA.

GO; GO. 0016740; F:transferase activity; IEA.

GO; GO. 0016740; F:transferase activity; IEA.

InterPro; IPRO008189; Corfpor Metransf.

InterPro; IPRO008189; Corfpor Metransf.

InterPro; IPRO008189; UST Metransferase; Complete protecome.

TIGRRAMS; TIGRO0096; TIGRO0096; I.

TIGRRAMS; TIGRO0096; TIGRO0096; I.

Transferases Methyltransferase; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21429245; PubMed=11544234; Hoskins J. Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAharey M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glass J.I.;

"Genome of the bacterium Streptococcus pneumoniae strain R6.";

"Genome of the bacterium Streptococcus pneumoniae strain R6.";

R BEL; AE008491; AAK999955.1;

R BGJ; G98020; G98020.

R GO; G0:0016020; G:membrane; IEA.

R GO; G0:0005215; F:transporter activity; IEA.

R GO; G0:0005215; F:transporter activity; IEA.

R GO; G0:0005215; BPD transporter

R InterPro; IPR000437; Prox lipoprot_S.

R InterPro; IPR000437; Prox lipoprot_S.

R Pfam; PF00528; BPD transp; I.

R PROSITE; PS00013; PROXAR LIPOPROTEIN; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 16; Length 283;
100.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter membrane-spanning permease-oligopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 AA; 31981 MW; EEC11B67310E6C1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 AA; 31176 MW; A08B18E83E18B750 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 16; Le
100.0%; Pred. No. 2.1e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 2.20
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 ROSLKLL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 ROSLKLL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=171101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
SEQUENCE 283 AA;
```

```
089402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   089402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    089402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDTDDTTDDTDDTTDDTDDTTDDTDDTTDDTDDTTDDTDDTTDDTDDTDDTTDDDTTDDTDDTTDDTDDTTDDTDDTTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDDTDD
₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; H89906; H89906.

QO; GO:01016020; C:membrane; IEA.

GO; GO:0004009; F:ATP-binding; IEA.

GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti...; IEA.

GO; GO:0000166; F:Nucleotide binding; IEA.

GO; GO:0000166; F:nucleotide binding; IEA.

InterPro; IPR003593; AAA ATPae.

InterPro; IPR003593; AAA ATPae.

InterPro; IPR003593; ABC_transporter.

Probom; PD000006; ABC_transporter.

Probom; PD0000066; ABC_transporter; I.

SMART; SM00382; AAA; I.
                                                                                                                                                                                                                                                                                                                                  STRAIN=N315;

MUDLINE=21311952; PubMed=11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,

Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,

Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,

Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,

Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T., Hattori M.,

Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22040717; PubMed=12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Baba T., Tuwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
"Genome and virulence determinants of high virulence community-
acquired MRSA.";
Lancet 359:1819-1827(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 16; Length 299; 100.0%; Pred. No. 2.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 299 AA; 34577 MW; 451484C431B3ABF0 CRC64;
                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein SA1156 (WM1206 protein)
SA1156 OR MM1206.
                                                                                                                                                                                                                            Staphylococcus aureus (strain N315), and
Staphylococcus aureus (strain MW2).
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               074388 PRELIMINARY; PRT;
074388;
01-NOV-1998 (TrEMELrel. 08, Created)
                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP003133; BAB42412.1; -. EMBL; AP004826; BAB95071.1; -.
                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                 NCBI_TaxID=158879, 196620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.v
                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 KLLQSEN 221
           189 IFWNILR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 KLLOSEN 69
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aureus.
                                                                                                    099UF7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 86
                                                                  RESULT 85
                                                                                   074388
               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=20478054; PubMed=11021991;
Sun L., Gurnon J.R., Adams B.J., Graves M.V., Van Etten J.L.;
"Characterization of a beta-1,3-glucanase encoded by chlorella virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=95131167; PubMed=7831789; In Z., Li Y., Zhang Y., Kutish G.F., Rock D.L., Van Etten J.L.; "Analysis of 45 kb of DNA located at the left end of the chlorella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Chlorovirus NCBI_TaxID=10506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=20013326; PubMed=10544099; MEDLINE=20013326; PubMed=10544099; Asiser A., Vollmert M., Tholl D., Graves M.V., Gurnon J.R., Xing Lisec A.D., Nickerson K.W., Van Etten J.L.; "Chlorella virus PBCV-1 encodes a functional homospermidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                    Lyne M., Rajandream M.A., Barrell B.G., Jimenez Martinez J; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, ALO31261, CAA20309.1; -.
EMBL, ALO31261, T40402; T40402; T40402; T800029; T80002; T80002; T80002; T80002; T80002; T80002; T80002; T80002; T80002; T80002; T80002; T800025; TRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 3; Length 301; 100.0%; Pred. No. 2.3e+02; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Van Etten J.L.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00498; FHA; 1. --
SMART; SMO0240; FHA; 1. --
PROSITE; PS50006; FHA DOMAIN; 1. SEQUENCE: PS50006; PAA DOMAIN; 1. SEQUENCE PS50006; PAA DOMAIN; 1. SEQUENCE PS50006; PAA PAA; PAA PAA; PAA PAA DAB PAA CRC64;
                                                                                                                                                        Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Forkhead nuclear signalling domain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paramecium bursaria chlorella virus 1 (PBCV-1)
                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-OCT-2003 (TrEMBLrel. 25, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virology 206:339-352(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virology 263:254-262(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virology 276:27-36(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 EEVSKSL 182
                                                                                                                                                                                                                         Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 EEVSKSL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A67R protein.
```

```
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 072A52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            087260
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7ZA52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        087260
              ************
                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=0157:H7 / RIMD 0509952;

MEDLINB=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Complete genome sequence of enterohemorrhagic Escherichia coli comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21074933, Jubmed=1120651;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Maynew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Maynew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
Van Etten J.L.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                          SEQUENCE FROM N.A.
Graves M.V., Van Etten J.L.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                        Gurnon J.R., Graves M.V., Van Etten J.L.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, 142280; AAC96435.1; -.
PIR; T17557; T17557.
                                                                                           Van Etten J.L.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Graves M.V., Van Etten J.L.; Graves M.V., Van Etten J.L.; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 AA; 33210 MW; 5397BE4D0A235C26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Res. 8:11-22(2001).

BMBL; AE005214; AAG54700.1; -.

BMBL; AP0025214; BAB33827.1; -.

PIR; D90679; D906.9.

PIR; H85529; H85529.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0006725; P:aromatic compound metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amnotation update)
2-hydroxy-6-ketonona-2,4-dienedioic acid hydrolase.
MHPC OR 20447 OR ECS0404.
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
2.1%; Score 7; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 TFDIASD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 TFDIASD 126
                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBX5K0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBX5K0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 88

QBX5K0

QBX5K0

AC QBX5K

AC QBX5K

AC QBX5K

AC QBX5K

AC QBX5K

AC QBX5K

AC QBX5K

AC QBX5K

AC QBX5K

AC QBX5K

AC QBX5K

AC QBX5K

AC DBCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

BCCC

  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence and analysis of the 60 kb conjugative, bacteriocin-producing plasmid pMRC01 from Lactococcus lactis DPC3147."; Mol. Microbiol. 29:1029-1038(1998).
EMBL, AECOCY, AAC56050.1; -. PIR, T43122, T43122, T63120.
GO; GO:0046821; C:extrachromosomal DNA, IEA.
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dougherty B.A., Hill C., Weidman J.F., Richardson D.R., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                     .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
                                                                                                                                                                                                                                                                              Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.1%; Score 7; DB 3; Length 312; Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zheng Y.-J., Tao Y., Zhang W., Jordan D.;
"Inhibition of fungal aldose reductase.";
Submitted (MAX-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY033888; AAK55762.1;
                                              InterPro; IRR000639; Epox hydrolase.
InterPro; IRR000379; Ser_estrs.
Pfam; Pr00561; abhydrolase; 1.
PRINTS; PR00111; ABHYDROLASE.
PRINTS; PR00412; EPOXHYDRLASE.
Hydrolase; Complete proteome.
SEQUENCE 309 AA; 34615 MW; E2B51850912969CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 AA; 34368 MW; 10FE14BC676B5C55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
hypothetical protein.
                                                                                                                                                                                                                                                                        Query Match
2.1%; Score 7; DB 16; Le
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
IPR000073; A/b hydrolase. IPR003089; AB_hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99000510; PubMed=9767571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                   253 ENLKLMM 259
                                                                                                                                                                                                                                                                                                                                                                                                                                         189 ENLKLMM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 QSLKLLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 QSLKLLG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactococcus lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=148305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aldose reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=DPC3147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pMRC01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROSB R.P.;
                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
```

```
Query Match
Best Local Similarity 100..
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 390:249-256(1997),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                      59 KEPPTEA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 KEPPTEA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Denizot F.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               006996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              966900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 966900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HDD COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON COCOSON CO
            SYNER
                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=JCM 10545 / 7;

MEDLINE=21456156; PubMed=11572479;

Kawarabayaai Y., Hinon Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Voshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
Oshima T., Kikuchi H.;
"Complete genome sequence of an aerobic thermoacidophilic
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perreten V., Schwarz F., Boeglin M., Cresta L., Dasen G., Teuber M.; "Antibiotic resistance spread in food.";
Nature 391:801-802(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perreten V., Schwarz F., Teuber M., Levy S.B.;
"Mdt(A), a New Efflux Protein Conferring Multiple Antibiotic
Resistance in Lactococcus lactis and Escherichia coli.";
Antimicrob. Agents Chemother. 45:1109-1114(2001).
                                                                 Score 7; DB 2; Length 314; Pred. No. 2.46+02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 2; Length 314;
100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Plasmid.
SEQUENCE 314 AA; 37078 MW; 8533511F7384C177 CRC64;
314 AA; 37078 MW; B6D0B01B2065C525 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0970H0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein ST1624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X92946; CAA63504.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
                                                                 Query Match 2.1%; Score 7; DB 2 Best Local Similarity 100.0%; Pred. No. 2.4 Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=21156959; PubMed=11257023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity luv...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
                                                                                                                                                                                                                                  166 RDFFKYV 172
                                                                                                                                                                                                                                                                                                            182 RDFFKYV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 RDFFKYV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 RDFFKYV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactococcus lactis.
Plasmid pX214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sulfolobus tokodaii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=111955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxiD=1358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sulfolobus
    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             032778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0970H0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 92
0970H0
AC 0970H
AC 0970H
DT 01-DB
DT 01-DB
DT 01-DB
DT 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 01-DB
CO 0
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCOSTABANCE REPAIRS NATION OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE COSTAGE OF THE C
    S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
RA Kunst F. Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Kunst F. Ogasawara N., Bessieres P., Bolotin A., Borchert S.,
RA Parvedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouilet S., Bruschi C. V., Caldwell B., Capuano V., Carter N.M.,
RA Brouilet S., Bruschi C. V., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Brouilet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Britz C., Fujita M., Fujita Y., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haidech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haidech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Nobayashi Y., Kochter P., Kohingstein G., Krogh S., Kumanto M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kobayashi Y., Kotterer P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Barro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Barro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Barro V., Pohl T.M., Portetelle D., Porwollik S., Ropfone F.,
Sakfuchi J., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sakfuchi J., Sakowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takamane M., Patanen M.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Tarkamane M., Vansmotch K., Yasumotco K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT "The Complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                             Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Z94043; CAB08044.1; --
EMBL; Z99121; CAB15458.1; --
EMBL; Z99121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
EMBL, AP000997: BAB66703.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 315 AA; 35692 MW; 3749E62D1671F43B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein yvdo.
                                                                                                                                                                                                                                                                                                              2.4e+02;
hes 0;
                                                                                                                                                                                                                                                                    DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320 AA.
                                                                                                                                                                                                                                                               2.1%; Score 7; DB 1
100.0%; Pred. No. 2.4
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98044033; PubMed=9384377;
```

```
Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QBLIF3
QBLIF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q97YG7
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8LIF2
                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Pectobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=45596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CBS 4435;
Hacker B., Habenicht A., Kies M., Mattes R.;
Hacker B., Habenicht A., Kies M., Mattes R.;
Hacker B., Habenicht Cloning and Characterization of the Xylose Utilisation: Cloning and Characterization of the Xylose Reductase from Candida tennis.";
Submitted (JUN-1998) to the BMBL/GenBank/DDBJ databases.
BMBL, ARC74484; AAC25601.1;
PDB, 1JEZ; 27-5EP-02.
PDB; 1K8C; 27-5EP-02.
GO; GO:0004032; F:aldehyde reductase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
ROJAS C.M., Ham J.H., Kim J.F., Beer S.V., Collmer A.;
"Erwinia chrysanthemi hrp/hrc genes and flanking regions.",
Submitted (CCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY169276; AAO34611.1;
InterPro; IPR008984; SMAD_FHA.
SEQUENCE 321 AA; 35671 MW; 70FEAD778E7A7570 CRC64;
                                                                                                                                                                                                                                            DB 16; Lv...
No. 2.46+02;
0; Indels
                                                                                                                                                                                                                                                                               Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 2; Length 321; 100.0%; Pred. No. 2.46+02; ative 0; Mismatches 0; Indels
                                                                                          InterPro; IPR02641; Patatin.
Pfam; PF01734; Patatin; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 320 AA; 35356 MW; 15909FEA37BC3125 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Xylose reductase (EC 1.1.1.21)
PIR; F70034; F70034.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0045735; F:nutrient reservoir activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322 AA
                                                                                                                                                                                                                                                                 Query Match
2.1%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 2.4
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 ADLOLID 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Erwinia chrysanthemi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 PPTEAVA 130
                                                                                                                                                                                                                                                                                                                                                                                                         84 ADLQLID 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PPTEAVA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Candida tenuis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           084BB3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q84BB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   074237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 94
084BB3
AC 084BB
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DT 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 95
074237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
      SO WE BENEFIT
                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCOCCOS ON THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                     ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Nipponbare;
Sasaki I., Matsumoto I., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Nipponbare;
Sasaki I., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 10; Length 322;
100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                2.1%; Score 7; DB 3; Length 322;
100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone:0J1316_A04[", Submitted (JÜL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone:P0503D09.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databagee.
EMBL; AP003822; BAC06992.1;
EMBL; AP005455; BAC16736.1;
                                                                                                                                                                   Oxidoreductase.
SEQUENCE 322 AA; 36021 MW; 4C74A8FBC9357690 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .l protein.
322 Aa; 37091 MW; 99434DFA7C2DCD21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (P0503D09.26 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0974G7;
01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Endoglucanase precursor (EC 3.2.1.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 AA
InterPro; IPR001395; Aldo/ket_red.
Pfam; PR00248; aldo ket_red; I
PRINTS; PR000029; ALDKETFDTASE;
ProDom; PD000288; ALDKETFDTASE;
PROSTITE; PS00798; ALDKETFO REDUCTASE 1; 1.
PROSTITE; PS00062; ALDOKETO REDUCTASE 2; 1.
PROSTITE; PS00063; ALDOKETO_REDUCTASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR008938; ARM.
InterPro; IPR004892; Mo25.
Pfam; PF03204; Mo25; 1.
                                                                                                                                                                                                                                                                    Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                 298 OPKLIEF 304
                                                                                                                                                                                                                                                                                                                                                                                               200 OPKLIEF 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 FDIASDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 FDIASDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 97
097YG7
ID 097YG
AC 097YG
DT 01-0C
DT 01-0C
DT 01-0C
```

Gaps

```
2.1%; Score 7; DB 2; Length 334;
100.0%; Pred. No. 2.5e+02;
Live 0; Mismatches 0; Indels
       334 AA; 37541 MW; 5935A9489C25EAD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity luv...
7, Conservative
                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
Plasmid IncP-beta R751
                                                                                                                                                          299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 PKLIEFL 305
                                                                               Local Similarity
Les 7; Conserva
                                                                                                                                                                                                          36 PKLIEFL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 PKLIEFL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transposase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thomas C.M.;
          SEQUENCE
                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                     P77600
P77600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QBGGX8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OBGGX8
                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 100
                                                                                                                                                                                                                                                                                     RESULT 99
                                                                                                                                                                                                                                                                                                               P77600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8GGX8
          ဝွ
                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                               ACCOOR NOT THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE READ OF THE REA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESOURNCE FROM N.A.

RECORDINGEROW N.A.

RECORDINGE TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO SUBJECT TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                  Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid IncP-beta R751.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 17; Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Davidson P., Thomas C.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U67194; AAC64435.1; --
EMBL; U60777; AAB03486.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 17; Le
100.0%; Pred. No. 2.5e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0046821; C:extrachromosomal DNA; IEA.
GO; GO:0004677; F:DNA binding; IEA.
GO; GO:0004803; F:transpoasea activity; IEA.
GO; GO:0006313; P:DNA transposition; IEA.
InterPro; IPR003346; Transposase_20.
InterPro; IPR003257; Transposase_9.
Pfam; PF02371; Transposase_9.
Pfam; PF01548; Transposase_9:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                          Sulfolobus solfataricus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 FDIASDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 FDIASDA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                               NCBI_TaxID=2287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thomas C.M.;
                                                                          Sulfolobus.
                                                  Archaea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P77472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P77472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 98
P77472
ID P7747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNPA
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 2; Length 334;
100.0%; Pred. No. 2.56+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Davidson P., Thomas C.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                            Davidson P., Thomas C.M.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thomas C.M.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U67194; AAC64438.1; -.
EMBL; U60777; AAB03489.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 AA; 37449 MW; 46436C5D66CCF2E3 CRC64;
                                                 01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0046821; C:extrachromosomal DNA; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004803; F:rransposase activity; IEA.
GO; GO:0006313; P:DNA transposition; IEA.
   334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq)
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JulerPro; IPR003346; Transposase_20.
InterPro; IPR002525; Transposase_9.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02371; Transposase 20; 1. Pfam; PF01548; Transposase 9; 1.
                                                                                                                                                                                                                                                                                                Enterobacteriaceae; Escherichia.
```

```
Ribera A., Roca I., Ruiz J., Gibert I., Vila J.;
"Partial characterization of a transposon containing the TET A determinant in one clinical isolate of Acinetobacter baumannii.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Acinetobacter.
                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 2; Length 334; 100.0%; Pred. No. 2.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                               EMBL; AY196695; AA038184 1; -...
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0004803; F:transposase activity; IEA.
GO; GO:0006313; P:DNA transposition; IEA.
InterPro; IRFR003346; Transposase 20.
Pfam; PF02371; Transposase 20; 1.
SEQUENCE 334 AA; 37467 MW; D629E2A1933B8F73 CRC64;
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 7; Conservative
                                        Acinetobacter baumannii.
                                                                                                                                                                                                                                                                                                                                                                                              299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serratia marcescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                            36 PKLIEFL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 PKLIEFL 42
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pDU1358.
                                                                                       NCBI_TaxID=470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=615;
           Transposase.
                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q84D05
Q84D05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           084D08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q84D08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 103
                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q84D08
          DOR RELATIONS SOON ON THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF T
                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                           Essa A.M., Julian D.J., Kidd S.P., Brown N.L., Hobman J.L.; "Mercury resistance in Enterobacteriaceae from the pre-antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Essa A.M., Julian D.J., Kidd S.P., Brown N.L., Hobman J.L., "Mercury resistance in Enterobacteriaceae from the pre-antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 2; Length 334; 100.0%; Pred. No. 2.5e+02; vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 2; Length 334; 100.0%; Pred. No. 2.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                            Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF457211, AANB7568.1, -. GO; GO:0003677; F:DNA binding; IEA. GO; GO:0004803; F:transposase activity; IEA. GO; GO:00048031; P:DNA transposation; IEA. InterPro; IPR00313; P:DNA transposase 20. InterPro; IPR003255; Transposase 9. Ffam; PF0217; Transposase 20; I. Ffam; PF0217; Transposase 20; I. SEQUENCE 334 AA; 37423 MW; CC86FE7FB842BADD CRC64;
                                                                                                                                                                                                      InterPro; IPR003346; Transposses 20.
InterPro; IPR002555; Transposses 9.
Pfam; PF00271; Transposses 9; 1.
Fran; PF01549; Transposses 9; 1.
SEQUENCE 334 AA; 37467 MW; FF745E317070903B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                         EMBL; AF457211; AAN87557.1; -. GO; GO:0003677; F:DNA binding; IEA. GO; GO:0004803; F:transposase activity; IEA. GO; GO:0006313; P:DNA transposition; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
 Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 24, C (TrEMBLrel. 24, L) (TrEMBLrel. 25, L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Veery Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
7, Conserve
                                                                                                                                                                                                                                                                                                                                                                       299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                     36 PKLIEFL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 PKLIEFL 42
                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
                                                            STRAIN=M634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transposase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003
01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=M634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q84FH4
Q84FH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OBGGX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DT 01
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

Gaps

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Serratia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.1%; Score 7; DB 2; Length 334; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Essa A.M.M., Hobman J.L., Brown N.L.;

Essa A.M.M., Hobman J.L., Brown N.L.;

Submit Arcas (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; ARCES 12005 1;

GO, GO:00046821; C:extrachromosomal DNA; IEA.

GO, GO:0004681; F:transposase activity; IEA.

GO, GO:000613; P:transposase activity; IEA.

InterPro; IPR003346; Transposase 20.

Pfam; PF02371; Transposase 20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 AA; 37467 MW; D629E2A1933B8F73 CRC64;
                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q84D05
ID Q6
AC Q6
DT 01
DT 01
```

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               093516;
                                                                                                                                                                               07WUV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
                                                                                                                                    RESULT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  093516
                                                                  셤
                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Partridge S.R., Hall R.M.; "18421 and 185075 have sub-terminal inverted repeats and target the terminal inverted repeats of Th21 family Francocca."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Partridge S.R., Hall R.M., "The IS1111 family members IS4321 and IS5075 have sub-terminal inverted repeats and target the terminal inverted repeats of Tn21
                                                                                    Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 2; Length 334; 100.0%; Pred. No. 2.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.1%; Score 7; DB 2; Length 334; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family transposons.";
Submitted (FBB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY123231, AA046066.1;
EMBL; AX242331, AA048506.1;
EMBL; AY242331, AA048504.1;
EMBL; AY242333, AA048504.1;
EMBL; AY242333, FORTENT CONDITIONS OF GO:00048777;
EMBL; AY242331, AA048504.1;
EMBL; AY242331, AA048504.1;
EMBL; AY242331, AA048504.1;
EMBL; AY242331, FORTENT CONDITIONS OF GO:00063131, FORTENT CONDITIONS OF GO:00063131, FORTENT CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDITIONS OF EMBLY CONDIT
                                                                                                                                                                                         Essa A.M.M., Hobman J.L., Brown N.L.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      terminal inverted repeats of Tn21 family transposons."; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                               334 AA; 37481 MW; BD8D1D57DDFA1A72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 AA; 37541 MW; 5935A9489C25EAD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                             334 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003346; Transposase_20.
Pfam; PF02371; Transposase_20; 1.
Plasmid.
SEQUENCE 334 AA; 37541 MW; 5935A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF02371; Transposase_20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enterobacteriaceae, Klebsiella.
                                                                                               Enterobacteriaceae; Serratia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klebsiella pneumoniae.
Plasmid pRMH760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 PKLIEFL 305
                                           Serratia marcescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 PKLIEFL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transposase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLASMID=pRMH760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLASMID=pRMH760;
                                                                  Plasmid pDU1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=573;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                           Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q84H92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           084H92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

Gaps

., 0

```
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Bakes S., Basham D., Brooks K., Chilingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrai J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Mhitehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella enterica servar Typhi CT18.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Partridge S.R., Hall R.M.;
"The IS1111 family members IS4321 and IS5075 have sub-terminal inverted repeats and target the terminal inverted repeats of In21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Klebsiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 2.1%; Score 7; DB 2; Length 334; Local Similarity 100.0%; Pred. No. 2.5e+02; les 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family transposons ";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY242532; AAO48503.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 AA; 37525 MW; D50466A1926FCB73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL513383, CAD09795.1; -. GO: 0046621; C: extrachromosomal DNA; IEA. GO; GO: 00046821; F: ENNA binding; IEA. GO; GO: 0004803; F: transposase activity; IEA. GO; GO: 0006313; P: DNA transposition; IEA.
                                                                                                                                                                                                                                                                                                        334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 413:848-852(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klebsiella pneumoniae.
Plasmid pRMH760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative transposase.
299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 PKLIEFL 305
                                                      36 PKLIEFL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 PKLIEFL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pHCM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fransposase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCOCCOS ON THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF THE STANTANT OF TH
```

```
NCBI TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLR6085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298AA6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             098AA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 110
            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davis R.M., Chillingworth T., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., "Complete genome sequence of a multiple drug resistant Salmonella enterics servorar Typhs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                          2.1%; Score 7; DB 16; Length 334; 100.0%; Pred. No. 2.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7; DB 16; Length 334;
Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                              Complete proteome.
334 AA; 37467 MW; 0D3D1D57DD8D0603 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37467 MW; D629E2A1933B8F73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AL513183; CALD09818.1; -. GO: 0046821; C: extrachromosomal DNA, IEA. GO: 00046821; C: extrachromosomal DNA, IEA. GO: 00004803; F: DNA binding; IEA. GO: 00004803; F: DNA transposition; IEA. InterPro; IPR003346; Transposase_20. InterPro; IPR02525; Transposase_9.
                                                                                                                                                                                                                                                                                                                                                                       334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.0%; Pred. No. 2.5 nes 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Created)
  InterPro; IPR003346; Transposase_20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21534947; PubMed=11677608;
                     InterPro, IPR002525, Transposase 7
Pfam, PF02371, Transposase 20, 1
Pfam, PF01548; Transposase 9, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF02371; Transposase 20; 1.
PF01548; Transposase 9; 1.
d; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2001 (TrEMBLrel. 18, 01-0CT-2001 (TrEMBLrel. 18, 01-0CT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 413:848-852(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative transposase.
                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                           299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 PKLIEFL 305
                                                                                                                                                                                                                                                    36 PKLIBFL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 PKLIEFL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pHCM1
                                                                              Plasmid; C
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q97X08;
                                                                                                                                                                                                                                                                                                                      RESULT 108
0934H6
AC 0934H6,
DT 01-DEC,
DT 01-DEC,
DD 01-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1-DEC,
DD 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 109
Q97X08
ID Q97X08
AC Q97X08
DT 01-0CT
DT 01-0CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  097X08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
DR
DR
DR
KW
SO
                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA RES. 7:331-338 (2000).

BNBL, AP003008; BAB52430.1; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:000166; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.

GO; GO:000166; F:nucleotide binding; IEA.

GO; GO:000166; F:nucleotide binding; IEA.

InterPro; IPR003593; AAA_ATPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Wether C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffrise B.C., Kozera C.J., Medina N., Peng X.,
Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Mochizuki Y., Vamada M., Tabata S., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIRI, G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; G90360; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                         Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 17; Length 334; 00.0%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.0%; Pred. No. 2.5
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABC transporter, ATP-binding component,
Endoglucanase precursor (EC 3.2.1.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-21332296; PubMed=11427726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE006803; AAK42142.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                          Sulfolobus solfataricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 FDIASDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 FDIASDA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                         NCBI_TaxID=2287;
```

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q97L54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            097L54
                                                                                                                                                                                                                                                                     0850A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 114
Q97L54
                                                                                                                                                                                                                                            RESULT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aatches
                                                                                                                                                                                                                                                         Q85QA5
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GERARA GERARA
                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=V583 / ATCC 700802;
MEDLINE=22550657; PubMed=12663927;
Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
"Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCSI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza Sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                   .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 16; Length 335; 100.0%; Pred. No. 2.5e+02; tive 0; Mismatches 0; Indels
                                                                                                        Query Match
2.1%; Score 7; DB 16; Length 335;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
          Pfam; PF00005, ABC tran; 1.
Probon; PD000006, ABC transporter; 1.
PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS00211; ABC TRANSPORTER 2; 1.
ATP-binding; Complete proteome.
SEQUENCE 335 AA; 35983 MW; 8CA1B1AB9649CAS6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 AA; 37306 MW; 225BA6D143BDB792 CRC64;
                                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 337 AA
                                                                                                                                                                                                                                           335 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7XIQ4;
01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
Hypothetical protein 0J1316_A04.107.
0J1316_A04.107.
InterPro; IPR003439; ABC_transporter.
                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE016955; AA082282.1; -.
TIGR; EF2571; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 299:2071-2074(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003777; DUF182.
Pfam; PF02655; XdhC_CoxI; 1.
Complete proteome.
SEQUENCE 335 AA; 37306 MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                      Conserved domain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis.";
                                                                                                                                                        229 LKLLGEL 235
                                                                                                                                                                                 199 LKLLGEL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 AILEKOD 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 AILEKOD 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7XIQ4
                                                                                                                                                                                                                                           Q831E0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 112
                                                                                                                                                                                                                  RESULT 111
                                                                                                                                                                                                                             RANG RANG S
                                                                                                                                                        ò
                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
;
0
                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koszul R., Malpertuy A., Frangeul L., Bouchier C., Thierry A., Duthoy S., Wincker P. Ferris S., Hennequin C., Dujon B.; "The complete mitcochondrial genome sequence of the pathogenic yeast Candida (Torulopsis) glabrata."; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                            STRAIN=cv. Nipponbare;
Sasaki I., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, BAC
                                                                                                                                                                                                                                                                             Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AJ511533, CAD54417.1; ...

CO, GO.0005739; C:mitochondrion, IEA.

GO, GO.0003735; F:structural constituent of ribosome; IEA.

InterPro, IPR007980; Yeast VARI.

Mitochondrion; Ribosomal protein.

SEQUENCE 339 AA; 40828 MW; E56F22DB96DBEC06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 8; Length 339; 100.0%; Pred. No. 2.5e+02; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; APRO3822; BAC79608.1; -. Hypothetical protein. Protein SEQUENCE 337 AA, 38866 MM; B43138F9464720C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Frangeul L.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-07-2001 (TrEMBLrel. 18, Created)
01-07-2001 (TrEMBLrel. 18, Last sequence update)
10-07-2003 (TrEMBLrel. 25, Last annotation update)
Putative transcriptional regulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0TN-2003 (TrEMBLrel. 24, Created)
01-0TN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mitochondrial ribosomal protein VARI.
                                                                                                                                                                                                                                                                             2.1%; Score 7; DB 10; Le
100.0%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Candida glabrata (Yeast) (Torulopsis glabrata).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 AA.
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 2.5
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                    177 FDIASDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                          177 FDIASDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 IMTKYIS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 IMTKYIS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=ATCC 2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 2001;
                                                                                                               clone:0J1316 A04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5478;
```

Page 37

```
PRELIMINARY;
         Q52481
Q52481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08L9L9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                           Noelling J., Breton G., Concidency M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.W., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing bacterium Clostriduum acetobutylicum.";
Bacterium Clostriduum acetobutylicum.";
EMBL, AEOOTS86; AAX78685.1;
PIR; B96987; B96987.
GO: GO:0030246; F:carbohydrate binding; IEA.
GO: GO:0030246; F:carbohydrate binding IEA.
InterPro; IPR00734; Sugar-bind.
Pfam; PF04198; Sugar-bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=1302A;
MEDLINE=21065167; PubMed=11134504;
Lee J., Klueener B., Tsiamis G., Stevens C., Neyt C., Tampakaki A.P., Panopoulos N.J., Noller J., Weiler E.W., Cornelis G.R., Mansfield J.W., Nurnberger T.; "HrpZPsph from the plant pathogen Pseudomonas syringae pv. phaseolicola binds to lipid bilayers and forms an ion-conducting pore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                     Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas syringae (pv. phaseolicola).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 7; DB 16; Length 344; 100.0%; Pred. No. 2.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 2; Length 345; 100.0%; Pred. No. 2.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Nati. Acad. Sci. U.S.A. 98:289-294(2001).
EMBL; AF268940; AAF99292.1; -
InterProc. IPR006961; HrpZ.
Pfan; PF04877; HrpZ; 1.
SEQUENCE 345 AA; 35250 MW; A4B0B23A67268CA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 AA; 38112 MW; 8898505500CE5D2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 AA.
                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325; PubMed=11466286;
  Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIVKILK 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 EIVKILK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 AQLAQEL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 AQLAQEL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome
                                                                  NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invitro."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 115
Q9F0B0
AC Q9F0B0
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01-MAR.
DT 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09F0B0
à
```

```
and comato are encoded by an operon containing Yersinia ysc homologs and elicit the hypersensitive response in tomato but not soybean."; Mol. Plant Microbe Interact. 8:717-732(1995).
EMBL; L41862; AABO136.1; ...
InterPro; IPR006961; HrpZ.
Pfam; PF04877; HrpZ; 1.
SEQUENCE 345 AA; 35290 MW; B73FB324B7F28DDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                      STRAIN=Race 4;
MEDLINE=96025089; PubMed=7579616;
Preston G., Huang H.C., He S.Y., Collmer A.,
"The HrpZ proteins of Pseudomonas syringae pvs. syringae, glycinea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                    Pseudomonas syringae.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome annotation.",
Genome Biol. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell 1 Peldmann K.;
Feldmann K.;
Frull-Length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY088359; AAM65898.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 7; DB 2; Length 345; 100.0%; Pred. No. 2.5e+02; ative 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 345 AA; 39841 MW; 2C46A3D3DEBB47AA CRC64;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 7; DB 10; Le ilarity 100.0%; Pred. No. 2.5e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR008938; ARM.
Interpro; IPR004892; Mo25.
Pfam; PF03204; Mo25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
'...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 TEXDLLT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 AQLAQEL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 AQLAQEL
                                                                                                                                                                                                                      NCBI_TaxID=317;
                                                                                       HrpZ protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
```

ô

RESULT 116 Q52481

```
359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=192;
                                                                                                                                                                            Brucella suis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                         OBFVE4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OBRMW1:
                                                                                             Q8FVE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OBRAWI
                                                                        RESULT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 121
                                  g
                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                ਨੇ
                                                                                                                                                                                                                                                                                                                                                        ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=9910339; PubMed=10382966;

Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jún-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.,
"Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                            STRAIN=Sprague-Dawley;
MEDLINE=22810130; PubMed=12909716;
Zylka M.J., Dong X., Southwell A.L., Anderson D.J.;
"Atypical expansion in mice of the sensory neuron-specific Mrg
                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·.
                                                                                                                                                                                                                                                                                                                              2.1%; Score 7; DB 11; Length 353; 100.0%; Pred. No. 2.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 7; DB 17; Length 357;
100.0%; Pred. No. 2.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aeropyrum pernix.
Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
357AA long hypothetical CARBAMOYLPHOSPHATE synthetase.
                                                                                                                                                                                                                                                                                                        353 AA; 40125 MW; CE3685C2D3A6A9E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40622 MW; FA21C414838695F4 CRC64;
                                                                             01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MRGB5 G protein-coupled receptor.
                                                                                                                                                                                                                                                        protein-coupled receptor family.", Proc. Natl. Acad. Sci. U.S.A. 100:10043-10048 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AP000059; BAA79463.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Desulfurococcaceae; Aeropyrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; C72746; C72746.
InterPro; IPR007356; DUF425.
Pfam; PF04243; DUF425; 1.
Complete proteome
SEQUENCE 357 AA; 40622 MW
                                                                                                                                                                                                                                                                                 EMBL; AF518243; AAQ08315.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 7; Conservative
                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                         Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                             226 RQSLKLL 232
                                                                                                                                                                                                                                                                                                                                                                                                   319 ROSLKLL 325
 190 TFKDLLT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APE0498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9YET3;
                                                         Q7TN44
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9YET3
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 119
                                  RESULT 118
                                             O7TN44
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9YET3
                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
MEDILINE 22247741; PubMed=12271122; Paulsen J.A., Heidelberg J.F., Read T.D., Seshadri R., Nelson K.E., Bisen J.A., Heidelberg J.F., Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J. Daugharty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.; "The Brucella suis genome reveals fundamental similarities between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gross J., Sperotto R.A., Vedoy C., Passaglia L.M.P., Schrank I.S.;
"The Azospirillum brasilense fixABCX operon: nucleotide sequence.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF489443; AAMO0319.1, -
GO, GO:0005489; F:electron transporter activity; IEA.
GO, GO:0005489; F:electron transport; IEA.
Interpro; IPR001308; ETF alpha.
PROSITE; PS00766; ETF alpha.
PROSITE; PS007696; ETF ALPHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Rhodospirillaceae; Azospirillum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 16; Length 358; 100.0%; Pred. No. 2.6e+02; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 AA; 39299 MW; DA2F02B1171B4C81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TF ALPHA; 1.
38708 MW; 89EBCCE6498F3D54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      animal and plant pathogens and symbionts.";
Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003462; ODC_Mu_crystall.
Pfam; PF02423; ODC_Mu_crystall; 1.
Complete proteome.
SEQUENCE 358 AA; 39299 MW; DA2F02B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE014583; AAN34071.1; -. TIGR; BRA0899; -.
                                                                                                                                                                                                                                                                                                                                                                                                                Ornithine cyclodeaminase.
ARCB OR BRA0899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Azospirillum brasilense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brucellaceae; Brucella.
NCBI_TaxID=29461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=1330 / Biovar 1;
290 IVEILLK 296
                                                                269 iVEILLK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 EKLLQSE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 EKLLÓSE 352
```

0

```
RESULT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9KS99
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART OF A PART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-16M / ATCC 21456 / Biotype 1;
MEDLINE=20020109; PubMed=1175668;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.;
The genome sequence of the facultative intracellular pathogen Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuba M., Yatsuki H., Kusakabe T., Takasaki Y., Nikoh N., Miyata T.,
Yamaguchi T., Hori K.,
"Molecular Evolution of Amphioxus Fructose-1,6-bisphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Branchiostoma belcheri (Amphoxius).
_Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO, GO:0004332; F.fructose-bisphosphate aldolase activity; IEA.
GO; GO:0006096; P:glycolysis; IEA.
InterPro; IPR000741; Aldolase I.
Pfam; PF00274; glycolytic_enzy; 1.
Probom; PD001128; Aldolase I; 1.
PROSITE; PS00158; ALDOLASE CLASS I; 1.
SEQUENCE 359 AA; 38493 MW; 9Ā0374AE531EEB18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brucella melitensis.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBI_TaxID=29459;
                      DB 2; Length 359; 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 5; Length 359;
100.0%; Pred. No. 2.6e+02;
Live 0; Mismatches 0; Indels
                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aldolase.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AB005035; BAA21101.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Ornithine cyclodeaminase (EC 4.3.1.12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 AA.
                                                                                                        Mismatches
                  Score 7; I
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
             Query Match
2.1%; Scc
Best Local Similarity 100.0%; Pr
Matches 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aldolase.
Branchiostoma belcheri
                                                                                                                                                                                     251 KPENLKL 257
                                                                                                                                                                                                                                                                       245 KPENLKL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 VKILKDN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 VKILKDN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P00883; 1ADO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Branchiostoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 122
017497
AC 017497
DT 01-JAN
DT 01-JAN
DT 01-JAN
DT 01-JAN
DE Aldola
OC Branchi
OC Branchi
OC Branchi
OX NCEL TR
RP SEQUENC
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
RT "MO1ecu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBYCY1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCY

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL

OOYCYL
                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DALUTE 406.477-483 (2000)

-1- FUNCTION: PROBABLY PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSPOCATION OF THE SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSPORT SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20406833; PubMed=10552301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Rad T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 16; Length 359; 100.0%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 16; Length 365;
100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0; Indels
EMBL; AE009677; AAL53639.1; -. GO, MAL5409559; AB3559; AB3559.
GO, GO:00166929; F:lyase activity; IEA.
GO, GO:0008473; F:ornithine cyclodeaminase activity; IEA.
InterPro; IRR03462; ODC_Mu_crystall.
Fam; PF02423; ODC_Mu_crystall.
Lyase; Complete proteome.
SEQUENCE 359 AA; 39460 MW; F29E90021EF950B5 CRC64;
                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00528; BPD transp; 1.
PROSITE; PS00402; BPD TRANSP INN MEMBR; 1.
Transmembrane; Transport; Complete proteome.
SEQUENCE 365 AA; 40698 MW; C783C9BAA49D24FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence upd
01-JUN-2003 (TrEMBLrel. 24, Last annotation u
Amino acid ABC transporter, permease protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0016021; C:integral to membrane; IEA. GO; GO:0005215; F:transporter activity; IEA. GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=El Tor N16961 / Serotype 01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000515; BPD_transp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE004215; AAF94518.1; -. PIR; F82210; F82210.
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                      214 EKLLOSE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                             347 EKLLÖSE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 GLLVTLI 163
                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 GLLVTLI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio cholerae.
                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VC1360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29KS99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09KS99
```

Gaps

. 0

Indela

```
N P.5.

N P.5.

N P.5.

A Yamada K., Chan M.M., Chang C.H., Dale J.M., Heuan V.M., Lee J.M.,

A Yamada K., Chan M.M., Chang C.H., Dale J.M., Heuan V.W., Lee J.M.,

A Onodera C.S., Quach H.L., Tang C.C., Toriumi M., Wong C., Wu H.C.,

A Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,

A Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,

A Tarabioposis Open Reading Frame (ORF) Clones.";

Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

B EMBL; A7096256; AAL07109.1;

DR EMBL; B7002750; AA022579.1;

DR EMBL; G96668; G96668; G96668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Shinn P., Tambunga G., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyem M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genomic sequence for Arabidopsis thaliana BAC FIN19 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
Koesema B., Lim B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MXY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
F1N19:7 (Hypothetical protein) (Putative peptide transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Full Length cDNA of gene F1N19.7 (GI:6633811).";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005489; F:electron transporter activity; IEA. GO; GO:0006118; P:electron transport; IEA. InterPro; IPR002109; Glutaredoxin. Pfam; PF00462; glutaredoxin; 1. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                   368 AA.
                 0; Mismatches
                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 7; Conservative
       7; Conservative
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F1N19.7 OR AT1G64500.
                                                                      40 EEVSKSL 46
                                                                                                                           76 EEVSKSL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 EEVSKSL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 EEVSKSL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   39SGW5;
                                                                                                                                                                                                                                                                                                                O9SGW5
                                                                                                                                                                                                                                             RESULT 127
          Matches
                                                                                                                                                                                                                                                                             Q9SGW5
                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D., Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Yu S., Bowser L., Carninoi P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Theologis A.; Theologis A.; Theologis A.; Theologis A.; Shinozaki K., Baki M., Shin Length CDNA of gene Atlg64500 (GI:15217659)."; Submitted (NoV-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; eudicotyledons; orde eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                       Vibrio vulnificus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 368;
                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ABC-type amino acid transport system, permease component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016806; AA011051.1;
GO; GO:0016202; C:membrane; IEA.
GO; GO:0016215; F:transporter activity; IEA.
GO; GO:006810; P:transport iEA.
InterPro; IFR000515; BPD_transp.
PROSITE; PS004015; BPD_transp.
PROSITE; PS00402; BPD_TRANSP_INN_MEMBR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 AA; 41096 MW; DE355603114A41A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20A65B0127DA24A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005489; F:electron transporter activity; IBA. GO; GO:0006118; P:electron transport; IEA. InterPro; IPR002109; Glutaredoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 2.1%; Score 7; DB 16; Le Local Similarity 100.0%; Pred. No. 2.7e+02; Les 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7; DB 10; Le
Pred. No. 2.7e+02;
                                      365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00462; glutaredoxin; 1.
SEQUENCE 368 AA; 40986 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; S
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Putative peptide transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY063982; AAL36338.1; -
                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 GLLVTLI 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 GLLVTLI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CMCP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28VZN7;
                               280999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O8VZN7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000 VZV

000
08D999
                                   A RAPER SERVICE OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
ö
                                                                  Gaps
                                                                  .;
0
                                 Length 368;
                                                              0; Indels
368 AA; 41016 MW; 396F8B0127C937A4 CRC64;
                              2.1%; Score 7; DB 10; Le
100.0%; Pred. No. 2.7e+02;
ative 0; Mismatches 0;
```

16 BIVKILK 22

8

```
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN=RIMD 2210633 / Serotype 03:K6;

MEDLINE=22508454; PubMed=12620739;

Makino K., Oshima W., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism

Lancet from that of V. cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lueneberg E., Zetzmann N., Hartmann M., Knirel Y.A., Kooistra O., Zaehringer U., Helbig J., Frosch M., "Cloning and functional characterization of a 30 kb gene locus required for lipopolysaccharide biosynthesis in Legionella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
                                                                                                                                                                                                                                                                  Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.1%; Score 7; DB 2; Length 369; Best Local Similarity 100.0%; Pred. No. 2.7e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368 AA; 41399 MW; A09AE5073B410381 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Int. J. Med. Microbiol, 290:37-49(2000).

EMBL, AJ007311; CAB65199.1; -.

Hypothetical protein.

SRQUENCE 369 AA; 42303 MW; 40955E0A9DFA2624 CRC64;
                                                                                                                                                   Last sequence update)
Last annotation update)
permease protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OGT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
2.1%; Score 7; DB 16; Le
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 AA
                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20496696; PubMed=11043980;
                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                        Amino acid ABC transporter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Legionellaceae; Legionella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Legionella pneumophila.
                                                                                                                                                                                                                                                                                                                          Vibrionaceae; Vibrio.
NCBL_TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 GLLVTLI 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 GLLVTLI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=RC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                         087P96
                                                       Q87P96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9RDY8
RESULT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 129
Q9RDY8
                                                          ACCOCC OCC ON THE STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DESCRIPTION OF STANDARD DES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
SEQUENCE FROM N.A.

TISSUE-Implantation stage endometrium;
Melner M.H., Ducharme N.A., Brash A.R., Winfrey V.P., Olson G.E.;
Melner M.H., Ducharme N.A., Brash A.R., Winfrest V.P., Olson G.E.;
"Differential Expression of Genes in the Endometrium at Implantation:
Upregulation of a Novel Member of the E2 Class of Ubiquitin
Conjugating Braymes.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AV330351; AAP93920.1; -.

SEQUENCE 369 AA; 42191 MW; 3B88532499960CF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to NICE-5 protein (EC 6.3.2.19) (Ubiquitin-conjugating enzyme E2) (Ubiquitin-protein ligase) (Ubiquitin carrier protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Straubberg R.;
Straubberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUIIIN TO OTHER PROTEINS (BY SIMILARITY).
--- PROTEINS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: ATP + UBIQUITIN + PROTEIN LYSINE = AMP + DIPHOSEHAIE + PROTEIN CONJUGATION; SECOND STEP.
-!- PATHWAY: UBIQUITIN CONJUGATION; SECOND STEP.
-!- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
THIOLESTER FORMATION (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.
EMBL; BC017708; AAH17708.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC017708; AAH17708.1; -. GO; GO:0016874; F:ligase activity; IEA. GO; GO:0004840; F:ligase activity; IEA. GO; GO:0004840; F:ubiquitin conjugating enzyme activity; IEA. GO; GO:0006842; F:ubiquitin-protein ligase activity; IEA. GO; GO:0006512; P:ubiquitin cycle; IEA. InterPro; IPR006575; RWD. InterPro; IPR006608; UBQ_conjugat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; Score 7; DB 6; Length 369; 100.0%; Pred. No. 2.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375 AA.
                                                                                                 369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
                                                                                                                                         Created)
                                                                                                                                                                                             Ubiquitin-conjugating enzyme UBCi.
Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00179; UQ_con; 1.
ProDom; PD000461; UBQ_conjugat; 1.
                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 NLAILEK 179
 18 EIVKILK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                       NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBWVN8;
                                                                                                 Q7YQ79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8WVN8
                                                         RESULT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 131
                                                                             27YQJ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8WVN8
g
                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
```

```
·:
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AYOB7612; AAM65366.1; -.

R GO; GO:005518; C:cell wall; IEA.

R GO; GO:0065218; C:cell wall; IEA.

R GO; GO:006223; F:peptidase activity; IEA.

R GO; GO:006233; F:peptidase activity; IEA.

R GO; GO:00045575; F:peptygalacturonase activity; IEA.

R GO; GO:0005575; P:polygalacturonase activity; IEA.

R GO; GO:0005575; P:polygalacturonase activity; IEA.

R GO; GO:0005575; P:proteclyais and peptidolysis; IEA.

R GO; GO:0005508; P:proteclyais and peptidolysis; IEA.

R InterPro; IRR000743; Glyco hydro 28.

R InterPro; IRR000508; Peptidase $26.

R Ffam; PF00295; Glyco hydro 28; 1.

R ROSITE; PS00761; SPASE I 3; 1.

R Cell wall; Glycosidase; Hydrolas.

Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Annower Anno
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            core eudicots; rosids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Pepermatophyta, Magnoliophyta; endicotyledons; core eudicots; rosid eurosids II; Erassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; "Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K.;
Feldmann K.;
Fell-Length cDNA from Arabidopsis thaliana ",
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES (POLYGALACTURONASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 377;
                                                                                                                                                               Length 375;
                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
SMART; SM00591; RWD; 1.
SMART; SM00212; UBCc; 1.
PROSITE; PSS0127; UBIQUITIN CONJUGAT_2; 1.
Ligase; Ubl. conjugation pathway.
SEQUENCE 375 AA; 42818 MW; 7DE07315E89178A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40865 MW; 4DD25136A4642102 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Polygalacturonase-like protein.
                                                                                                                                                         DB 4; Lend
10. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 10; Le
100.0%; Pred. No. 2.7e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
                                                                                                                                         2.1%; Scc.
100.0%; Pred. No. 2.
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        377 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity luv...
Lag 7; Conservative
                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Biol. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                           179 NLAILEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 LIEFLSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 LIEFLSS 307
                                                                                                                                                                                                                                                             24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8LAH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9M7X3;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8LAH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9M7Y3
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 133
Q9M7Y3
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                             ò
  SO KW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

```
01-0CT-2002 (TrBMBLrel. 22, Created)
01-0CT-2002 (TrBMBLrel. 22, Last sequence update)
01-0CT-2003 (TrBMBLrel. 25, Last amountation update)
01-0CT-2003 (TrBMBLrel. 25, Last amountation update)
Similar to NICE-5 protein (EC 6.3.2.19) (Ubiquitin-conjugating enzyme
E2) (Ubiquitin_protein ligase) (Ubiquitin carrier protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Straugherg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYZES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER PROTEINS (BY TIMILARITY).
                                                                                                                                                                    Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AC023912; AAF63821.1; -.
GO; GO:0005618; C:cell wall; IEA.
GO; GO:0016620; C:membrane; IEA.
GO; GO:0016620; C:membrane; IEA.
GO; GO:0016620; C:membrane; IEA.
GO; GO:0016620; F:peptidase activity, acting on glycosyl bonds; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0008575; P:carbohydrate metabolism; IEA.
GO; GO:0006508; P:polygalacturonase activity; IEA.
GO; GO:0006508; P:polygalacturonase activity; IEA.
InterPro; IPR000743; Glyco-hydro-28.
InterPro; IPR000508; Peptidase.
InterPro; IPR000508; Peptidase.
InterPro; IPR000508; Peptidase.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Frant.
Fra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. Columbia;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
Maili R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F3E22 genomic sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- CATALYTIC ACTIVITY. AIP + UBIQUITIN + PROTEIN LYSINE = AMP + DIPHOSPHATE + PROTEIN N-UBIQUITYLLYSINE.
-1- PATHWAY: UBIQUITIN CONJUGATION; SECOND STEE.
-1- PATHWAY: UBIQUITIN CONJUGATION; SECOND STEE.
-1- MISCELLANBOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
THIOLESTER FORMATION (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE UBIQUITIN-CONJUGATING ENZYME FAMILY.
EMBL; BC029111; AAH29111.1; -
GO; GO:0016874; F:ligame activity; IEA.
GO; GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.
GO; GO:0004842; F:ubiquitin-protein ligame activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 10; Length 377; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fram; Erver., 200710; PbH1; 4.
PROSITE; PS00761; SPASE_I_3; 1.
Cell wall; Glycosidase; Hydrolase.
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [POLYGALACTURONASES].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 LIEFLSS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 LIEFLSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                          F3E22.9 protein.
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08K2Z8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 134
Q8K2Z8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DDR NO DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
```

0;

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team,
the RIKEN Genome Exploration Research Group Phase I & II Team,
the RIKEN Genome Exploration Research Group Phase I & II Team,
the Morital Fig. 10 of the mouse transcriptome based on functional annotation of
60,770 full-length cDNNs.";
Nature 420:563-573 (2002)
BMB1, AK081215, BR0180111;
GO; GO:0004840; Fubliquitin conjugating enzyme activity; IEA.
GO; GO:0006512; P:ubliquitin cycle; IEA.
InterPro; IRR000668; UBQ.conjugat.
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                 Query Match 2.1%; Score 7; DB 11; Length 378; Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 7; DB 11; Length 378; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; LEACOUS, 1.

Pram, PF00179; UQ con; 1.

ProD012012; UBCC; 1.

SMART; SW0012012; UBCC; 1.

PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.

PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
GO, GO:0006512; F:ubiquitin cycle; IEA.
InterPro; IPR00608; UBQ_conjugat.
Pfam; PF00179; UQ_con; 1.
Pr05004; DBC0,1.
SMART; SM0012; UBCc,1.
PROSITE; PS50127; UBCUITIN CONUGAT_2; 1.
Ligase; UBL conjugation pathway.
SEQUENCE 378 AA; 42923 MW; D1690A9C4BC6DBDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein F13D11.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          378 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Hippocampus; MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similar to NICE-5 protein homolog. 3010021M21RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                              182 NLAILEK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 NLAILEK 188
                                                                                                                                                                                                                                                                                                                                                           24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08BUN2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       019391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8BUN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 136
2019391
AC 019391
AC 019391.
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        019391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8BUN2
           ò
                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

```
Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Taspin A., Scott J., Beanan M., Brinkac L., Daugherty S., Baboy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Gelblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Shewanella.
                                                                            "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 5; Length 379;
100.0%; Pred. No. 2.8e+02;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                           "The sequence of C. elegans cosmid F13D11.", Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                  Waterston R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                     EMBL, U40939; AAA81703.2; -. PIR, T16059; T16059. WormPep; F13D11-4; CE30950. Hypothetical protein. SEQUENCE 379 AA; 42494 MW; 221F2D4EB8BB3138 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR; 800694; -. GO; Coytoplasm; IEA. GO; GO:0005524; F.ATP binding; IEA. GO; GO:0005524; F.ATP binding; IEA. GO; GO:0004335; F: Galactokinase activity; IEA. GO; GO:0006312; F: Kinase activity; IEA. GO; GO:000612; P: Rinase activity; IEA. GO; GO:000612; P: Rinase activity; IEA. GO; GO:000612; P: Rinase activity; IEA. GO; GO:0016310; P: Phosphorylation; IEA. InterPro; IPR000705; Galactokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nat. Biotechnol. 20:1118-1123 (2002).
EMBL; AE015515; AAN53772.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MR-1;
MEDLINE=22297686; PupMed=12368813;
                 STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GALK OR SO0694.
Shewanella oneidensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291 VEILLKN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 VEILLKN 64
                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                              STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=70863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Galactokinase.
                                                             Waterston R.;
                                                                                                                                                                                                         Fulton L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OBEIY3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8EIY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
```

```
29JRN4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09JRN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBCX72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBCX72
           Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ठ
                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                         2.1%; Score 7; DB 16; Length 381;
100.0%; Pred. No. 2.8e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
2.1%; Score 7; DB 5; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRANT=Bristol N2;
Wilson R., Wamsley P.;
"The sequence of C. elegans cosmid H19M22.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF040648; AAK26140.1; -. Wormbep; H19M22.czc; CE26978. Hypothetical protein. SEQUENCE 386 AA; 43533 MW; BBE7BCE17601E57D CRC64;
                                                                                                                                                                                                                  381 AA; 41510 MW; C799B46FC8BE44E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-UUN-2001 (TrEMBLrel. 17, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387 AA
               InterPro; IRR006204; GHMP kinase.
InterPro; IPR006206; Mev galkinase.
Pfam; PF00288; GHMP kinases; 1.
PRINTS; PR00473; GALCTOKINASE.
PRINTS; PR00960; LMBPPROTEIN.
TIGRPAMS; TIGR00131; gal kin; 1.
PROSITE; P800657; GHMP KINASE ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8EY27;
01-MAR-2003 (TrEMBLrel. 23, Created)
InterPro; IPR006203; GHMPknse_ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
The 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                          154 AVAQLAQ 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 AQLAQEL 280
                                                                                                                                                                                                                                                                                                                                                  65 AVAQLAQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 AQLAQEL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Bristol N2;
Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9BKP3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09BKP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8EY27
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOW WE WE WAY SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE SEE THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8EY27
  q
                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                   Ren S.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE011592; AAN51589.1; -.
GO; GO:0016747; F:transferase activity, transferring groups o. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suzuki N., Nakano Y., Yoshida Y., Nako H., Yamashita Y., Koga T.; "Genetic analysts of the gene cluster for the synthesis of serotype aspecific polysaccharide antigen in A. actinomycetemcomitans."; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AB04656, BAB03209.1; --
GO, GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                               Bacteria, Spirochaetes, Spirochaetales, Leptospiraceae, Leptospira.
NCBI_TaxID=173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Actinobacillus.
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O.T.M. (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Antibiotic resistance protein (Antibiotic efflux protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 2; Length 390; 100.0%; Pred. No. 2.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   387 AA; 44605 MW; 4B3A7BC91D8661FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          390 AA; 44354 MW; 2B9267E002D35382 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative glycosyltransferase.
Actinobacillus actinomycetemcomitans (Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 390 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.1%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 2.8
Matches 7; Conservative 0; Mismatches
                             01-JUN-2003 (TrEMBLrel. 24, Last annotatio
Probable intercellular adhesion protein C.
                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002656; Acyl transf 3.
Pfam; PF01757; Acyl_transf 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001296; Glyco trans 1.
Pfam; PF00534; Glycos transf_1; 1.
Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                Leptospira interrogans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            actinomycetemcomitans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 PKLIEFL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 IMTKYIS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 IMTKYIS 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
SEQUENCE 387 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=SUNYaB 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=714;
```

```
NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=1021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                    QBDGBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q92VE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 144
                                                                                                                                                         DDT REPRESENTED THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=HTBB31 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A Katoh H., Nakahara Y., Ikeuchi M.;

Katoh H., Nakahara Y., Ikeuchi M.;

Tuchoning and expression of the cyal gene from thermophilic
Thermosynechococcus (formerly Synechococcus) elongatus BP-1.";

Thermosynechococcus (formerly Synechococcus) elongatus BP-1.";

L submitted (DEC-2000) to the EMEL/GenBank/DDBJ databases.

BMBL; AB052847; BAB20624.1; -

R GO; GO:0004383; F:quanylate cyclase activity; IEA.

R GO; GO:0007242; F:lyase activity; IEA.

R GO; GO:0007242; P:intracellular signaling cascade; IEA.

InterPro; IPR001054; G cyclase.

R InterPro; IPR01054; G cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·,
                     Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 16; Length 396; 100.0%; Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.1%; Score 7; DB 2; Length 399; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 AA; 42992 MW; 60BE167BC1C51569 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399 AA; 44620 MW; CF4957D52C3D7DIA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, APONGGOS, BACLSOSZ.1, --
GO, GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR007114; MFS.
InterPro; IPR008818; Sub transporter.
Pfam; PF00083; sugar tr; 1.
PROSITE; PS508SO; MFS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          399 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00498; FHA; 1.
Pfam; PF00211; guanylate cyc; 1.
PROSITE; PS50006; FHA DOMAIN; 1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                             environments.";
Nucleic Acids Res. 30:3927-3935(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermosynechococcus elongatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 SPHKTOP 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 SPHKTOP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 LKGYEAP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 LKGYEAP 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=146786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adenylate cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 142
09F1L6
AC 09F1L6
DT 01-MAR
DT 01-OCTR
DD AGENY1
OS Thermon
OC Bacter:
OC NCEL TR
RP SEQUENT
RP SEQUENT
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT "Cloul
RT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09F1L6
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

```
Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
Golding B., Puehler A.;
"The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
fixing endosymbiont Sinorhizobium meliloti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
EMBL, AL603644; CAC49159.1;
                                                                                                                                                                                                                                                                                              MEDLING=2222144; PubMed=12240834;
Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto ! Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium DNA Res 9:123-130(2002).

EMBL, APODS377; BACC9962.1; -. GO; GO:0004383; F:guanylate cyclase activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 16; Length 399 ilarity 100.0%; Pred. No. 2.9e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                               Synechococcus elongatus (Thermosynechococcus elongatus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399 AA; 44620 MW; CF4957D52C3D7DIA CRC64;
                                                                                                                                                                                     Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
399 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein RB0759.
RB0759 OR SMB21255.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50006; FHA DOMAIN; 1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
CCMplete proteome.
SEQUENCE 399 AA; 44620 MW; CF4957D52C31
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21396508; PubMed=11481431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00498; FHA; 1...-
Pfam; PF00211; guanylate_cyc; 1.
SMART; SM00044; CYCc; 1.
SMART; SM00240; FHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro, IPR000253; FHA.
InterPro, IPR001054; G cyclase.
InterPro, IPR008984; SWAD_FHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pSymB (megaplasmid 2)
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 LKGYEAP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 LKGYEAP 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                  Adenylate cyclase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
```

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=77768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9XAY2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8M431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 148
                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9XAY2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8M43:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCOCC OD DET BE SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER SENDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/61; TISSUB=Retina;
MEDLINE=22354683; PubMed=12466851;
The FAMTOM consortium.
The FAMTOM consortium.
The FAMTOM Consortium.
The FAMTOM Consortium.
The FAMTOM Consortium.
The FAMTOM Consortium.
The FAMTOM Consortium.
The FAMTOM Consortium.
The FAMTOM Consortium.
The FAMTOM Consortium.
The FAMTOM Consortium.
The FAMTOM Consortium.

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length consortium.
"Analysis of the mouse transcriptome based on functional annotation of Mature 420:563-573 (2022).

EMBL; AK044657; BAC32021.1; -.
EMBL; AK044657; BAC32021.1; -.
GO, GO:0005739; C:mitochondrion; IDA.

InterPro; IPR001401; Dynamin.
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22735913; PubMed=12835416;
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 11; Length 402;
100.0%; Pred. No. 2.9e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                       / Match 2.1%; Score 7; DB 16; Length 400; Local Similarity 100.0%; Pred. No. 2.9e+02; nes 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                               0; Indels
PIR; G95936; G95936.
GO; G0:0046821; C:extrachromosomal DNA; IEA.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 400 AA; 42766 MW; 3F775E554DDF5FIF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     402 AA; 46232 MW; E660EC93BC32E74E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           402 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dynamin-like 120 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plenctomycetaceae; Pirellula.
NCBI_TaxID=117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00350; dynamin; 1.
PRINTS; PR00195; DYNAMIN.
NON_TER 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100. hes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhodopirellula baltica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                               140 KASEEVS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 LIGELIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 Licelii 216
                                                                                                                                                                                                                                                                                                               37 KASEEVS 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7UWG3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 145
28BLL3
AC QBBLL3
DT 01-MAR.
DT 01-MAR.
DT 01-CCT.
DT 01-CCT.
DX MUS MUS
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC BUKALY
CC 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBBLL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 146
Q7UWG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7UWG3
                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
   S KW DS
                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

```
STRAIN-M384;
McEwan N.R., Walker N.D., Wallace R.J.;
"A long open reading frame in the rumen bacterium Prevotella albensis
M384 has homology to unidentified open reading frames in other
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dubach J., Patterson B.D., Briggs M.B., Venzke K., Flammand J., Stander P., Scheepers L., Kays R.; "Molecular genetic variation across the southern geographic range of the African lion, Panthera leo.";
Schlesner H., Amann R., Reinhardt R., "Complete genome sequence of the marine planctomycete Pirellula sp. strain 1.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Rissipedia, Felidae, Panthera.
                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                DB 16; Length 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 2; Length 407; 100.0%; Pred. No. 2.9e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organisms.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                   Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).

EMBL, BX294136; CAD72400.1; -

Hypothetical protein; Complete protecme.

SEQUENCE 402 AA; 43264 MW; 4165BF55C907C188 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407 AA; 42560 MW; 6FC6C897060762D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein (Fragment). Prevotella albensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407 AA.
                                                                                                                                                                                                2.1%; Score 7; DB 10100.0%; Pred. No. 2.99ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AJ243361, CAB46012.1, ... InterProv. IRRO04813, Tetrpept_transpt. Pfam, PF03169, OPT, 1. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prevotellaceae, Prevotella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Panthera tigris (Tiger).
                                                                                                                                                                                                                                                                                                   294 LLKNOPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 LIVILIA 228
                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                  28 LLKNOPK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 LLVTLIA 84
```

·,

```
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7TSS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9ATH0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7TSS2
                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC OCC OCC OCT REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE REPRESENT THE R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     슝
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ubbach J., Patterson B.D., Briggs M.B., Venzke K., Flammand J.,
Stander P., Scheepers L., Kays R.;
"Molecular genetic variation across the southern geographic range of
"Molecular genetic variation across the southern geographic range of
the African lion, Panthera leo.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AFB8521; AMM46205.1;
"R GO; GO:0008137; F:NADH dehydrogense (ubiquinone) activity; IEA.
GO; GO:0008137; F:NADH dehydrogense (ubiquinone) activity; IEA.
GO; GO:0006118; P:Nather dehydrogense activity; IEA.
GO; GO:0006120; P:mitcchondrial electron transport, NADH to u. .; IEA.
InterPro; IPR0019916; NADHUb_oxred5.
InterPro; IPR0019916; NaDHUb_oxred6.
InterPro; IPR001906; Rieske dom.
Pfam. PR001461. Oxidored q1.
InterPro; IPR005806; Rieske dom.
                                                                                                                                                                                                                                                                                                                                                                                                           ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Panthera.
                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                              Query Match 2.1%; Score 7; DB 8; Length 407; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 7; DB 8; Length 407; 100.0%; Pred. No. 2.9e+02; tive 0; Mismatches 0; Indels
  Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                    407 AA; 45157 MW; 29C65A27F1854410 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 407 AA; 45183 MW; 70048488F6268B84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2002 (TrEWBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
NADH dehydrogenase subunit 5 (Fragment).
                                                                                                                                                                                                                                NAD; Oxidoreductase; Ubiquinone; Mitochondrion. NON_TER 107 407 407 SEQUENCE 407 AA, 45157 MW, 29C65A27F1854410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00361; oxidored g1; 1.
PRINTS; PR01434; NADHDHGNASES.
NAD; Oxidoreductase; Ubiquinone; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 LLVTLIA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Panthera leo (Lion).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 LLVTLIA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                             78 LLVTLIA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 LLVTLIA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=TSV3550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8M432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 149
Q8M432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
SEQUENCE FROM N.A. Altham I., Koehler M., Engel W.; Altmann M.E., Schulze E., Adham I., Koehler M., Engel W.; "Isolation and characterization of the human UBE2Q gene and its murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=129/SV;
Altmann M.E., Schulze E., Adham I., Koehler M., Engel W.;
"Isolation and characterization of the human UBB2Q gene and its murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-UTN-2001 (TrEMBLrel. 17, Created)
01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Aminolevulinate denydratase (EC 4.2.1.24) (Delta-aminolevulinic acid dehydratase) (Porphobilinogen synthase) (ALADH).
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Raphanus sativus (Radish).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 7; DB 11; Length 422;
100.0%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 422;
                                                                                                                                                                                                                                                                                                                                                         ortholog.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY112698; AAM60814.1; -.
SEQUENCE 422 AA; 46127 MW; 106FF7E59DF65555 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ortholog.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY112699; AAM60815.1; -.
SEQUENCE 422 AA; 46131 MW; FAAS3C0CA87B8A5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
O727B8 PRELIMINARY; PRT; 422 AA.
01-077-2033 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-07T-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
2.1%; Score 7; DB 4; L
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. wc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                               Ubiquitin-conjugating enzyme E2Q. UBE2Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ubiquitin-conjugating enzyme E2Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 NLAILEK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 NLAILEK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 152
09ATHO
AC 09ATHO
DT 01-JUN
DT 01-JUN
DE Aminol
DE Aminol
DE Gebydr
GN ALAD.
OS BARANA
```

ô

RESULT 150 07Z7E8

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berthe T., Klein-Eude D., Balange A.P.;
"Study of 5-aminolevulinate dehydratase in radish seedlings: Are there housekeeping and light-induced enzymee?";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: 2 5-AMINOLEVULINATE = PORPHOBILINOGEN + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
NCBI_TaxID=3726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 426;
0. 3e+02;
ches 0; Indels
                                                                                                                                                                                                                                                                                                                                         HSSP; PISO02; 1B4E.
GO: GO:0016829; F:lyase activity; IEA.
GO: GO:0004655; F:porphobilinogen synthase activity; IEA.
GO; GO:0006783; F:heme biosynthesis; IEA.
InterPro; IPR001731; AlaD_dehydratase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00490; ALAD; 1.
PRINTS; PR00144; DALDHYDRTASE.
ProDom; PD002304; AlaD dehydratase; 1.
PROSITE; PS00169; DALA DEHYDRATASE; 1.
Lyase; Porphyrin biosynthesis.
SEQUENCE 426 AA; 46552 MW; 0C239C00B77B1CAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 AA; 50205 MW; A3EF05AC290C93BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Scor.
100.0%; Pred. No. Ju.
0; Mismatches
                                                                                                                                                                                                                                                                 -1- SUBUNT: HOMOOCTAMER (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE ALADH FAMILY.
EMBL; AF332195; AAK15323.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF04055; Radical SAM; 1.
Pfam; PF0919; UPF0004; 1.
SMATT, SM00729; Elps; 1.
TIGRFAMs; TIGR01579; MiaB-like-C; 1.
TIGRFAMs; TIGR00089; TIGR00089; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01278; UPF0004; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fe-S oxidoreductases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 LLRDKSP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLRDKSP 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
SEQUENCE 436 AA;
                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358
                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 153
1097JJ4
AC 097JJ4
AC 097JJ4
AC 097JJ4
AC 097JJ4
DT 01-OCT-
DT 01-OCT-
DT 01-OCT-
DE Re-S 00
CC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
OC Clostric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  097334
  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       임
```

```
Mypulist; MYPU 4130; -

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004009; F:ATP binding; IEA.

GO; GO:0004009; F:ATP-binding; IEA.

GO; GO:000166; F:nucleotide binding; IEA.

DR GO; GO:0000810; P:transport; IEA.

DR GO; GO:0000810; P:transport; IEA.

DR GO; GO:0000810; P:transport; IEA.

InterPro; IPR003439; AAA ATPass.

DR PROMO35; ABC tran; 1.

DR PRODOM; PD0000006; ABC transporter; 1.

DR PROSTIE; PS00211; AAA; I.

DR PROSTIE; PS00211; AAA; I.

DR PROSTIE; PS00211; ABC TRANSPORTER 1; 1.

DR PROSTIE; PS0093; ABC TRANSPORTER 2; 1.
                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=UAB CTIF;
MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Perris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helioobacter hepaticus.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helioobacteraceae; Helicobacter.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of the murine respiratory pathogen
                                                                      ó.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
FKBP-type peptidyl-prolyl cis-trans isomerase (Trigger factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
      Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 16; Length 440;
100.0%; Pred. No. 3.1e+02;
iive 0; Mismatches 0; Indels
                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           01-0cT-2001 (TrEMBLrel. 18, Created)
01-0cT-2001 (TrEMBLrel. 18, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
01igopeptide ABC transporter ATP-binding protein OPPP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 AA; 50792 MW; 1327EB0EDEAF0B9B CRC64;
      DB 16; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 AA.
   2.1%; Score 7; DB 1
100.0%; Pred. No. 3.1
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
EMBL; AL445564; CAC13586.1; -.
PIR; E90563; E90563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
Query Match
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
1es 7; Conservative
                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                         231 LLGELIL 237
                                                                                                                                                                                  428 LIGELIL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 IVKILKD 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycoplasma pulmonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 IVKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome SEQUENCE 440 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q7VINB
Q7VINB;
                                                                                                                                                                                                                                                                                                                                        0980F3
                                                                                                                                                                                                                                                                               RESULT 154
Q98QF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7VINB
                                                                                                                                                                                                                                                                                                                                                                                                  DDT REPARENT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY O
                                                                                                                            à
                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
```

0

```
NCBI_TaxID=55601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7SXY7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q7SXY7
                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT TO DESCRIBE TO THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A., "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
SEQUENCE FROM N.A.
STRAIS-ATC 51449 / JBI;
STRAIS-ATC 51449 / JBI;
SUEZDRO-2709201; PubMed=12810954;
Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P.,
Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
Helland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,
Schauer D.B., Shen Z., Meber J., Frosch M., Fox J.G.;
"The complete genome sequence of the carcinogenic bacterium
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Listonella.
                                                                                                                                                                                                                                                                                               2.1%; Score 7; DB 16; Length 442; 100.0%; Pred. No. 3.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the EMBL/GenBank/DDBJ databases
                                                                                                                                                                    Helicobacter hepaticus.",
Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906 (2003).
EMBL; AE017145; AAP77163.1;
Isomerase; Complete protesome.
SEQUENCE 442 AA; 50710 MW; DE9377336D28834C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 443 AA; 51998 MW; 2BBD1D59F237B074 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 24, Last sequence update) (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            444 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 2.1%; Score 7; DB 5
Local Similarity 100.0%; Pred. No. 3.1
les 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio anguillarum (Listonella anguillarum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dictyostelium discoideum (Slime mold)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22092622; PubMed=12097910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baumgart C.;
Submitted (MAR-2003) to the
EMBL; AC115608; AAL92378.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 418:79-85(2002).
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
7; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLre
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                291 VEILLKN 297
                                                                                                                                                                                                                                                                                                                                                                                                                         296 VEILLKN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 LIEFLSS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIEFLSS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=AX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8T2G0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        056568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QS6568
1D QS
AC QS
DT 01
DT 01
DT VI
GN VI
OS VI
OC VI
    g
                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

```
ALESTONE DOLL OF The STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sutterfield Y.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
NCBI_TaxID=7955,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                            Milton D.L., Norgvist A., Wolf-Watz H.; "Sequence of a novel virulence-mediating gene, virc, from Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 100.0%; Pred. No. 3.2e+02; 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 2; Length 444;
100.0%; Pred.•No. 3.2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC055195; AAH55195.1; -. Hypothetical protein.... ""18086797841BABE CRC64;
                                                                                                                                                                                                                                                   Gene 164:95-100(1995).

EMBL; U17054; AAA86985.1; -.

EMRL; U17054; AAA86985.1; -.

EIR; U17054; PR001440; TPR.

InterPro; IPR0018941; TPR-1ike.

SEQUENCE 444 AA; 51461 MW; 78F0B5901907717F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             444 AA; 51111 MW; 77898CC82F41BABE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           444 AA.
                                                                                            MEDLINE=96060845; PubMed=7590330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sednences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 AQELYSS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 AQELYSS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserva
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                            anguillarum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA
                                              STRAIN-NB10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IISSUE=Body;
```

0

```
Hypothetical
SEQUENCE 45
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 084RN6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q84RN6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q7XUF9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q84RN6
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Ecker J., Theologis A., Davis R.W.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY BELLOMGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                   01-UNY-2002 (TrEMBLrel. 21, Created)
01-UNY-2002 (TrEMBLrel. 21, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 7; DB 1
100.0%; Pred. No. 3.2
tive 0; Mismatches
                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25, Putative enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POLYGALACTURONASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
            325 LIKQIRD 331
                                                  188 LIKQIRD 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 LIEFLSS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 LIEFLSS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8FJ04;
                                                                                                                                                   OBRWK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08FJ04
                                                                                                           RESULT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08FJ04
ID 08
AC 08
DT 01
DT 01
DE DT
                                                                                                                                                   D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D D T D T D D T D D T D D T D D T D D T D D T D D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T 
          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                          SEQUENCE FROM N.A.
STRAIN=OG:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
MEDLINE=22388234; PubMed=12471157;
Melch R.A. Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
MEXTERNELY emosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
GO:0003824; F:catalylic activity; IEA.
GO:0003825; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Becherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 7; DB 16; Length 452; 100.0%; Pred. No. 3.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 10; Length 453; 100.0%; Pred. No. 3.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang R., Han B., Hong G.F.; Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AL627380; CAD79706.1; -.. GQ; GQ:00003674; C:nucleus; IEA. GQ; GQ:0003677; F:DNA binding; IEA. InterPro; IPR0016652; Kelch, rep. InterPro; IPR0016652; Kelch, 4. SNART; SM00612; Kelch; 4. SNART; SM00612; Kelch; 3. PROSITE; PS000344; MRB_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   452 AA; 51206 MW; 49A96E64FE8E3C79 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ıl protein."
453 AA; 50562 MW; 6A8ABFC386D0AAA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein H0302E05.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          453 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000873; AMP-bind.
Pfam; PF00501; AMP-binding; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 DIASDAF 184
Escherichia coli 06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 DIASDAF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 VLVADFL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 VLVADFL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                           NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4530;
```

PRT;

PRELIMINARY;

```
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                CPE0896
                                                                                  Q8XLZ4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9AWX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 165
Q9AWX3
                              RESULT 164
                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22482865; PubMed=12594514;
Langk/ABr R.B., Cliften P.F., Johnston M., Piskur J.,
"Yeast genome duplication was followed by asynchronous differentiation
of duplicated genes.";
                                                                                                                                                                                                                                                                                                                               Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., Chen L., Ran D.L., Weng Q.J., Zhang L., Lu Y.L., Mu J., Yu Z., Lu T.T., Zhang Y.J., Lu Y.C., Li Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Mu M., Submitted (DBC-2001) to the BML/GenBank/DDBJ databases.

Submitted (DBC-2001) to the BML/GenBank/DDBJ databases.

SEQUENCE 453 AA; 50532 MW; 6A8ABFDD795AAA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoldeae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.1%; Score 7; DB 3; Length 459; Best Local Similarity 100.0%; Pred. No. 3.2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CBS4309;
Langkjaer R.B., Cliften P.F., Johnston M., Piskur J.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY144952; AA032515.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 459 AA; 48585 MW; 3EC9C765C08E9A23 CRC64;
                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                459 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 7; DB 1.1
100.0%; Pred. No. 3.2
Itive 0; Mismatches
                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces castellii (Yeast).
                                         01-0CT-2003 (TrEMBLrel. 25, C1
01-0CT-2003 (TrEMBLrel. 25, L2
01-0CT-2003 (TrEMBLrel. 25, L2
0J991113 30, 7 protein.
0J991113 30, 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 421:848-852(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 VLVADFL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             311 SSGLLVT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 VLVADFL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 SSGLLVT 81
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=27288;
                                                                                                                                                                                                                                                                    NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CBS4309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 163
2875W3
AC 2875W3
AC 2875W3
DT 01-JUN
DE PHO87
OC SACCHA:
OC BUKATYO
OC SACCHA:
OC BUKATYO
OC SACCHA:
OC BUKATYO
OC SACCHA:
OC BUKATYO
OC SACCHA:
OC BUKATYO
OC SACCHA:
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUCKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKATYO
OC BUKAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q875W3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=13 / Type A;
MEDLINE=21664373; PubMed=11792842;
Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
Shinatu T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                      Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.1%; Score 7; DB 16; Length 475; Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AP002908, BAB32936.1, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53567 MW; B889927345727429 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           flesh-eater.";
Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).
BMBL, Abullass and Sci. U.S.A. 99:996-1001 (2002).
GO: GO: 0005524; F:ATP binding; IEA.
GO: GO: 0016391; F: Kinase activity; IEA.
GO: GO: 0006508; F: Subtilase activity; IEA.
InterPro: IRR003594; ATPbind ATPase.
InterPro: IRR000399; Peptidase_S8.
Pfam. PF02518; HATPase_c; 1.
                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative ribosomal RNA apurinic site specific lyase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             476 AA.
                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last seque
01-OCT-2003 (TrEMBLrel. 25, Last annot:
Two-component sensor histidine kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gramene; 09AWX3; -
GO; GO:0016829; F:lyase activity; IEA.
InterPro; IPR001810; F-box.
InterPro; IPR006566; FBD.
InterPro; IPR008945; Skp1_Skp2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00387; HATPase c; 1.
PROSITE; PS00136; SUBTILASE ASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kinase; Complete proteome.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00646; F-box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 EVSKSLQ 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 EVSKŠLQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone: P0013G02."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAC
DE REPRENTATION OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PACE OF SOME PAC
```

```
Query Match
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Myocilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 072609;
                                                                                                                                                                                                                                                                           Q924K5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          672FQ9
                                                                                                                                                                                                                              RESULT 168
Q924K5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 169
Q7Z6Q9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                          à
                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Пр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AKO26184; BAB15387.1; ---
SEQUENCE 485 AA; 54051 MW; 4474E549ACD560C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22784745; PubMed=12886019;
MEDLINE=22784745; PubMed=12886019;
Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,
Latorne A., Rausell C., Kamerbeek J., Gadau J., Hoelldobler B.,
van Ham R.C.H.J., Gross R., Moya A.;
"The genome sequence of Blochmannia floridanus: comparative analysis of reduced genomes."
Proc. Natl. Acad. Sci. U. 3. 100:9388-9393(2003).
EMBL; BX248584; CAD83664.1; -.
Ligase; Complete protecome.
SEQUENCE 480 AA; 54194 MW; 2C8C6455543D369F CRC64;
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ol-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MCR-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein FLJ22531.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, ant endosymbionts, Candidatus Blochmannia.
                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                        Query Match 2.1%; Score 7; DB 10; Length 476; Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.1%; Score 7; DB 16; Length 480; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                             476 AA; 51900 MW; 43FF7DC3DDD1305C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
UDP-N-acetylmuramate:alanine ligase (EC 6.3.2.8).
WMCRC OR BFL143.
Candidatus Blochmannia floridanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25, Created)
                                             PROSITE; PS50181; FBOX; 1.
SMART; SM00579; FBD; 1.
SMART; SM00256; FBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                        355 KTDKASE 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 MNLLRDK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452 MNLLRDK 458
                                                                                                                                                                                                                                        34 KTDKASE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=203907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                      Lyase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            Q7VQ17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09H677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 167
Q9H677
                                                                                                                                                                                                                                                                                                                                                                                 OTVOITA
ALD
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DIT
OYA
DI
OYA
DI
OYA
DI
OYA
DI
OYA
DI
OYA
DI
OYA
DI
OYA
DI
OYA
DI
OYA
DI
OYA
DI
OYA
DI
OYA
DI
DR
DR
SO
SO
                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Ahmed F., Tomarev S.I.;
Ahmed F., Tomarev S.I.;
"Rat Myoc/Tigr gene: structure and changes in mRNA level in the retina with induced ganglion cell damage.";
Submitted (UUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF289235; AAK83081.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
DJ45466.1 (Myocilin, trabecular meshwork inducible glucocorticoid response (TIGR)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 11; Length 489; 100.0%; Pred. No. 3.4e+02; tive 0; Mismatches 0; Indels
2.1%; Score 7; DB 4; Length 485; 100.0%; Pred. No. 3.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; Score 7; DB 4; Length 490; 100.0%; Pred. No. 3.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paritt R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003112; Olfac_like.
Pfam: PF02191; OLF; 1.
SEQUENCE 489 AA; 55094 MW; 688D5BB9126E9006 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z98750; CAD92590.1; -. SEQUENCE 490 AA; 55336 MW; 70BCB267AB52428B CRC64;
                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                              489 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               490 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.1%
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                             231 LLGELIL 237
                                                                                                                                            161 LLGELIL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 NLLRDKS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 NLLRDKS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
```

**0866N2** 

```
EMBL, AY190130, AAC40254.1; -...EMBL, AY190128, AAC40254.1; JOINED. EMBL, AY190129, AAC40254.1; JOINED. INTEFPC, IPRO3112; Olfac_like. Pfam; PF02191; OlF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                            Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 NLLRDKS 137
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                       NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7955;
                01-JUN-2003
01-OCT-2003
                                                                   Myocilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7SXV4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7SXV4
                DDT REPRESENTED BY SO DE STANDER SO DE STANDER SERVICE SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO DE STANDER SO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Ahmed F., Tomarev S.I.;
Ahmed F., Tomarev S.I.;
Ahmed F., Tomarev S.I.;
Ahmed F., Tomarev S.I.;
Anded ganglion call damage.";
Submitted (JUL-2000) to the EMEL/GenBank/DDBJ databases.
Submitted (JUL-2000) to the EMEL/GenBank/DDBJ databases.
InterPro; IPR03312; Olfac_like.
Pfam; PP02191; OLF; 1.
SNART; SM00284; OLF; 1.
SNART; SM02284; OLF; 1.
SEQUENCE 490 AA; 55314 MW; 2B5C5475BC2A0425 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·:
                                                                                                                                                                                                                                                                                                                                                                                Shepard A.R., Jacobson N., Sui H., Steely H.T., Lotery A.J., Stone B.M., Clark A.F.;
Stone B.M., Clark A.F.;
Rabbit myocilin cloning Implications for human myocilin glycosylation and signal peptide usage.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.1%; Score 7; DB 11; Length 490; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 7; DB 6; Length 490; 100.0%; Pred. No. 3.46+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     490 AA; 54885 MW; F975AC169461FD49 CRC64;
                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                        490 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q863A3;
01-JUN-2003 (TrEMBLrel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 NLLRDKS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 NLLRDKS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                              Myocilin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                           Q866N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0924K4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q924K4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q863A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 171
Q924K4
RESULT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
```

Q863A3 ID Q8 AC Q8 DT 01

g

```
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=AB; TISSUE=Body;

MEDINE=2238825; PubMed=12477932;

Rausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hisch F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brahler M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Roas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergran B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Raywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20576076; PubMed=11133859; Fingert J.H., Clark A.F., Craig J.E., Alward W.L., Snibson G.R., McLaughlin M., Tuttle L., MacKey D.A., Sheffield V.C., Stone E.M.; Evaluation of the myocilin (MYOC) glaucoma gene in monkey and human steroid-induced ocular hypertension."; Invest. Ophthalmol. Vis. Sci. 42:145-152(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brāchydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Mecazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostarlophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Fingert J.H., Clark A.F., Craig J.E., Alward W.L., Snibson G.R., McLaughlin M., Tuttle L., Mackey D.A., Sheffield V.C., Stone E.M., Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                             Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 6; Length 491;
100.0%; Pred. No. 3.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 AA; 55513 MW; 3D18DEE0BA4D6ABD CRC64;
(TrEMBLrel. 24, Last sequence update) (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492 AA.
```

·.

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-cv. Nipponbare;
McCombie W.R., Spiegel L., de la Bastide M., Preston R., Ferraro K.,
Kuit K., Nascimento L., Zutavern T., Balija V., Bell M., Baker J.,
Santos L., Miller B., Katzenberger F., Muller S., King L., Yang C.,
Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
"Genomic sequence for Oryza sativa, Nipponbare strain, clone
OJ1003C07, from chromosome 10, complete sequence.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group).
Oryza sativa (yiridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnollophyta, Lilliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                      ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Nipponbare,
The Rice Chromosome 10 Sequencing Consortium,
"In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Nipponbare;
Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
Submitted (MAX-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC113335; AAM08826.1; -.
EMBL; AE017084; AAP53374.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 7; DB 10; Length 496;
Pred. No. 3.5e+02;
                                                                                                                                                                                       DB 13; Length 492;
                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                       Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                il protein.
496 Aa; 52120 MW; 133CE5C5CBA88753 CRC64;
                                                                                                                   EMBL; BC055232; AAH55232.1; -.
Hypothetical protein.
SEQUENCE 492 AA; 56252 MW; 4A2AD535B329AE78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative protein phosphatase 2C (Hypothetical protein)
           and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                       3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               496 AA.
                                                                                                                                                                                    Query Match
2.1%; Score 7; DB 1.
Best Local Similarity 100.0%; Pred. No. 3.4
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0003824; F:catalytic activity; IBA.
InterPro; IPR001932; PP2C-like.
Pfam; PF00481; PP2C; 1.
                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, Created)
                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00332; PP2Cc; 1.
SMART; SM00331; PP2C_SIG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 300:1566-1569(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity luv...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                        SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Body;
                                                                                                                                                                                                                                                                                282 SLOAMKE 288
                                                                                                                                                                                                                                                 45 SLQAMKE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gramene; Q8S5N3; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              08S5N3;
                                                                                                                                                                                                                                                                                                                                                            Q8S5N3
                                                                                                                                                                                                                                                                                                                              RESULT 174
                                                                                                                                                                                                                                                                                                                                               Q8S5N3
ò
                                                                                                                                                                                                                                                                              g
```

```
and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chamoun Z., Mann R.K., Nellen D., Bellotto M., Beachy P.A., Basler K., "Drosophila melanogaster skinny hedgehog (ski)."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proceins in intracellular bacteria and eukaryotes, plant plastids, identification of unique biochemical properties of the ATP/ADP-transport protein from Holospora obtusa and Caedibacter caryophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Linka N., Hurka H., Lang F., Burger G., Winkler H.H., Urbany C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Phylogenetic analysis of non-mitochondrial nucleotide transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Holosporaceae; Caedibacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Arthropoda, Héxapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 7; DB 2; Length 499; 100.0%; Pred. No. 3.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allowing an efficient energy parasitism.";
Submitted (ARR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ44110; CAD29686.1; --
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005471; F:ATP binding; IEA.
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGRO0769; AAA; 1.
SEQUENCE 499 AA; 56443 MW; 49923A8BA0F445EE CRC64;
                                                                                                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Skinny hedgehog (SD13634p).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 500 AA.
                                                                                                                                                              499 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004667; ADP_ATP_car.
Pfam; PF03219; TLC; 1.
                                                                                                                                                                                                                                                                                                                                Nucleoside triphosphate protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                 Caedibacter caryophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
430 VSKSLQA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 GLLVTLI 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 GLLVTLI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=28906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Linka N., Hu
Neuhaus E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                    2842J1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                095VY0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q95VY0
                                                                                                                                                              0842J1
                                                                                             RESULT 175
0842J1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395VY(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
a
                                                                                                                                                                                                SO DE RESTANTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DEL CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DEL CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DEL CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DEL CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DEL CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DEL CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DEL CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA CORRESTA DE LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

```
RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Galle R.E., Garge R.A., Lewis S.E., Richards S., Ashburner M., Hederson S.N., Raton G.G., Worthan J.R., Yandell M.D., Zhang O., Chen L.X., Raton G.G., Worthan J.R., Yandell M.D., Zhang O., Chen L.X., Bernadon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Baril J.F., Agbayami A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Barkaktaroglu L., Beasley E.M., Bellew R.M., Basu A., Baxendale J., Barkaktaroglu L., Beasley E.M., Burlis K.C., Busam D.A., Burlis H., Cadleu E., Center A., Chaldra I., RA Burlis R.C., Cableu E., Conter M., Cadleu E., Conter J.M., Cadleu E., Conter M., Cadleu E., Conter M., Cadleu E., Conter M., Cadleu E., Conter M., Cadleu E., Conter M., Cadleu E., Conter M., Cadleu E., Downes M., Dougon-Rocha S., Punkow B.C., Dunn P., RA Burlis R.C., E., Downes M., Dugan-Rocha S., Punkow B.C., Dunn P., Roslen C., Gabrielian A.E., Gary N.S., Galbart W.M., Glasser K., Andrei B., Beller R., Kodira C.C., Ferraz C., Ferriera S., Plaisser R., Allali M., Kalush F., Karpen G.H., Kaz Z., Galbart M., Glasser R., Allali M., Kalush F., Karpen G.H., Kaz Z., Calbart M., Glasser R., Allali M., Kalush F., Karpen G.H., Kaz Z., Kulp D., Lai Z., Liang Y., Lin X., Mattei B., McIntosh T.C., McIeod M.P., McIntosh T.C., Marzt C., Moris S., Morlis S., Morlis S., Morlis S., Morlis S., Morlis S., Morlis S., Wulp D., Lai Z., Liang X., Mattei B., McIntosh T.C., McIeod M.P., McIntosh T.C., Scheeler F., Shen H., Ralush S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O., Zhen J., Kate S., Wu Margy D.M., Naskern D.Y., Yang S., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X., Wang X.
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                               GO; GO:0007225; P:patched receptor ligand processing; IMP. InterPro; IPR004299; MBOAT fam. PF03062; MBOAT; 1. SEQUENCE 500 AA; 58148 MW; 5193D7823CB216B8 CRC64;
                                                                                                                                                                                        Score 7; DB 5; Length 500;
Pred. No. 3.5e+02;
                                                                                                                                                                                                                                  0; Indels
(JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                               500 AA.
                                                                                                                                                                                    Query Match
2.1%; Score 7; DB 5
Best Local Similarity 100.0%; Pred. No. 3.5
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
                     EMBL; AF398410; AAK97480.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG11495 protein (SIGHTLESS).
RASP OR CG11495.
                                                           FlyBase; FBgn0024194; rasp.
                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                   124 LLVTLIA 130
                                                                                                                                                                                                                                                                       78 LLVTLIA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Berkeley;
  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                              99VZU2 ;
                                                                                                                                                                                                                                                                                                                                                                               RESULT 177
                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                               qq
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                  Lee J.D., Treisman J.B.

"Sightless has homology to transmembrane acyltransferases and is required to generate active Hedgehog protein.";

Curr. Biol. 11:1147-1152(2001).

EMBL; AR03477; AR47725.1; -.

EMBL; AR93157; AR47725.1; -.

EMBL; AR93157; Parthed receptor ligand processing; IMP.

GO: GO:0007225; P: Patched receptor ligand processing; IMP.

InterPro; IRR04299; MBOAT_fam.

Pfam; PF03062; MBOAT; 1.

SEQUENCE 500 AA; 58105 MW; 4498DC306976F2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 5; Length 500; 100.0%; Pred. No. 3.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 5; Length 502; 100.0%; Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wallis J.M.,
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G_PATCH; 1.
56846 MW; ACBDF9F6782F59D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL032649; CAA21702.2; -.
PIR; T27190; T27190.
WormPep; Y55D9A.2a; CE28712.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR000467; G patch.
Pfam; PF01585; G-patch; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    511 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. No.
                                                     SEQUENCE FROM N.A.
MEDLINE=21400488; PubMed=11509241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99069613; PubMed=9851916;
Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SMO0443; G_patch; 1.
PROSITE; PS50174; G_PATCH; 1.
SEQUENCE 502 AA. __ec...
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YSSD9A.2a protein.
YSSD9A.2 OR YSSD9A.2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 LLVTLIA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 LLVTLIA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 NEKEPPT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 NEKEPPT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
Les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9XWG6; Q9U244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           095015
095015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95MX60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95MX60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             095015
ID 09
ACCOCCOORDINATION OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
```

```
D9KND4
          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DT-2003 (TrEMBLrel. 25, Last annotation update)
Y55D9A.2b protein.
Y55D9A.2 OR Y55D9A.2B.
Caenorhabditis elegans.
Ebukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genomic sequence for Arabidopsis thaliana BAC F17L21 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hangen N., Howing B., Koo T., Lam B., Lee J. Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriuni M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 7; DB 5; Length 511;
100.0%; Pred. No. 3.6e+02;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                Wallis J.M.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ecker J.R.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR000466, G patch.
Pfam; PR01585; G-patch; 1.
SMART; SM00443; G_patch; 1.
PR05ITE; PS50174; G PATCH; 1.
SEQUENCE 511 AA; 57873 MW; 587CE67B8CECE4F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         investigating biology.";
Science 282:2012-2018(1998).
EMBL; AL032649; CAA21703.2; -.
PIR; T27191; T27191.
WormPep; Y55D9A.2b; CE28713.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005676; F:nucleic acid binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        520 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequ
01-OCT-2003 (TrEMBLrel. 25, Last anno
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     477 NEKEPPT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 NEKEPPT 63
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                        NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9FZL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A PACO PETER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER RAPER
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

```
..
0
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Lee J., Lenz C., Li J., Liu A., Liu J., Schwartz J., Southwick A.,
Thaveri M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Theologis A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Theologis A., Ecker J.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAINEL TOT NIG661 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E. K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 10; Length 520;
100.0%; Pred. No. 3.6e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                    Ecker J.R.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                       Ecker J.R.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR008938; ARM.
InterPro; IPR008531; DUP813.
InterPro; IPR000357; HEAT.
Prom: PF05668; DUF813; 1.
PROSITE; PS50077; HEAT REPEAT; 1.
SEQUENCE 520 AA; 56056 MW; 337977D7766EE9CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Methyl-accepting chemotaxis protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           521 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AC004557; AAF99750.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 406:477-483(2000).
EMBL; AE004347; AAF95945.1; -.
PIR; E82508; E82508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 LIEFLSS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 LIEFLSS 246
SEQUENCE FROM N.A.
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9KND4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09KND4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAC DATE OF THE PROPERTY OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF TH
```

```
NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P0702H08.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9LGI6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8LQS7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        915760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC Q9
AC Q9
DT Q1
DT Q1
DT Q1
DT Q1
OD DE PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8LQS7
                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-0157:187 / EDL933 / ATCC 700927;
BEDLINE-21074935; PubMed=11206551;
PETNA N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                              Query Match
2.1%; Score 7; DB 16; Length 521;
Best Local Similarity 100.0%; Pred. No. 3.68+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC028240; AAH28240.1; -.
Hypothetical protein.
SEOURNCE 522 AA; 58061 MW; C7A910052E10E9E1 CRC64;
                                                                                                                                                         521 AA; 57258 MW; F86E09D49F2DA855 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein z0521.
                    PRINTS; PRO0260; CHEMTRNSDUCR.
SMART; SMO0204; HAMP; 1.
SMART; SMO0203; MA; 1.
PROSITE; PSS0111; CHEMOTAXIS_TRANSDUC_2; 1.
PROSITE; PSS00885; HAMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.1%; Score 7; DB 4 Best Local Similarity 100.0%; Pred. No. 3.6 Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similar to hypothetical protein FLJ22531.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel, 22, 01-OCT-2002 (TrEMBLrel, 22,
Pfam; PF00015; MCPsignal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                  177 LLVTLIA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 LLGELIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 LLGELIL 167
                                                                                                                                                                                                                                                                                          78 LLVTLIA 84
                                                                                                                                 Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8XE85;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002
                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QBN6TO;
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 182
Q8N6T0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OBNETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8XE85
    à
                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE PACTOR OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
SEQUENCE FROM N.A.

STRAIN-C157:H7 / RIMD 0509952;

STRAIN-C156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterchemorrhagic Escherichia coli
"Ol57:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Nipponbare;
Sasaki T., Mateumoto T., Yamamoto K.;
"Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC
clone:P0702H08.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.1%; Score 7; DB 16; Length 523; Best Local Similarity 100.0%; Pred. No. 3.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; A2003350; BAB91860.1; -. GENGGS7; -. GENGGS7; -. SEQUENCE 530 AA, 59292 MW; F8C866F1331B8A07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001646; Speptide_repeat.
Pfam, PP00805; Pentapeptide, "Hypotherical protein; Complete proteome.
SEQUENCE 523 AA; 60952 MW; 11E5D0F0FFB4DD86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            530 AA; 59292 MW; F8C866F1331B8A07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0C903.20 protein (P0030H07.3 protein).
00099G03.20 OR P0030H07.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
2.1%; Score 7; DB 10; Le
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    530 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                        DNA Res. 8:11-22(2001).
EMBL, AE005221; AAG54768.1; -.
EMBL, AP002551; BAB33895.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLre
01-MAR-2003 (TrEMBLre
P0702H08.17 protein.
                                                                                                                                                                                                                                                                                                                                                   PIR; D85538; D85538.
PIR; H90687; H90687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 PLAKIIL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356 ÞLAKÍTL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        514 AQLAQEL 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 AQLAQEL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
```

```
T19D16.24.
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     023691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        023691
                                                                                                                                                                                               000781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 188
023691
                                                                                                                                                                         RESULT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                             Matches
                                                                                                                                                                                      000781
        Z K K K K K
                                                                                                                    à
                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The r144 major histocompatibility complex class I-like gene of rat cytomogalovirus is dispensable for both acute and long-term infection in the immunocompromised host.";
J. Virol. 74:1045-1050(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20473137; PubMed=11018281; Gruijthuijsen Y.K., Beuken E., Bruggeman C.A., Vink C.; "Rat cytomegalovirus R89 is a highly conserved gene which expresses a spliced transcript.";
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Maastricht;
MEDLINE=20091365; PubMed=10623772;
Beisser P.S., Kloover J.S., Grauls G.E., Blok M.J., Bruggeman C.A.,
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza,
                                                                                                                                                                                                                                                                                                                                   6
                                                       SEQUENCE FROM N.A.
STRAIN-cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20366325; PubMed=10906222; Vink C., Beuken E., Bruggeman C.A.; "Complete DNA sequence of the rat cytomegalovirus genome."; J. Virol. 74:7656-7665(2000)
                                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 10; Length 534; 100.0%; Pred. No. 3.7e+02; tive 0; Mismatches 0; Indels
                                                                                                            Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                clone:P0030H07.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002522; BAB036520.1;
EMBL; AP003045; BAB44041.1;
                                                                                                                                                                                                                                   InterPro; Free PPR.
InterPro; IPR002885; PPR.
InterPro; IPR008941; TPR-like.
Pfam; PF01535; PPR; 10.
TIGRFAMS; TIGR00756; PPR; 10.
SEQUENCE 534 AA; 61225 MW; 96CD7BC918119DD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Muromegalovirus.
NCBI_TaxID=79700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                     549 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat cytomegalovirus (strain Maastricht)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-201 FROM N.A.
                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                    16 EIVKILK 22
                                                                                                                                                                                                                                                                                                                                                                         85 EIVKILK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=Maastricht;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Maastricht;
                                    NCBI_TaxID=4530;
                                                                                                                                                                                                                              Gramene; Q9LGI6;
                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9DW53;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9DW53
                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vink
                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D., Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis thaliana chromosome 1 BAC T19D16 genomic sequence."; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                      2.1%; Score 7; DB 12; Length 549;
100.0%; Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 7; DB 10; Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 5; Length 551;
100.0%; Pred. No. 3.8e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 293324; CAB07534.1; -.
Hypothetical protein.
Virus Res. 69:119-130(2000).

EMBL; AF235689; AAF99237.1; -.

InterPro. 1 PR003360; US22.

PFam; PF02333; US2; 1.

SEQUENCE 549 AA; 61955 MW; D9B3680F32436D87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 AA; 60874 MW; BC99686CD23A2F68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         554 AA; 60902 MW; 8188B41F9AE27BBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                               Local Similarity 100.0%; Pred. No. 3.8 nes 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            554 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-OCT-2003 (TrEMBLrel. 25, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel, 05, 01-JAN-1998 (TrEMBLrel, 05, 01-OCT-2003 (TrEMBLrel, 25, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=LV-561;
Ortiz G., Segovia M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; F86244; F86244.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                        323 ILCGTNE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 VTLIADL 373
                                                                                                                                                                                                                                                       52 ILCGTNE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Subtelomeric ORF."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 VTLIADL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
```

```
STRAIN=C57BL/6J; TISSUE=Eye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00350; dynamin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 LLGELIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 LiGELIL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 EILLKNQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 EILLKNO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0949V9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9SKE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 191
Q949V9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9SKE2
                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCOCCOS SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GERARA
                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wormbep, F11E7.2; CE20532.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
GO; GO:0006885; P:regulation of pH; IEA.
InterPro; IPR006153; Na H porter.
Pfam; PF00999; Na H Exchanger; 1.
SEQUENCE 558 AA; 61977 MW; CCE9DD6E134CBB6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5; Length 558; 0. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lennard N.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harris B.R.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                Pred. No. 3.8e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 7; DB 5
100.0%; Pred. No. 3.8
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, Z68106, CAA92125.2, -.
EMBL, Z49153, CAA92125.2, JOINED.
EMBL, Z49153, CAD30426.1, -.
EMBL, Z68106, CAD30426.1, JOINED.
PIR, T22075, T22075.
100.08; Pro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dynamin-like 120 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2002 (TrEMBLrel. 21, 01-OCT-2003 (TrEMBLrel. 25,
                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                               161 AILEKOD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 PIVEILL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       457 PIVEILL 463
                                                                                                                                                  26 AILEKQD 32
                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1] -
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F41E7.2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                RESULT 189
Q20274
AC Q20274
DT Q1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OUN
DT O1-OU
                                                                                                                                                                                                                                                                                                                                                                                                                      920274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08BK99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8BK99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 190
088K99
1D 088K99
AC 088K99
DT 01-MAR
DT 01-MAR
DT 01-CT
DE DYNAMII
OS MARMIN
OC ENEATY
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMAI
OC MAMMA
                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                   QD
                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RA Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,
RA Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,
RA Jang P.K., Lee J.M., OnoGera C.S., Quach H.L., Tang C., Toriumi M.,
RA Yamamura Y., Yu G., Yu S., Bowesr L., Carninci P., Chen H., Chenk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
RA Ecker J.R., Theologis A., Tracy S.E., Shinozaki K., Davis R.W.,
RY Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W.,
RA Ecker J.R., Theologis A., Tracy S.E., Shinozaki K., Davis R.W.,
RY Submitted (JUL-201) to the EMBL/GenBank/DDBJ databases.
BR Entl. Length C. DAR ARA2798 1; --
BR EMBL, AVGOS061, ARA2798 1; --
BR InterPro: IPRO04993; GH3:
BR Ffam; PF03321; GH3: 1.
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
Hanalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative auxin-responsive protein apuate,
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II, Brassicales; Brassicaceae, Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 11; Length 567;
100.0%; Pred. No. 3.9e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 10; Length 575; 100.0%; Pred. No. 3.9e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               64377 MW; CA9D6BC0FC7AAD52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9SKE2, Q9LKI2;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-UNY-2002 (TrEMBLrel. 21, Last sequence update)
01-OTV-2003 (TrEMBLrel. 25, Last annotation update)
Putative auxin-responsive protein (FIN219).
AT2G46370 OR FIN219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        575 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  575 AA
                                                                                                                                                                                                                        MGD; MGI:1921393; Opal.
GO; GO:0005739; C:mitochondrion; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                         InterPro, IPR001401; Dynamin.
                                                                                                                                                                                                EMBL; AK053861; BAC35561.1;
                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0195; DYNAMIN.
SMART; SM00053; DYNC; 1.
SEQUENCE 567 AA; 64377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
```

```
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8M434;
                                                                                                                                                                                                                                                                                                                                                                         Q7X8T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8M434
                                                                                                                                                                                                                                                                                                                         RESULT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 195
                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                 Q7X8T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8M434
       8 2 2 8 S
                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                     "FIN219, an auxin-regulated gene, defines a link between phytochrome A and the downstream regulator COP1 in light control of Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                         STRAIN=cv. Columbia;
Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
Fraser C.M., Venter J.C.,
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Yamada K., Chan M.M., Chang C.H., Dale J.M., Heuan V.W., Lee J.M.,
Quach H.L., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
Yu G., Yuan S., Chen H., Cheuk R., Jones T., Kim C.J., Nguyen M.,
Palm C.J., Shinn P., Southwick A., Tripp M.G., Wu T., Davis R.W.,
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20381006; PubMed=10921909;
Hsieh H.-L., Okamoto H., Wang M., Ang L.-H., Matsui M., Goodman H.,
Deng X.-W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels . 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 7; DB 10; Length 575; 100.0%; Pred. No. 3.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ecker J.R., Theologis A.;
"Arabidopsis Open Reading Frame (ORF) Clones.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ACCO6525, AAD33040.2;
EMBL; AF279129; AAF86349.1;
EMBL; AX150437; AAN12979.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berks M.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF03321; GH3; 1.
SEQUENCE 575 AA; 64350 MW; 2E4304B03DA6DE59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes Dev. 14:1958-1970(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel.* 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2003 (TrEMBLrel. 24, R102.7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR004993; GH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                              STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 EILLKNQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A84902; A84902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EILLKNO 40
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                      NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berks M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   021893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 193
1021893
AC 021893
AC 021893
DT 01-NOV.
DT 01-UNOV.
DE R102.7
GN R102.7
GN R102.7
CC RIABDAIIO
CC RIABDAIIO
CC RIABDAIIO
CC RIABDAIIO
CN RABDAIIO
RR SEQUENT
RR SEQUENT
RR SEQUENT
RR SEQUENT
RR SEQUENT
RR SEQUENT
RR SEQUENT
RR SEQUENT
RR SEQUENT
RR SEQUENT
RR SEQUENT
RR SEQUENT
RR SEQUENT
RR SEQUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUENT
RR SEGUEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             021893
  DP
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                     Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=KPR98;
Dubach J., Patterson B.D., Briggs M.B., Venzke K., Flammand J.,
Stander P., Scheepers L., Kays R.;
"Molecular genetic variation across the southern geographic range of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ol-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
05.NNBa0023J03.20 protein (OSJNBa0024J22.9 protein).
05.NNBA0023J03.20 OR OSJNBA0024J22.9.
05.NNBA0023J03.20 OR OSJNBA0024J22.9.
05.NNBA0023J03.20 OR OSJNBA0024J22.9.
05.NNBA0023J03.20 OR OSJNBA0024J22.9.
05.NNBA0023J03.20 OR OSJNBA0024J22.9.
06.NNBA0023J03.20 OR OSJNBA0024J02.9.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0024J03.
06.NNBA0023J03.20 OR OSJNBA0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Felidae, Panthera.
                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 10; Length 593;
100.0%; Pred. No. 4e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                  Length 587;
                                                                                                                                                                                                                                                                                                0; Indels
EMBL; Z70309; CAA94361.1; -.
PIK; T24103; T24103.
WOTHDEP; R102.7; CE06335.
SEQUENCE 587 AA; 66150 MW; 64C5A0F8BCC9973D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           593 AA; 66432 MW; 14E4AA7B18333FC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NADH dehydrogenase subunit 5.
                                                                                                                                                                                                    2.1%; Score 7; DB 5; L
100.0%; Pred. No. 4e+02;
trive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                593 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 606 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                            7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  356 KKTDKAS 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   572 AILEKOD 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Panthera leo (Lion).
                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               33 KKTDKAS 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 AILEKOD 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9689;
```

```
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,

Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,

Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,

Miranda M., Narusaka M., Mayyen M., Palm C.J., Sakurai T., Satou M.,

Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VI-COLLEGE DECEDIO.

FONT.4/AT5G52560.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carminci P., Charles H., Cheuk R., Hayashizaki Y., Ishida J., Oznenici P., Charles T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Karlin-Neumann G., Rawai J., Kim C., Koesema E., Lam B., Lin J., Sakurai T., Satou M., Nayuen M., Palm C.J., Sakurai T., Satou M., Seki M., Nayuen M., Palm C.J., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "Full Length CDNA of gene F6NY.4/ATSG52560 (GT:8953711)."; "Full Length CDNA of gene F6NY.4/ATSG52560 (GT:8953711)."; EMBL; AR360236; AAK264093.1; -.
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE ANN. 3.1...

Moreau J., Lebreton S.;

Moreau J., Lebreton S.;

"Small G protein XRalB cross-talks with Ras/Raf/MAPK pathway to control the morphogenetic movement of gastrulation.";

Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ304845; CAC19674.1;

InterPro; IPR000198; RhoGAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Full Length cDNA of gene F6N7.4/AT5952560 (GI:8953711)."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 7; DB 13; Length 611;
100.0%; Pred. No. 4.1e+02;
/ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 611 AA; 71592 MW; 2AE1A5D64F74B5C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RalB-binding protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             614 AA.
                                                                                                                                                                               Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00324; RhoGAP; 1.
PROSITE; PS50238; RHOGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00620; RhoGAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                  Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 LRRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 LRRQIGT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             090511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SO DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR READ DR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                  the African lion, Panthera leo.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBU databases.
EMBL; AR38614; AMM46197.1; -.
GO; GO:0008137; E:NADH dehydrogenase (ubiquinone) activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
InterPro; IPR001316; NADHub oxidored.
InterPro; IPR001156; Oxidored.g1.
InterPro; IPR001156; Oxidored.g1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-JCM 10545 / 7;
MEDLINE-21456156; PubMed=11572479;
Kawarabbayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Oshi K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Res. 8.123-140(2001).

EMBL; AP000984; BAB65993.1; -.

GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.

GO; GO:0005976; P:polysaccharide metabolism; IEA.

InterPro; IPR000165; Glyco_hydro_15.

InterPro; IPR008928; Glyco_hydro_15.

Ffam, PF00723; Glyco_hydro_15.

Ffam, PF00723; Glyco_hydro_15.

Ffam, PF00723; Glyco_hydro_15; 1.

SEQUENCE 606 AA; 70032 MW; F98C6DFB1446BD92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 17; Length 606; 100.0%; Pred. No. 4.18+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
2.1%; Score 7; DB 8; Length 606;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00361; oxidored q1; 1.
Pfam; PF00662; oxidored q1; 1.
PRINTS; PR01434; NADHDHGNASES.
NAD; Oxidoreductaes; Ubiquinone; Mitochondrion.
SEQUENCE 606 AA; 68282 MW; 1E23B012895BE04B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein ST0973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 SLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        558 SLKLIGE 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 LLVTLIA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sulfolobus tokodaii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 LLVTLIA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=111955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sulfolobus.
```

097300

RESULT 196

셤

ò

611 AA.

PRT;

PRELIMINARY;

Q9DDA3; **Q9DDA3** 

RESULT 197

**Q9DDA3** 

Query Match

ò

ö

0;

```
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                       Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLR5867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O98AT0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D98AT0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=RAG-1;
Nakar D., Gutnick D.L.;
"Genomic organization of the wce region of Acinetobacter lwoffii RAG-1 required for emulsan biosynthesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature D., Gutnick D.L.;

"A protein tyrosine kinase of Acinetobacter Iwoffii RAG-1 is involved to memlsan biosynthesis.",

Submitted (UN-1999) to the EMBL/GenBank/DDBJ databases.

BMBL, AJ243431; CAB57208.1; -.

PIR; 144840; 144840.

GO, GO:0009058; P:biosynthesis; IEA.

InterPro; IPR003869; Polysac Capp.

Pfan; PF02719; Polysac Capp.

Pfan; PF02719; Polysac Capp.

Pfan; PF02719; Polysac Gap.

Pfan; PF02719; Polysac Gap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702,
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Moraxellaceae, Acinetobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                 DB 10; Length 614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 2; Length 624;
100.0%; Pred. No. 4.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                       Query Match
2.1%; Score 7; DB 10; Length 614
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
      GO; GO:0016779; F:nucleotidyltransferase activity; IEA.
                                                                                                                                   al protein.
614 AA; 67852 MW; A83D823026E1BDA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
At1g27210/T7N9_27 (Expressed protein) (At1g27210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Putative dTDP-glucose-4,6-dehydratase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        625 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                 GO; GO:0008152; P:metabolism; IBA.
InterPro; PRR02618; UDRGP.
Pfam; PF01704; UDRGP; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acinetobacter lwoffii
                                                                                                                                                                                                                                                                                                                                                                                                                          261 LYSSGLL 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 LLVTLIA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 LLVTLIA 62
                                                                                                                                                                                                                                                                                                                                                          73 LYSSGLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=28090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-RAG-1;
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 200
Q93ZH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9RMC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           093 ZH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 199
Q9RMC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09RMC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OCCOCO CONTRACTOR OF COCOCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COCOCO COC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAN TERMENT OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
          % ₹ B B B B
                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A.,
Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Pahim C.J., Quach H.L., Sakurai T., Satou M.,
Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G.,
Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis ORP clones.",
Submitted (MAX-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AX057340, AAL09780.1,
EMBL, BY140087, AAM98228.1,
EMBL, BY140087, AAM98228.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nikayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Icomplete genome structure of the nitrogen-fixing symbiotic bacterium
Cheuk R., Chen H., Kim C.J., Koesema B., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M., Palm K.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 10; Length 625; 100.0%; Pred. No. 4.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                          "Arabidopsis cDNA clones."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF05668; DUF813; 1.
PROSITE; PS50077; HEAT REPEAT; 1.
SEQUENCE 625 AA; 67541 MW; 387B03D99CF9262B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  631 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABC transporter, ATP-binding protein, ExsA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR008938; ARM.
InterPro; IPR008531; DUF813.
InterPro; IPR000357; HEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity luv...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 LIEFLSS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 LIEFLSS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
```

```
permease domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prochlorococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1219;
                                                                                                                                                                                                                           NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q7V9L8
Q7V9L8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR01812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
    g
         DNA Res. 7:331-336(2000).

REMBL; AP003007; BAB52242.1; -.

REMBL; AP003007; BAB52242.1; -.

RO; GO:0005224; F:ATP binding; IEA.

GO; GO:000166; F:ATP-binding; IEA.

GO; GO:000166; F:RATP-binding; IEA.

GO; GO:000166; F:RATP-binding; IEA.

GO; GO:000166; F:RATP-binding; IEA.

GO; GO:000166; F:RATP-binding; IEA.

GO; GO:000166; F:RATP-binding; IEA.

GO; GO:000166; F:RATP-binding; IEA.

GO; GO:000166; F:RATP-binding; IEA.

GO; GO:000166; F:RATP-binding; IEA.

GO; GO:000166; F:RATP-binding; IEA.

GO; GO:000166; F:RATP-binding; IEA.

FOR THEPPO; IPR00143; ABC transporter; I.

FroDom; PD0000064; ABC transporter; I.

FRODOM; PD0000064; ABC TRANSPORTER, I.

FROSTIE; PS0091; ABC TRANSPORTER, 2; I.

ROSTIE; PS0091; ABC TRANSPORTER, 2; I.

ROSTIE; PS0091; ABC TRANSPORTER, 2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN—ATCC 50358;

MEDLING—E233190; Pubmed=12446799;
SIMPSON A.G.B. Lukes J., Roger A.J.;

Simpson A.G.B., Lukes J., Roger A.J.;

"The Evolutionary History of Kinetoplastids and Their Kinetoplasts.";

Mol. Biol. Bvol. 19:2071-2083(2002).

Mol. Biol. Evol. 19:2071-2083(2002).

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0003754; F:Chaperone activity; IEA.

InterPro; IPRO01494; Hsp90.

Pfam; PF00181; HSP90.

Pfam; PF00181; HSP90.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length 631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Buglenozoa; Kinetoplastida; Bodonidae; Bodo.
NCBI_TaxID=127146;
                                                                                                                                                                                                                                                                                                                                                                                                                631 AA; 69489 MW; A7DAEB1F457A6985 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72719 MW; 02DF994CA541EAD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) Heat shock protein 90 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 16; Le
100.0%; Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 5; Ler
100.0%; Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 3.3.
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       634 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match Local Similarity 100.0%; Pred. No. 3.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00775; HEATSHOCK90.
SMART; SM00387; HATPase_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    634
Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 DIASDAF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 DIASDAF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 EKQDKKT 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          634 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 EKQDKKT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bodo saliens
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 202
081820
AC 081820
AC 081820
DT 01-MAR
DT 01-MAR
DT 01-CT
B Heat of
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
CO ENERTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  081820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSP-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 203
Q8KJ66
ID Q8KJ66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
RT
DR
DR
DR
DR
DR
DR
DR
SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

PRELIMINARY;

Q8KJ66

```
Mesorhizobium loti strain M7A.;

I. Bacteriol. 184:3086-3095(2002).

BMB1, AL672114; CAD31371.1; -.

CG, GO:0016620; C:membrane; IEA.

GO; GO:00016020; E:ATP binding; IEA.

GO; GO:000166; F:ATP binding; IEA.

GO; GO:000166; F:nuclectide binding; IEA.

GO; GO:000166; F:nuclectide binding; IEA.

GO; GO:000166; F:nuclectide binding; IEA.

GO; GO:000166; F:nuclectide binding; IEA.

RO; GO:000166; F:nuclectide binding; IEA.

GO; GO:000166; F:nuclectide binding; IEA.

RO; GO:000166; F:nuclectide binding; IEA.

GO; GO:000166; F:nuclectide binding; IEA.

RO; GO:000140; ABC_transporter.

Romar: PF00064; ABC membrane; 1.

Rem; FF00065; ABC_transporter; 1.

ROD; FF00005; ABC_transporter; 1.

ROD; GO:00011; ABC_TRANSPORTER_1; 1.

ROSITE; PS00211; ABC_TRANSPORTER_2; 1.

ROSITE; PS00211; ABC_TRANSPORTER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable SACCHARIDE EXPORTING ABC transporter protein, ATP-binding and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M., Barbe V., Duprat S., Galperin M.Y., Koonin B.V., Le Gall F., Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B., Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P., Wolf Y.I., Hess W.R.;
"Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxyphotocrophic genome.";
Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sullivan J.T., Trzebiatowski J.R., Cruickshank R.W., Gouzy J., Brown S.D., Elliot R.M., Fleetwood D.J., McCallum N.G., Rossbach U., Stuart G.S., Weaver J.E., Webby R.J., de Bruijn F.J., Ronson C.W.; "Comparative sequence analysis of the symbiosis island of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prochlorococcus marinus.
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
                                                                                                                                                                                                                                                                                                           Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 2; Length 643; 100.0%; Pred. No. 4.3e+02; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         643 AA; 70759 MW; DA6253137BF605B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Metallo-beta-lactamase superfamily hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 647 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21999272; PubMed=12003951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=SARG / CCMP 1375 / SS120;
MEDLINE=22810154; PubMed=12917486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 DIASDAF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 DIASDAF 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PACTOR AND PROPERTY OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STREET OF STR
```

```
InterPro; IPR000357; HEAT.
Pfam; PF05668; DUF813; 1.
PROSITE; PS50077; HEAT REPEAT; 1.
PROSITE; 649 AA; 70051 MW; 40A16FF2F185CCCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                Q8KFR3
                                                                                                                                                                                                                                                                                                                                                        RESULT 206
Q8KFR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7V430
ID Q7
AC Q7
       88 B B B
                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi B., Corn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AC000348, ARP, 3987011, -. InterPro; IPR008531, ARM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Pall C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lee J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genomic sequence for Arabidopsis thaliana BAC T7N9 from chromosome
                                                                                                                                                        ô
                                                                                                 Query Match 2.1%; Score 7; DB 16; Length 647; Best Local Similarity 100.0%; Pred. No. 4.3e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ecker J.R.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ecker J.R.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases
                       Hydrolase, Complete proteome.
SEQUENCE 647 AA; 71209 MW; A46F67B9CE9FBBAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   649 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                              PRT;
EMBL; AE017166; AAQ00856.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                        326 IKQIRDL 332
                                                                                                                                                                                                                                                       292 IKQIRDL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T7N9.27
                                                                                                                                                                                                                                                                                                                            RESULT 205
                                                                                                                                                                                                                                                                                                                                                      Q9LFX
     SOW
                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                   ADDRING SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVIC
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO, GO: 0016620; C:membrane; IEA.
GO; GO: 0016524; F:ATP binding; IEA.
GO; GO: 0004009; F:ATP-binding; IEA.
GO; GO: 0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
GO; GO: 0006810; F:ATP-binding; IEA.
GO; GO: 0006810; P: transport; IEA.
InterPro; IPR001140; ABC—IM—transpt.
InterPro; IPR00140; ABC—IM—transpt.
InterPro; IPR003439; ABC—transporter.
Pfam; PF00664; ABC—membrane; 1.
Pfam; PF000055 ABC—transporter; 1.
Probom; PD0000066; ABC—transporter; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=TLS / ATCC 49652 / DSM 12025;

MEDLINE=22103685; PubMed=12093901;

A MEDLINE=22103685; PubMed=12093901;

Bisen J.A., Nelson K.E., Pauleen I.T., Heidelberg J.F., Wu M.,

A Dodson R.J., Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,

Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

A Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,

A Mathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,

Vamathevan J., Tettelin H., Bryant D.A., Fraser C.M.;

The complete genome sequence of Chlorobium tepidum TLS, a

photosynthetic, anaerobic, green-sulfur bacterium.";

Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514 (2002).
                                                                           Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
                    Score 7; DB 10; Length 649;
Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 16; Length 653; 100.0%; Pred. No. 4.4e+02; tive 0; Mismatches 0; Indels
                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73148 MW; 4A6DDC186EAF97EE CRC64;
                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel, 22, Created)
01-OCT-2002 (TrEMBLrel, 22, Last sequence update)
01-OCT-2003 (TrEMBLrel, 25, Last annotation update)
     2.1%; Scor.
100.0%; Pred. No. 4...
                                                                                                                                                                                                                                                                                                   653 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     656 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00211; ABC_TRANSPORTER_1; 1. PROSITE; PS50893; ABC_TRANSPORTER_2; 1. ATP-binding; Complete_protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                      ABC transporter, ATP-binding protein. CT0259.
                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE012804; AAM71505.1; -.
Query Match
Best Local Similarity 100.0
Then 7; Conservative
                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                       301 LIEFLSS 307
                                                                                                                                                                         240 LIEFLSS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 LIEFLSS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 LIEFLSS 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlorobium tepidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       653 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlorobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q7V430
Q7V430;
```

```
..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                 MEDINE=22825698; PubMed=12917642; Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P., Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M., Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A., Webb E.A., Zinser E.R., Chisholm S.W.; and Genome divergence in two Prochlorococcus ecotypes reflects oceanic niche differentiation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                           Bacteria; Cyanobacteria; Prochlorophytes; Prochloroccaceae;
                                                                                                                                                                                                                                                                                                                                                                 . Match 2.1%; Score 7; DB 16; Length 656; Local Similarity 100.0%; Pred. No. 4.4e+02; es 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11; Length 658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases EMBL; BC049983; AAH49983.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              658 AA; 72605 MW; 7A3ECED9287071B0 CRC64;
                                                                                                                                                                                                                                                                                                                                    656 Aa; 71066 MW; 25650D8348BFFDA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter, multidrug efflux type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 11; Le 100.0%; Pred. No. 4.4e+02; live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 662 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         658 AA
                                                                            Prochlorococcus marinus (strain MIT 9313)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                         Nature 424:1042-1047(2003).
EMBL; BX572101; CAE22317.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 13, C
(TrEMBLrel. 23, L
(TrEMBLrel. 24, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.v.
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                           105 LRRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                           494 LRRQIGT 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     596 EEVSKSL 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 EEVSKSL 46
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    Complete proteome
                                                                                                                   NCBI_TaxID=74547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                          Prochlorococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (
01-MAR-2003 (
01-JUN-2003 (
CG5316-PB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9VDX2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     080V96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O9VDX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9VDX2
   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEDTTE
                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
;
0
                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.B., Rubin G.M.,
                                           Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neptera; Endopterygota; Diptera; Brichycera; Brospera; Brosphilidae; Drosophila; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Celniker, S.;
Celniker, S.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AYIBBS2, AAMST0692.1, -.
R PLYBAS, FBGR0038704, CG5316.
R InterPro; IPR001310; HIT.
R InterPro; IPR00130; Aff C2H2.
R Ffam; PP001230; HIT; 1.
R Ffam; PP001230; HIT; 1.
DR SWART; SN00355; ZnF C2H2; 1.
SR SWART; SN00355; ZnF C2H2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 663;
                                                                                                                                                                                                                                                                                  DB 5; Length 662;
0. 4.4e+02;
cches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                    Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003726; AAF55666.2; -.
FlyBase; FBGN0038704; CG5316.
InterPro; IPR00310; HIT.
InterPro; IPR00310; AIT.
Pfam; PF00120; HIT; 1.
Pfam; PF00096; Zf_CC2H2.
SMART; SM00355; ZnF_CC2H2.
SMART; SM00355; ZnF_CC3H2.
SMART; SM00355; ZnF_CC3H2.
SMART; SM00355; ZnF_CC3H2.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 7; DB 5; Les
Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 5
Local Similarity 100.0%; Pred. No. 4.4
es 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBCCN1;
01-MAR-2003 (TrEMBLrel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.1%; Sest Local Similarity 100.0%; Matches 7; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 ISKPENL 255
                                                                                                                                                                                                                                                                                                                                               249 ISKPENL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ISKPENL 17
                                                                                                                                                                                                                                                                                                                                                                             11 ISKPENL 17
                               SEQUENCE FROM N.A.
                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GM01362p.
                                                                                                                                                                                                                                                                                Query Match
                                                                                                             FlyBase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08MSG8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 211
Q8CCN1
ID Q8CCN1
AC Q8CCN1
DT 01-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSCCN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBMSG8
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 210
                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
RRI
RRI
RRI
RRI
RRI
RRI
DR CDR
DR CDR
DR CDR
DR CDR
                                                                                                                                                                                                                                                                                                                                                                             Оp
```

```
MGD; MGI:2444084; Napllo.

GO; GO:0005351; F:sugar porter activity; IEA.

GO; GO:0005401; P:phosphoenolpyruvate-dependent sugar phospho. . .; IEA.

InterPro; IPR001114; HPr SerP.

InterPro; IPR007111; NACHT NTPase.

InterPro; IPR004020; PAAD_DAPIN_dom.
                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUB=Olfactory brain;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.;
Nature 420:563-573 (2002).
EMBL; AK03246; BAC27872.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

STRAIN-cv. Columbia;
Vysotsakaia V.S., Schwartz J.R., Yu G., Toriumi M., Liu S., Lenz C.,
Li J., Kremenetskaia I., Luros J., Altafi H., Gonzalez A., Araujo R.,
Buehler E., Conn L., Conway A.B., Dunn P., Hansen N., Huizar L.,
Kim C., Palm C.J., Rowley D., Shinn P., Walker M., Davis R.W.,
Ecker J.R., Federspiel N.A., Theologis A.,
"Arabidopsis thaliana chromosome 1 BAC F508 sequence.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eurosids, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Columbia;
Theologis A.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
slumitted (DEC-1998) to THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AC005990; AAC98010.1; -.
PIR; B86369; B86369.
GO; GO:0005524; F:ATP binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; her.,
No. 4.5e+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00589; PTS HPR SER; 1.
SEQUENCE 673 AA; 76367 MW; EE773C592BEC7054 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
PAAD and NACHT containing protein.
NAPLIO OR 6430548120RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              731 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 1
100.0%; Pred. No. 4.5
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F508.10, Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF05729; NACHT; 1. —
Pfam; PF02728; PAAD DAIN; 1.
PS051TE; PS50824; DĀPIN; 1.
PROSITE; PS50837; NACHT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 LTRHKVL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 LTRHKVL 395
                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F508.10 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9ZUE0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9ZUE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
```

```
RESULT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 215
                        28WZU0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9KQC3
                                                à
                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22482865; PubMed=12594514;
LangkjAEr R.B., Cliften P.F., Johnston M., Piskur J.;
"Yeast genome duplication was followed by asynchronous differentiation
of duplicated genes ";
Nature 421:848-852(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000371; Src thr.pkin_AS.
Fam; PP00069; Prot kinase.
Probom; PD000001; Prot kinase, 1.
PROSITE; PS00107; PROTEIN_KINASE ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 731 AA; 77639 MM; 45D93AD5C45001B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                  2.1%; Score 7; DB 10; Length 731;
100.0%; Pred. No. 4.8e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=623-6C;
Langkjaer R.B., Cliften P.F., Johnston M., Piskur J.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AX144849; AA032413.1;
GO; GO:0016462; F:pyrophosphatase activity; IEA.
GO; GO:0005415; F:transporter activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:000814; P:sodium ion transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 3; Length 732;
100.0%; Pred. No. 4.8e+02;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           732 AA; 80605 MW; CB4DF258D567C314 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces bayanus (Yeast) (Saccharomyces uvarum).
                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                           732 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro, IPR00585; Hemopexin.
InterPro, IPR001898; Na/Bul symport.
InterPro, IPR008162; Pyrophosphatase.
InterPro, IPR004331; SPX.
                                                                                                                                                                                                                                                                                                                                                  Q876G2;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00939; Na_sulph_symp; 1.
Pfam; PF03105; SPX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00024; HEMOPEXIN; 1. PROSITE; PS00387; PPASE; 1.
                                                                                                                                                                    Ouery Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                   519 KVLVADF 525
                                                                                                                                                                                                                                         195 KVLVADF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        593 SSGLLVT 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSGLLVT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4931;
                                                                                                                                                                                                                                                                                                                                                                                                            (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=623-6C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                              RESULT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                        ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=EI TOR N16961,

MEDLINE=20406833; DubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Frager C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Schulsel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G., Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                            Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes, Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.1%; Score 7; DB 3; Length 734; Best Local Similarity 100.0%; Pred. No. 4.8e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0016020; C:membrane; IEA.
GO; GO:0015093; F:ferrous iron transporter activity; IEA.
GO; GO:0015684; P:ferrous iron transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      German Neurospora genome project;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL66990; CAD21116.1; -.
InterPro; IRO08862; Tcp11.
Pfam; PF05794; Tcp11.
SEQUENCE 734 AA; 81374 MW; 5B8F9A16C66359CF CRC64;
                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TEMBLrel. 24, Last annotation update)
Ferrous iron transport protein B.
                734 AA.
                                                                                       Created)
            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003373; FeoB.
InterPro; IPR006073; GPP1 0BG.
InterPro; IPR005225; Small_GTP.
Pfam; PF02421; FeoB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 406:477-483(2000).
EMBL; AE004281; AAF95223.1; -.
                                                                      01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
    PRELIMINARY;
                                                                                                                                                                                                       Related to SOK1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     510 AQELYSS 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B82122; B82122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 AQELYSS 76
                                                                                                                                                                                                                                                                                          Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=666;
                                                                                                                                                                                                                                                 B8J24.140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
QBWZU0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9KQC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HID DE RELATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
Tetrahymenina; Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                       .,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mochizuki K., Gorovsky M.A.;
Mochizuki K., Gorovsky M.A.;
"Analysis of a piwi-related gene implicates small RNA in DNA
rearrangement in Tetrahymena.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, ABUSALII; BACO2573.1;
InterPro; IPR003106; PAZ.
InterPro; IPR003165; Piwi.
                                                                                                                                                                        DB 16; Length 758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 4; Length 777; 100.0%; Pred. No. 5.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                  Query Match 2.1%; Score 7; DB 16; Length 758 Best Local Similarity 100.0%; Pred. No. 5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL BC006574; ARH05074.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEAM; PF02170; PAZ; 1.
Pfam; PF02171; Piwi; 1.
PROSITE; PS50821; PAZ; 1.
SEQUENCE 780 AA; 89525 MW; 58D3FE686D6FE288 CRC64;
                                                                                 Complete proteome. Sall4 MW; EC194EE2D28FEF28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              777 AA; 86029 MW; 6BA69AB781A99956 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (Fragment)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       777 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           780 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                  TIGRFAMS; TIGRO0437; feoB; 1.
TIGRFAMS; TIGRO0231; small GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
PRINTS; PR00326; GTP1OBG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piwi-related protein.
                                                                                                                                                                                                                                                                                                                                                       332 LVTLIAD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        715 EEVSKSL 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 EEVSKSL 46
                                                                                                                                                                                                                                                                                            79 LVTLIAD 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER
SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8MXZ9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8MXZ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9BSF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8MXZ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O9BSF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATA DATA BANDA DATA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BANDA BAN
S KAR BR
                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetrahymena thermophila.
Eukaryota, Alveolata, Ciliophora, Oligohymenophorea, Hymenostomatida,
Tetrahymenina, Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Rosenauer A., Martindale D.W.;
"The characterization of cnjA, a Tetrahymena gene active only during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=84067828; PubMed=66446127;
Martindale D.W., Bruns P.J.;
"Cloning of abundant mRNA species present during conjugation of
Tetrahymena thermophila: identification of mRNA species present
exclusively during maiosis.";
MAI. Cell. Biol. 3:1857-1865(1983).
                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 7; DB 5; Length 780; 100.0%; Pred. No. 5.1e+02; tive 0; Mismatches 0; Indels
                        DB 5; Length 780; . 5.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Martindale D.W., Rosenauer A.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; AY19021. AAM17972.2;
InterPro; IPR003100; PAZ.
InterPro; IPR003165; Piwi.
Pfam: PF02170; PAZ; 1.
Pfam: PF02171; Piwi; 1.
PROSITE; PS50821; PAZ; 1.
PROSITE; PS50821; PAZ; 1.
SEQUENCE 780 AA; 89552 MW; 51DCDFBZBAF1184 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  01-077-2002 (TrEMBLrel. 22, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thesis (1993), McGill University, Thesis Office,
                                                                                                                                                                                                                                                                                                                                                    780 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          786 AA.
                        2.1%; Score 7; DB 5
100.0%; Pred. No. 5.1¢
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anabaena sp. (strain PCC 7120).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100...
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WD-40 repeat-protein.
                                                                                                                                        228 SLKLLGE 234
                                                                                                                                                                                                  97 SLKLLGE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 SLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 SLKLLGE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CnjA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALR4559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8YNK6
                                                                                                                                                                                                                                                                                                                                                 Q8MQL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 219
                                                                                                                                                                                                                                                                                        RESULT 218
                                                                                                                                                                                                                                                                                                                         ОВМОГЛ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OBYNK6
                                                                                                                                                                                                                                                                                                                                                                                SO DER LE REPRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA PRESENTATION DE LA P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
RESULT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           066933
                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 5192976; Dubmed=11932238;

A Balagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

A FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

A Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

A Zimmer A., Barber R.D., Cann I., Graham D.B., Grahame D.A., Guss A.M.,

RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

RA Hedderich R., Junyam L.A., White R.H., de Macario E.C.,

RA Springer T.A., Umayam L.A., White R.H., de Macario E.C.,

RA Springer R.M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Metcalf W.W., Birren B.,

Metcalf W.W., Birren B.,
                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.", Genome Res. 12:532-542(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                        Gaps
MEDLINE=21595285; PubMed=11759840; Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kibhida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                 "Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
Methanosarcinales; Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 17; Length 791; 100.0%; Pred. No. 5.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 16; Length 786;
100.0%; Pred. No. 5.1e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                            PRINTS, PRO0320; WD40; 7.

PRINTS, PRO0320; GPRCTEINBRPT.

SMART; SM00320; WD REPEATS 1; 1.

PROSITE; PSS0082; WD_REPEATS 2; 5.

PROSITE; PSS0082; WD_REPEATS 2; 5.

COMPLETE; PSS0084; WD_REPEATS REGION; 1.

COMPLETE PSS0084; WD_REPEATS REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l protein; Complete proteome.
791 AA; 90717 MW; 50BC61629A0CFES7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein MA0561.
                                                                                              cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
EMBL; AP003596; BAB76258.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                               791 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanosarcina acetivorans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE010717; AAM04005.1;
Hypothetical protein; Compl
                                                                                                                                      PIR; AG2375; AG2375.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                       Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                        282 NLAILEK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 DKASEEV 228
                                                                                                                                                                                                                                                                                                                                                 24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 DKASEEV 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8TT76
                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 220
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        원
```

```
MEDLINE=2160851; PubMed=11743194; Miller N., Blanchard M., Godner B., Hinkle G., Gattung S., Miller N., Blanchard M., Godner B., Stodner B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Lartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Gielo C., Slater S.; Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens CSB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21608550, PubMed=11743193; Mooks D.E., Kitajima J.P., Nood D.W., Setubal J.C., Kaul R., Mooks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Roues G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                     Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiane, Rhizobiane, Agrobacterium group; Agrobacterium. WCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 7; DB 16; Length 818; 100.0%; Pred. No. 5.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     818 AA; 90067 MW; 06A011D8EE9D234E CRC64;
                                                                                                                                                                    ATU2575 OR AGR C_4665.
Agrobacterium tumefaciens (strain C58 / ATCC 33970)
                                                                                                                Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                           Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mannose-1-phosphate guanyltransferase.
MPG OR AO 718.
                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; iPR006979; Gal_bind_like.
Complete proteome.
SEQUENCE 818 AA; 90067 MW: 06201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE009203; AAL43556.1; -. EMBL; AE008170; AAK88298.1; -. PIR; A97668; A97668. PIR; AF2892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 294:2317-2323(2001).
                                                      01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 100.8
Matches 7; Conservative
   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 KLLGELI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPG OR AQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            066933
QBUCC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REAK OOS GE DIT
```

```
ö
                                                                                                                                                                                                                    Nature 392:353-358(1998).

BNBL; AR000704; AAC06893.1; -

PIR A70363; A70363.

GO; GO:0016868; Fintramolecular transferase activity, phosph. . .; IEA.

GO; GO:0016868; Firmcleotidyltransferase activity; IEA.

GO; GO:001689; Firmcleotidyltransferase activity; IEA.

GO; GO:0009058; Picarbohydrate metabolism; IEA.

InterPro; IPR001451; Hexapep_transf.

InterPro; IPR001451; Hexapep_transf.

InterPro; IPR005844; PG_PMM_ABAI.

Pfam; PF00132; hexapep_transferase.

Ffam; PF00132; hexapep_transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CO-92 / Biovar Orientalis;

MEDLINE=21470413; PubMed=11586360;

Parkhill J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quall M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague.",

BMBL, AJ4151; CAC91096.1;

PIR; AD0279; AD0279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                            MEDLINE=98196666; PubMed=9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 2.1%; Score 7; DB 16; Length 846; Local Similarity 100.0%; Pred. No. 5.5e+02; No. 5.7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 7; DB 16; Length B31;
100.0%; Pred. No. 5.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00483; NTP_transferase; 1.
Pfam; PF02878; PGM PMM 1; 1.
Transferase; Complete proteome.
SEQUENCE 831 AA; 93607 MW; F39513DC53594EA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00334; MYB 2; 1. Hypothetical protein; Complete proteome. SEQUENCE 846 AA; 95345 MW; DFB8859195F1C4C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001005; Myb_DNA binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative virulence factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
Les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219 SENYVTK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   533 SENYVTK 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=632;
STRAIN=VF5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 223
(08ZE91
DT 01-MAR.
DT 01-MAR.
DT 01-CT.
DT 01-CT.
DT 01-CT.
DT 01-CT.
DT 01-CT.
DT 01-CT.
DT 01-CT.
DT 01-CT.
DT 01-CT.
DT 01-CT.
DT 01-CT.
DT 01-CT.
DT 01-CT.
DT 01-MAR.
DT 01-CT.
DX YETSIN.
CO Bacter.
CO Bacter.
CO Bacter.
CO Bacter.
CO Bacter.
CO Bacter.
CO Bacter.
CO Bacter.
CO Bacter.
CO Bacter.
CO Bacter.
RA FELLWE.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
RA BAKER.
R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08ZE91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best
ò
```

```
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., Perry R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=13 / Type A;
MEDLINE=21664373; PubMed=11792842;
Shimizu T., Ohtanin K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium perfringens.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

EMBL; AP003192; BAB81700.1; -.

GO: GO:0005622; C:intracellular; IEA.

GO: GO:0008409; F:5'-3' exonuclease activity; IEA.

GO: GO:000577; F:DNA binding; IEA.

GO: GO:0004518; F:UNA-directed DNA polymerase activity; IEA.

GO: GO:0004518; F:unclease activity; IEA.

GO: GO:0006260; P:DNA replication; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 16; Length 846;
100.0%; Pred. No. 5.5e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of Yersinia pestis KIM.";
"Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).

BMBL, AE013812, AAM85685.1;
GO, GO:0005634; G:nucleus; IEA.

GO; GO:0005677; F:DNA binding; IEA.

InterPro; IPR001005; Wyb. DNA_binding.

BROSITE; PS00334; WWYB 2; 1.

SEQUENCE 846 AA; 95319 WW; DF8899FDESFIC4C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                  846 AA.
                                                                                                                                                                                                                                    Created)
                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.1%
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                 Putative virulence factor.
                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 IVEILLK 296
564 IVEILLK 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              564 iVEILLK 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                                                                                                                                                   Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLA OR CPE1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     flesh-eater.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clostridium.
                                                                                                                                                                                                 Q8DOH5;
                                                                                                                                                              QBDOH5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8XIW9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 225
                                                                                                RESULT 224
                                                                                                                                      QBDOHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
   g
                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE REPRESENTATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
```

. 0

ô

Gaps

.. 0

```
Sensor protein KdpD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           635 AQLAQEL 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   815 EEVSKSL 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 EEVSKSL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 AQLAQEL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 887 AA;
                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDPD OR PSPTO2245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; PSPT02245;
             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=323;
                                                                                                      TISSUE=Testis;
                                                                                                                                                                                                                                                             NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q883V3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0883V3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q883V3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S
Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project."; Sugano S.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 2.1%; Score 7; DB 4; Length 875; Local Similarity 100.0%; Pred. No. 5.6e+02; Nes 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 875 AA; 97099 MW; 10A0E9147A9BFCB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   866 AA; 99118 MW; E7F786F720146615 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
10-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.1%; Score 7; DB 16; Le Best Local Similarity 100.0%; Pred. No. 5.6e+02; Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 875 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          877 AA.
InterPro; IPR002421; 5.3 exonuclease.
InterPro; IPR001098; 5.3 exo. C.
InterPro; IPR001098; DNA_pol.
InterPro; IPR002298; DNA_pol.
InterPro; IPR002518; Exo. N.1.
InterPro; IPR00513; Exo. N.1.
InterPro; IPR00513; Exo. N.1.
InterPro; IPR00518; HHH 1.
Pfam; PF00476; DNA_pol. N.1.
Pfam; PF00476; DNA_pol. A; 1.
SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HHH; 1.
SMART; SM00278; HHH; 1.
SMART; SM00278; HHH; 1.
SMART; SM00278; HHH; 1.
IGRPAMS; TIGR00593; POLAC; 1.
TIGRPAMS; TIGR00593; POLAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein FLJ21610. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 DEKNYLI 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           813 EEVSKSL 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 DEKNYLI 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EEVSKSL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
SEQUENCE 866 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissum=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OBND03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8ND03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 226
029H706
AC 029H706
AC 029H706
DT 01-MAR-
DT 01-MAR-
DT 01-MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC DL MAR-
DC 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              907H60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCC By High Coc Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market Market 
             음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-DC3000;
Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Buell R., Joardar V., Van Aken S., Feldblyum T., Gwinn M.,
Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
White O., Fraser C., Collmer A.;
"Complete sequence of Pseudomonas syringae.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, ADD16663; AAO55761.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A GO; GO: 0016020; C: membrane; IEA.

R GO; GO: 0016301; F: ATP binding; IEA.

R GO; GO: 0016301; F: F: ATP binding; IEA.

R GO; GO: 0016301; F: ATP binding; IEA.

R GO; GO: 0006315; F: Word-component sensor molecule activity; IEA.

R GO; GO: 000165; F: Tesponse to stress; IEA.

R GO; GO: 000165; P: signal transduction; IEA.

R InterPro; IPR004359; Bact sens pr.C.

R InterPro; IPR004369; Bact sens pr.C.

R InterPro; IPR005467; His kinase.

R InterPro; IPR005467; His kinase.

R InterPro; IPR005467; His kinase.

R InterPro; IPR00516; Usp. dom.

R Pfam; PF00518; HARTase c; 1.

R Pfam; PF00512; KdpDi.

R Pfam; PF00512; KdpDi.

R Pfam; PF00512; KdpDi.

R Pfam; PF00512; VdpDi.

R Pfam; PF00512; VdpDi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 16; Length 887;
100.0%; Pred. No. 5.7e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                           Query Match
2.1%; Score 7; DB 4; Length 877;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
Blum H., Bauersachs S., Mewes H.W., Weil B., Wiemann S.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AL834491; CAD39149.1; -. Hypothetical protein.
                                                                                                                                                                                877 AA; 97314 MW; 95630B42D96FC29D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              887 AA; 96814 MW; B45A5C89EE8B6D69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00344; BCTRLSENSOR.
PROSITE; PS50109; HIS KIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
```

```
RESULT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q88AL5
                                                                                                                                                                                                                        Q9FSE5
                                                                                                                                                                                                                                                                           SOW REPRESENTATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LangkjAEr R.B., Cliften P.F., Johnston M., Piskur J., "Yeast genome duplication was followed by asynchronous differentiation of duplicated genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces castellii (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 3; Length 916; 100.0%; Pred. No. 5.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 902;
                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.1%; Score 7; DB 2; Length 902; Best Local Similarity 100.0%; Pred. No. 5.8e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lampidis R., Kreft J.;
Lampidis R., Kreft J.;
"PlcA/PrfA operon of Listeria seeligeri.";
Submitted (ARR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X9704; CAA65738.1;
InterPro; IPR001899; Gram pos anchor.
InterPro; IPR00437; Prok lipoprot S.
TIGRFAMS; TIGR01167; LPRTG anchor; I.
PROSITE; PS00013; PROKAR LIPOPROTEIN; I.
SRQUENCE 902 AA; 99419 MW; BDADDIIEF7C056DI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CBS4309;
Langkjaer R.B., Cliften P.F., Johnston M., Piskur J.;
Submitrad (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY144951, AA032514.1;
GO; GO:0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00939; Na sulph symp; 1.
Pfam; PF03105; SPX; 1.
SEQUENCE 916 AA; 101476 MW; B18AC6008B6F69A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005215; F:transporter activity, IEA. GO; GO:0006814; P:sodium ion transport; IEA. InterPro; IPR001898; Na/sul_symport. InterPro; IPR004331; SPX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           916 AA.
                                                                                            902 AA.
                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CBS4309;
MEDLINE=22482865; PubMed=12594514;
                                                                                                                                                                      01-JUL-1997 (TrEMBLrel. 04, 01-JAN-1998 (TrEMBLrel. 05, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.(
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 421:848-852(2003).
                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              684 IVKILKD 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 IVKILKD 23
                                                                                                                                                                                                                                                                                                                                                          Listeria seeligeri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=27288;
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=SLCC3379;
                                                                                                                                                                                                                                                                                                  ORF A protein
                                                                                                                                     007686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q875W4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 230
089784
AC 087584
AC 087584
DT 01-0707
DT 01-0707
DE PHO897
DC SACChAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACCHAN
CO SACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0875W4
RESULT 229
007686
AC 007686
AC 007686
DT 01.4UL
DT 01.5UL
DE ORF A 00.5C
CS Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC Bacter
CC 
                                                                                            007686
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=DC3000;
Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=cv. Kusabue; TISSUE=Leaf;
MEDLINE=20453114; PubMed=10998053;
Schaffrath U., Zabbai F., Dudler R.;
"Characterization of RCI-1, a chloroplastic rice lipoxygenase whose synthesis is induced by chemical plant resistance activators.";
Eur. J. Biochem. 267:5935-5942 (2000).
EBRBL; AJ270938; CAC01439.1; -.
HSSP; P08170; 2SBL.
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 7; DB 10; Length 922; 100.0%; Pred. No. 5.9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           922 AA; 104687 MW; BODDOC172A2DFAE0 CRC64;
                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Lipoxygenase (EC 1.13.11.12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-QCT-2003 (TrEMBLrel. 25, Last annotation update)
Cation efflux family protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005506; F:iron ion binding; IEA.
GO; GO:0016165; F:lipoxygenase activity; IEA.
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000907; Lipoxygenase.
InterPro; IPR0009076; PLAT_LH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1053 AA.
                                                                                                                                                                                               922 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PP00305; lipoxygenase; 1.
PRINTS; PR00087; LIPOXYGENASE.
PROSITE; PS0071; LIPOXYGENASE_1; 1.
PROSITE; PS00081; LIPOXYGENASE_2; 1.
                                                                                                                                                                                                                                                      (TrEMBLrel. 16, Created)
                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100. Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 DLLTRHK 195
                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (Rice).
                                                775 SSGLLVT 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 DLLTRHK 70
75 SSGLLVT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gramene; Q9FSES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase.
                                                                                                                                                                                                                                                         01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSPTO0375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q88AL5
                                                                                                                                                                                               Q9FSE5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 232
ठ
```

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 027764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      927764
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92776
         ò
                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=ATCC 19089 / CE15;

MEDINE=21176989, bubMed=11259647;

Mierman W.C., Feldblyum T.V. Laub M.T., Paulsen I.T., Nelson K.E.,

A Nierman W.C., Neldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

By Detocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

By Detocka I., Nelson W.C., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

Salzberg S.L., Venter J.C., Shapiro L., Fraser C. M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

REBL; AR036569; AAK22909.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                 Query Match 2.1%; Score 7; DB 16; Length 1053; Best Local Similarity 100.0%; Pred. No. 6.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16; Length 1055;
White O., Fraser C., Collmer A.; "Complete sequence of Pseudomonas syringae."; Submitted (MAR-2013) to the EMBL/GenBank/DDBJ databases. EMBL; AE016857; AA053919.1; -- IIGR; PSPT00375; -- InterPro; IPR001036; Acrilvin_res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                           1053 AA; 113670 MW; EDB6A557CE363D71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1055 AA; 112904 MW; F31D4E15E0C8CD78 CRC64;
                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO, GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0006810; F:ransporter activity; IEA.
GO; GO:0006810; F:ransport, IEA.
InterPro; IPR008969; Carboxypep_reg.
InterPro; IPR00531; TonB_boxC.
Pfam; PP00593; TonB_dep_Rec; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1094 AA.
                                                                                                                                                                                                                                                               PRT; 1055 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 2.1%; Score 7; DB 1
Local Similarity 100.0%; Pred. No. 6.6
hes 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
                                                                       Pfam; PF00873; ACR tran; 1.
PRINTS; PR00702; ACRIFLAVINRP.
                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                             Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                      OmpA-related protein.
                                                                                                                                                                                                     647 TLIADLO 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 LRDKSPN 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 LRDKSPN 291
                                                                                                                                                                               81 TLIADLO 87
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                               Complete proteome.
SEQUENCE 1053 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                         09A9P9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8TAB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8TAB3
                                                                                                                                                                                                                                    RESULT 233
Q9A9P9
                                                                                                                                                                                                                                                             09A9P9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8TAB3
ID Q8
AC Q8
DT 01
       ð
                                                                                                                                                                               à
```

```
Murakami K., Tanabo, Tarada S.;
Murakami K., Tanabo, Tarada S.;
"Structure of a Plasmodium yoelii gene-encoded protein homologous to
"Structure of a Plasmodium yoelii gene-encoded protein homologous to
the Ca(2+)-ATPase of rabbit skeletal muscle sarcoplasmic reticulum.";
J. Cell Sci. 97:487-495(1990).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- STHILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
EMBL; X55197; CAA38982.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                 Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·.
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
BA99E24.1.1 (Protocadherin 19 (Hypothetical protein KIAA1313))
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein; Calcium; Calcium-binding; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:001601; EC: integral to membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005528; F:ATP binding; IEA.
GO; GO:000588; F:Calcium-transporting ATPase activity; IEA.
GO; GO:0006816; F:Calcium ion transport; IEA.
GO; GO:0006812; P:Cation transport; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:0008152; P:proton transport; IEA.
GO; GO:0015925; P:proton transport; IEA.
InterPro; IPR001757; ATPase_E1-E2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 4; Length 1094;
100.0%; Pred. No. 6.8e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 1094 AA; 120316 MW; EFD59CF996F2EFFE CRC64;
                                                                                                                                                                                                                                                                                                                                       Chapman J.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=91161669; PubMed=2150071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00232; CADHERIN 1; 5.
PROSITE; PS50268; CADHERIN 2; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A45761; A45761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 SSGLLVT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P04191; 1EUL.
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmodium yoelii.
                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996
```

0

```
301 LIEFLSS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baumgart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q803P9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     080329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               086J27
                                                                                                                                                                                                                                                                                                                                                                           RESULT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                  Q803P9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        086J27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | March | Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=MSB8 / DSM 3109;

X MEDLINE=99287316; PubMed=10360571;
A Haft DH., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
A Haft DH., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
A McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
A Heidelberg J., Sutton G.G., Pleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
Tevidence for lateral gene transfer between Archaea and Bacteria from Invalure 399:323-329(1999).
R EMBL, AROINT74, AAD36257.1; -.
R PDB; AZZ287; AZZ287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                           INTERPRETABLE OF CALLON ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE N.
INTERPRETABLE OF CALION ATPASE N.
INTERPRETABLE OF PROUGES AT HYDENE OF C.
INTERPRETABLE OF THROUGES OF THE SECOND OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE N.
INTERPRETABLE OF THE SECOND OF CALION ATPASE N.
INTERPRETABLE OF CALION ATPASE N.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATPASE C.
INTERPRETABLE OF CALION ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 1115; .. 6.9e+02; ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromosome segregation SMC protein, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 5
100.0%; Pred. No. 6.9
iive 0; Mismatches
InterPro; IPR005782; Calcium_ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      784 IVKILKD 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermotoga maritima.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 IVKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09X0R4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09X0R4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DR DR DR KW KW KW SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR SO DR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               임
```

```
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gloeckner G., Eichinger L., Száfranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
2.1%; Score 7; DB 16; Length 1170;
100.0%; Pred. No. 7.2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 7; DB 13; Length 1189;
100.0%; Pred. No. 7.3e+02;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.1%; Score 7; DB 5; Length 1243; Best Local Similarity 100.0%; Pred. No. 7.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC044389; AAH44389.1; -. SEQUENCE 1189 AA: 134074 MW; 1D1838616CC21928 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1243 AA; 147185 MW; 32638DF439FB585C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
Dictyostellum discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyostellida, Dictyostellum.
                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to kinectin 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=AX4;
MEDLINE=22092622; PubMed=12097910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2003) to the EMBL; AC115608; AAO51792.1; Hypothetical protein.
Query Match 2.1
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 262 LRDKSPN 268
                                                                                                               170 KYVELST 176
                                                                                                                                                                    310 KYVELST 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 LRDKSPN 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=AX4;
```

```
PRT; 1280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
        STRAIN=Sprague-Dawley; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 TEAVAÇL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 SLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     493 SIKLIGE 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 TEAVAQL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
                                                                                                                             P19491;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9FTA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 241
Q9FTA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                     Rumenapf T., Strauss E.G., Strauss J.H.;
"Aura virus is a New World representative of Sindbis-like viruses.";
Virology 208:621-633(1995).
                                                                                                                                                                                                                                                                   Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12; Length 1244;
5. 7.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1244 AA; 137116 MW; FB6B682234ED2F46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruemenapf T.H.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
N-methyl-b-aspartate receptor NMDAR2C subunit.
Rattus norvegicus (Rat).
                                                                                                                           PRT; 1244 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Preα. ...
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 7; D
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=95266268; Pubmed=7747434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF126284; AAD13623.1; -.
HKSP; P03316; 1XXF.
MEROPS; C09.001; -.
MEROPS; S03.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                         PRELIMINARY;
|||||||
501 LIEFLSS 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 KYVELST 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                912 KYVELST 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       NCBI TaxID=44158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00798;
SEQUENCE 1244 ?
                                                                                                                                                                                                                            Polyprotein 2.
                                                                                                                                                                                                                                               Aura virus.
                                                                                                                                                                                                                                                                                      Alphavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q62644
Q62644;
                                                                            RESULT 239
Q86925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 240
062644
AC 062644
DT 01-NOV.
DT 01-COTOV
DT N-methy
OC Mutanian
COX NCBL TR
                                                                                                                         Q86925
                                                                                                                         HERE THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF THE PACE OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicocyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Boulter J., Pecht G.; "Nucleotide Sequence of rat NMDA receptor subunit gene NMDAR2C."; Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; U08259; AAA17832.1; -. PIR; B45219; B45219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R.,
De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
Villaroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W.,
Rudd S., Lemcke K., Mayer K.P.X.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                           R GO; GO:0016020; C:membrane; IEA.
R GO; GO:0016020; C:membrane; IEA.
R GO; GO:0005234; F:glutamate-gated ion channel activity; IEA.
GO; GO:0004970; F:inotropic glutamate receptor activity; IEA.
GO; GO:0004970; F:inotropic glutamate receptor activity; IEA.
R GO; GO:0006472; F:receptor activity; IEA.
R GO; GO:0006811; F:rensporter activity; IEA.
R GO; GO:0006215; F:ransporter activity; IEA.
R GO; GO:0006911; P:ion transport; IEA.
R InterPro; IPR001320; Ion glu receptor.
R InterPro; IPR001310; SBP/Glu_receptor.
R InterPro; IPR001311; SBP/Glu_receptor.
R Pfam; PP00060; Iig chan; 1.
R PRINTS; PR00177; NMDARECEPTOR.
R SWART; SM00079; PBPe; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 11; Length 1250; 100.0%; Pred. No. 7.6e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 10; Length 1280;
100.0%; Pred. No. 7.7e+02;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1250 AA; 136706 MW; D45A8BF27B2A79BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEOUENCE 1280 AA; 144481 MW; ED59CE0B9EA89E43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Aradidopsis sequencing project;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL392174; CAC08331.1;
InterPro; IPR002885; PPR.
InterPro; IPR003885; PPR.
InterPro; IPR008481; TPR.
InterPro; IPR00841; TPR-like.
Pfam; PF01555; PPR; 26.
IIGREAMS; IIGR00756; PPR; 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9FTA4;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
```

ô

```
1303 AA; 153737 MW; 5B122456F4FBEF9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1184 SLKLIGE 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 SLKLLGE 234
                                                                                                                                                                                                                                                                                                    611 LIÉFLSS 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                 301 LIEFLSS 307
                                                                                                                       Local Similarity
es 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER
NON TER
SEQUENCE
Receptor.
SEQUENCE
                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBBN38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9SL02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QBBN3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 245
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 244
                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9SL02
                                                                                                                                                                                                                                                                                                                                                                                                                                      QBBN38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SO OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCC COLOR REPRESENTATION OCCURRENTATION OCCURRENTATION OCCURRENTATION OCCURRENTATION OCCURRENTATION OCCURRENTATION OCCURRENTATION OCCURRENTATION OCCURRENTATION OCCURRENTATION OCCURRENTATION OCCURRENTATION OCCURRENTATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
   S &
                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to G-protein-coupled receptor at plasma membrane; interactions in two-hybrid system with Gpa2p; Gprlp.
Dictyostellum discoideum (Blime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=AX4;
MEDLINE=22092222; PubMed=12097910;
MEDLINE=22092222; PubMed=12097910;
Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
"Sequence and analysis of chromosome 2 of Dictyostellum discoideum.";
Nature 418:79-85(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A., "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
BMBL, AC115608; AAOS1793.1; --
GO, GO.0004648; P. Protein serine/threonine kinase activity; IBA.
GO, GO.0006468; P. Protein amino acid phosphorylation; IBA.
InterPro; IPR008271; Ser thr pkin AS.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 5; Length 1297;
100.0%; Pred. No. 7.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein. - - SEQUENCE 1297 AA; 152631 MW; 47F8435D354A5297 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; ARC115681; AAOS2391.1; -.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR002110; ANK.
                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1303 AA.
                                                                                                                                     1297 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Prec. ....
                                                                                                                                                                                                                                                                                                 Hypothetical protein.
Dictyostelium discoideum (Slime mold)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22092622; PubMed=12097910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 418:79-85(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 LIEFLSS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    532 LIEFLSS 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=AX4;
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=AX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=AX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                     Q86J26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 243

Q86HYO
AC Q86HYO
DT 01-JUM
DT 01-JUM
DT 01-JUM
DT 01-JUM
DT 01-CTT
DE Similar
DE SIMILAR
OX NCBL
RR [1]
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR MEDLINI
RR MEDLINI
RR MEDLINI
RR MEDLINI
RR MEDLINI
RR MEDLINI
RR MEDLINI
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
RR SEQUEN
                                                               RESULT 242
086426
AC 086426
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJW
DT 01-UJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 086HY0
                                                                                                                                     086J26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

```
..
0
                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Spleen;
MFDLINB=223546683; PubMed=12466851;
The FANTOM Consortium,
the FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the MINION of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nanalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
MADIATE 420:563-573 (2002).
EMBL; AK086535; BAC40035.1; -.
MGD; MGI:107448; Lyst.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Columbia;
Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vankken S.E.,
Lin X., Kaul S., Shea T.P., Fujii C.Y., Ronning C.M., Benito M.-I.,
Carreta A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
Fraser C.M., Venter J.C.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSELO2; Q9M6P9;
01-MAY-2000 (TYEMBLEE]. 21, Last sequence update)
01-UTN-2003 (TYEMBLEE]. 25, Last annotation update)
01-OCT-2003 (TYEMBLEE]. 25, Last annotation update)
Putative RAD50 DNA repair protein (DNA repair-recombination protein)
(A12431970/RS22D22.28).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 11; Length 1310;
100.0%; Pred. No. 7.9e+02;
ive 0; Mismatches 0; Indels
Length 1303;
                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1310 AA; 146042 MW; 1E1E97EBBBC45BFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              (TremBirel. 23, Created)
(TremBirel. 23, Last sequence update)
(TremBirel. 24, Last annotation update)
2.1%; Score 7; DB 5; Le: 100.0%; Pred. No. 7.9e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1316 AA.
                                                                                                                                                                                                                                                                                                                                                                   PRT; 1310 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lysosomal trafficking regulator (Fragment).
```

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AC00623; AAD15407.2; -...
EMBL; AC168748; AAR36810.1; -..
EMBL; AX168748; AAR36810.1; -..
EMBL; AX168748; AAR36810.1; -..
EMBL; AX19771; AAM98090.1; -..
EMBL; BT00522; AA064758.1; -..
PIR; D84727; D84727. Cimembrane; IEA.
GO; GO:0016020; Cimembrane; IEA.
GO; GO:000524; F:ATP binding; IEA.
GO; GO:0006281; P:DNA repair; IEA.
GO; GO:0006810; P:transport; IEA.
GO; GO:006810; P:transport; IEA.
InterPro; IPR004349; ABC transporter.
                                                                       White C.I.; "I shall a stable of the Arabidopsis RAD50 gene leads to plant sterility and
                                                                                                                                                                             Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y., Chang V.H., Dale J.M., Deng J.M., Hayashizaki Y., Lan B., Lee J.M., Lin J., Miranda M., Narusaka M., Narusaka M., Narusaka M., Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., "Arabidopsis cDNA clones.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                    Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lan B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S. Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
                 STRAIN=cv. Columbia;
MEDLINE=21097002; PubMed=11169180;
Gailego M.E., Jeanneau M., Granier F., Bouchez D., Bechtold N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 10; Length 1316; 100.0%; Pred. No. 7.9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007517; Rad50_zn_hook.
Pfam; PF04423; Rad50_zn hook; 1.
TIGRPAMs; TIGR00606; rad50; rad50, rad50; seQUENCE 1316 AA; 152814 MW; 89DC4F6BCA39B0E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I.JUN-2002 (TrEMBLrel. 21, Created)
1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1327 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyostelium discoideum (Slime mold)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22092622; PubMed=12097910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity lou...
Lac 7; Conservative
                                                                                                         MMS sensitivity.";
Plant J. 25:31-41(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1070 AEIVKIL 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 AEIVKIL 21
                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
   FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=AX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQ8T2G2
IDD Q6
AC QC
DT 011
DDT 011
DDE Hy
DDE HY
OOS DI
OOS DI
OOS BE
RRN [1]
임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        German Neurospora genome project;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; Ad451012; CAC18142.1;
R GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005634; C:nucleus; IEA.

GO; GO:0005635; P:regulation of transcription, DNA-dependent; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

R InterPro; IPR00337; PT_Umok.

R Pfam; PF02178; AT hook.

R Pfam; PF02178; AT hook; 2.

R Pfam; PF02178; AT hook; 2.

R R Pfam; SN00329; ATHOOK; 2.

R SMART; SN00384; AT hook; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G., Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; Score 7; DB 3; Length 1458;
100.0%; Pred. No. 8.6e+02;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1458 AA; 162988 MW; 7563160FA7D7442A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.1%; Score 7; DB 5; L
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 7; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
Related to c-module-binding factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1119 AQLAQEL 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 LIEFLSS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              569 LIEFLSS 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 AQLAQEL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5141;
                                                                                                                                                                                      STRAIN=AX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B2108.50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9HE72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRARE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

RESULT 248

Page 78

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Berkeley,
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., ILI P.W., Hoskins R.A., Gacayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxeer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=22065263; PubMed=12070089;
Parsons M.J., Pollard S.M., Saude L., Feldman B., Coutinho P., Hirst E.M., Stemple D.L.,
"Zebrafish mutants identify an essential role for laminins in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hekapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            notochord formation.";

Development 129:1137-3146(2002).

E EMBL, AF466049; AAM61767.1;

R GO: 0005578; C:extracellular matrix; IEA.

R GO: 0005198; F:extracellular matrix; IEA.

R TINEPTPO: IPRO06209; EGF like.

R InterPro: IPRO06219; Laminin EGF.

R Ffam; PR00635; laminin EGF.

R Ffam; PR00655; laminin Merm; 1.

R PAMN: SMORIS; Baminin Nerm; 1.

R PRINTS; SMORIS; EGF Lam; 13.

R SMART; SMORIS; EGF Lam; 13.

R PROSITE; PS01186; EGF Lim; 13.

R PROSITE; PS01186; EGF Lim; 13.

R PROSITE; PS01186; EGF Lim; 13.

R PROSITE; PS01186; EGF Lim; 13.

R PROSITE; PS01186; EGF Lim; 13.

R PROSITE; PS01186; EGF Lim; 13.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R PROSITE; PS01186; EGF Lim; 14.

R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 2.1%; Score 7; DB 13; Length 1785; Local Similarity 100.0%; Pred. No. 1e+03; nes 7; Conservative 0; Mismatches 0; Indels
                                                                                                                     01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
CG9088 protein (LD40310p).
                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Danio rerio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1838 AA.
                                             PRT; 1785 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1501 LİKÇİRD 1507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325 LIKQIRD 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7955;
                                                                                                                                                                                                                                                              Laminin beta 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09VMJ7
                                    QBJHV7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 249
Q9VMJ7
                                                                                                                                                                                                                                                                                                           LAMB1
Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HODER REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF THE REPORT OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
```

```
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
RA Chedson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J. Evangelista C.C., Ferrac C., Ferrica S., Fleischmann W.,
RA Godek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,
Ralush F., Karpen G.H., Wei M.-H., Ibegwam C.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Harris M.,
Alalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ina X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Martei B., McIntosh T.C., McLeod M.P., McCherson D.,
RA Mulson D.R., McIntosh T.C., McLeod M. P., McCherson D.,
RA Nount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Strupski M.P., Smith T.,
RN Bland S.M., Woodage T., Wonley K.C., Wu D., Yang S., Yao Q., Zheng L.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.,
RA Zhong X.H., Zhong W., Zhong W., Zhou X., Zhu S., Zhu X., Zhu S., Zhan M., Zhong X.,
RA Zhong X.H., Zhong W., Zhong W., Zhou X., Zhu S., Zhu X., Zhu S., Zhan M., Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Brokstein P., Hong L., Pris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Pfam; FP02373; jmjc; 1. | Pfam; PP02373; jmjc; 1. | Pfam; PP02373; jmjc; 1. | Pfam; PP02028; PHD; 3. | Pfam; PP02928; AFC5HC2; 1. | Pfam; PP02928; AFC5HC2; 1. | Pfam; PP02928; AFC5HC2; 1. | Pfam; PP02928; AFC5HC2; 1. | Pfam; PP02928; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AFC9F2; AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; Score 7; DB 5; Length 1838; 100.0%; Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003612; AAF52319.1; -
EMBL; AY095051; AAM11379.1; -
FlyBase; FBgn0031759; lid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. Mc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001606; ARID.
InterPro; IPR003347; TF JmjC.
InterPro; IPR003349; TF_JmjN.
InterPro; IPR004198; Znf_CSHC2.
InterPro; IPR001965; Znf_PHD.
Pfam; PF01388; ARID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1258 KNPAEIV 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 KNPAEIV 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
PRESULT 250

0861V6

0861V6

0861V6

0861V6

0861V6

0861V6

01-UTN-2003 (TrEMBLrel. 24, Created)

DT 01-UTN-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-UTN-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-UTN-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-UTN-2003 (TrEMBLrel. 26, Last sequence update)

DT 01-UTN-2003 (TrEMBLrel. 26, Last sequence update)

DT 01-UTN-2003 (TrEMBLrel. 26, Last sequence update)

DT 01-UTN-2003 (TrEMBLrel. 26, Last sequence update)

DT 01-UTN-2003 (TrEMBLrel. 26, Last sequence update)

NCBL_TAXID-A489;

RA 01-OCT-2003 (TrEMBLrel. 26, Last sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence seq
```

Search completed: April 12, 2004, 10:36:50 Job time : 60 secs

97 VTQIFNN 103 ||||||| 611 VTQIFNN 617

දුරු අධ

Abp08677 Human ORF

5 ABP08677

16

```
April 12, 2004, 10:28:43 ; Search time 59 Seconds (without alignments) 1613.873 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                     US-10-025-730-1
337
1 MKKMPLFSKSHKNPAEIVKI......FADEKNYLIKQIRDLKKTAP 337
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                               1586107 seqs, 282547505 residues
                                                                                                                                                                                                                     Post-processing: Listing first 300 summaries
                                      - protein search, using sw model
                                                                                                                      OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                    A Geneseq 29Jan04:*
1: geneseqp1980s:*
2: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                              0
                                                                                       Title:
Perfect score:
                                                                                                                      Scoring table:
                                                                                                                                                              Word size :
                                       OM protein
                                                                                                                                                                                                                                       Database :
                                                                                                                                               Searched:
                                                                                                       Sequence:
                                                       Run on:
```

		* Query			SUMMARIES	
Score Match Length				DB	qr	Description
37 100.0		337		Э	AAY94247	Aay94247 Human cal
37 100.0 337	337	•	•	4	AAB82090	Aab82090 Human Acu
	337		•	4	AAM39078	Aam39078 Human pol
27 67.4	.4 237	•	4		AAM40864	
8 55.8	5.8	289 4	4		AAB94139	
3 6.8	۳.	341 3	m		AAY94248	Aay94248 Mouse cal
3 6.8	ω.	341 4	4.		AAB48970	Aab48970 Human ANI
3 6.8	∞.	350 4	4		AAB20387	Aab20387 Human acu
3 6.8	∞.	496 4	4		AAE10858	Aael0858 Gal4-huma
23 6.8 552 4	8.	552 4	4		AAE10859	Aael0859 LexA-huma
7 5.0	٥.	354 4	4		ABG23844	Abg23844 Novel hum
4.5	rv.	339 3	m		AAY94249	Aay94249 Drosophil
5 4.5	'n.	339 4	4		ABB60392	a
4.2	.5	377 3	٣		AAY94250	
3.6		383 4	4		ABG23843	Abg23843 Novel hum
12 3.6 639 4	9.	639 4	4		ABG25372	Abg25372 Novel hum
2.4	4.	139 3	ო		AAG41153	Aag41153 Zea mays
2.4	4.	148 3	m		AAG41152	Aag41152 Zea mays
2.4	4.	154 3	m		AAG41151	Aag41151 Zea mays
8 2.4 464 4	₽.	464 4	4		ABB59571	Abb59571 Drosophil
	4.	923 4	4		ABB58067	Abb58067 Drosophil
7 2.1 44 4	.1	44 4	4		ABG03535	Abq03535 Novel hum
7 2.1 46	.1	46	. ,	_	AAG55362	Aag55362 Arabidops
۲.	.1	51 4	4		ABB53042	Abb53042 Escherich
7 2.1 83 5	2.1 83 5	83	ш		ABP05605	Abp05605 Human ORF

JE6// Human C	89310 Human E	76204 Human G	19956	74439	71944	1422	29337	39088	31106	15091	1481	30715	23888	15275	54954	11479	24494	53772	11773	729	24179	18312	45274	23886	71583	73387	35090	17865	17866	27865 37360	45273	32843 23650	15089	1447	06308	85255	51052	24493	31788	52729	73473	49289	37733	35155	52146	15325	w61390	339772 365679	Abu07341 Human TIG	e54515
1867	3931	620	9097	7443	7194	3142	933	3908	3110	503	44.4	3071	2388	1527	5495	1147	2449	3377	7711	567	2417 3388	1831	1527	388	7158	7338	509	2105 1786	1786	2786 3736	1527	3284 3365	508	7144 7368	0630	3525	5105	2449	33333	5272	7347	1928	3773	3515	5214	1532	5139	3977	ABU07341	5451
Ω <u>-</u>	4	9 (	o 4	4	9 .	4 0	7	41 u	4	mι	- ~	1 m	m	m s	r vo	۱ بې	വ വ	4,	o m	ı,	ۍ د	7	m ~	'n	φ.	n m	m	n (1	7	4r ru	m'	ω φ	mı	ა 4	m	0 <b>4</b> 1	m r	N.	ى م	4	ഗ സ	'n	01 C	14	ស រ	<b>Λ</b>	(2)	m 4	* 4	7
7 0	0 0 0	66	ם מ	٠ <u>-</u>	-16	2	~	r -	· 0	0 0	<b>n</b> C	, ii	<b>~</b> i	<del>-</del> -	4	O O	2	ini	nία	-	သော	0	00	0	00	0 0	OI C	NM	(0)	w 44	4.	4 4	4	9 1	- 1	~ &	00	10	NO	LO I	ınα	9	o a	n 01	0	$\sigma$	90	90	200	0
					•			•					•	•													•										•				•		•		•	•		•	17.	•

Aay07418 HSV-1 TK Aaw97150 HSV-1 TK Aaw97150 HSV-1 TK Aby97150 HSV-1 TK Aby974502 Human TFR Aby99202 Thymidine Aby99202 Thymidine Aby99203 Thymidine Aby99203 Thymidine Aby99203 Thymidine Aby99203 Human bon Aam5857 Peptide # Aam7831 Human bon Aam5857 Human bon Aam585929 Human pep Aar5484 Ion chann Aby95929 Human pep Aar55929 Human pep Aar5627 Amphiphil Abo11924 Human zin Aby1026 Human zin Aby1026 Human ner Aby1026 Human ner Aby1026 Human bon Aam415122 Corticotr Aby1026 Hybride # Aam76952 Human bon Aam67659 Human bon Aam67659 Human bon Aam67659 Human bon Aby1026 Hybrid po Aam67659 Human bon Aam67659 Human iv Aby1027 Transplan Aaw191026 Transplan Aaw31027 Transplan Aaw31027 Transplan Aam68966 Staphyloc Aby1027 Transplan Aam68966 Staphyloc Aby1027 Boptide # Aby1027 Boptide # Aby1027896 Peptide # Aby1027896 Peptide # Aby1027896 Peptide # Aby1067891 Human rep Aby10851 Furan bra Aby10851 Furan bra Aby10851 Human bra Aby10851 Human bra Aby10861 Human rep Aby10861 Human rep	Aag18732 Zea many Aag18732 Zea many Aau14265 Human nov Aa004708 Human noul Abg09887 Novel hum Aaw92823 Human tra Aaw92823 Human tra Aaw92813 Human dig Aa005232 Human pol Ad32508 Human nov Ad67826 Endometri Aab34514 Human sec Aag76342 Human col Aau45084 Propionib Abm42089 Propionib Abm38818 Propionib Abm38818 Propionib Aau454299 Propionib Abm49642 Propionib Abm49642 Propionib Aau49642 Propionib Aau49642 Propionib Aau49642 Propionib Aau49642 Propionib Aau49642 Propionib Abm49642 Propionib Abm49642 Propionib Abm49642 Propionib Abm49642 Propionib Abm496438 Propionib Abm496438 Propionib Abm496438 Propionib Abm496438 Propionib
AAYO7418 AAW97150 AAW97150 AAW97150 AAW97150 AAW37114 AAW22114 AAW3850 AAW3850 AAW3850 AAW3850 AAW3850 AAW3850 AAW3850 AAW3850 AAW3850 AAW3850 AAW3850 AAW4122 AAW415122 AAW415122 AAW61223 AAW415127 AAW61220 AAW31757 AAW61220 AAW31757 AAW63516 AAW31757 AAW62510 AAW31757 AAW63516 AAW31757 AAW62510 AAW31757 AAW62510 AAW31757 AAW62510 AAW31757 AAW62510 AAW31757 AAW62510 AAW31757 AAW62510 AAW31757 AAW62510 AAW66253 AAW66253 AAW66253 AAW66253 AAW62850 AAW66253 AAW66253 AAW62850 AAW62850 AAW62850 AAW62850 AAW6283	
これまままままままままままままままままままままままままままままままままままま	
22222222222222222222222222222222222222	
Aaw66669 Human TIG Aaw70496 Trabecula Aaw70496 Trabecula Aaw70496 Trabecula Aaw89391 Human TIG Aaw89391 Human TIG Aaw89391 Human Tra Aay93937 A trabecula Aay93371 A trabecula Aa93374 Human TIG Ab975692 Human TIG Ab975692 Human TIG Ab975692 Human TIG Ab975692 Human TIG Ab975692 Human TIG Ab975692 Human TIG Ab975692 Human TIG Ab975692 Human TIG Ab97230 Arabidops Aa93219 Arabidops Aa93219 Arabidops Aa932073 Arabidops Aa932074 Arabidops Aa932075 Arabidops Aa932074 Arabidops Aa932074 Arabidops Aa932074 Arabidops Aa932074 Arabidops Aa932074 Arabidops Aa932074 Arabidops Aa932074 Arabidops Aa932074 Arabidops Aa932074 Arabidops Aa932076 Arabidops Aa932077 Arabidops Aa932077 Arabidops Aa932077 Arabidops Aa932077 Arabidops Aa932077 Arabidops Aa932077 Arabidops Aa932077 Arabidops Aa932077 Arabidops Aa932077 Arabidops Aa932077 Arabidops Aa932077 Arabidops Aa932077 Arabidops Aa932077 Arabidops Aa91207 Arabidops Aa91208 Arabidops Aa91208 Arabidops Aa91213 Human pro Ab01254 Bruman S77 Aae17312 Human S77 Aae17312 Human S77 Aae17313 Human pro Ab09658 Amino aci Ab09659 Amino aci Ab09659 Amino aci Ab09659 Amino aci Ab09669 Amino aci Ab09660 Amino aci Ab09860 Amino aci Ab09860 Amino aci Ab08680 Amino aci Ab08680 Amino aci Ab08680 Amino aci Ab08680 Amino aci Ab08680 Amino aci Ab08680 Amino aci Ab08680 Amino aci Ab08680 Amino aci	Aaw23593 Human LYS Aar45945 Glutamic Abb77986 Amino aci Abg76501 DNA encod Aaw23595 Murine Ly Aab90551 Human sec Abg65473 Human alb Aau99587 Novel hum Aau99587 Novel hum Aau99587 Novel hum Aau99587 Novel hum Aau99587 Novel hum Aau99587 Novel hum Aau99587 Novel hum Aau9587 Novel hum Abb102425 Drosophil Abb6425 Drosophil Abb6425 Drosophil Abb16425 Prosophil Abb16425 Prosophil Abb16425 Human CNN Aww22017 Utrophin. Aaw22017 Utrophin. Aaw22017 Human CAS Abu03359 Human CAS Abu03359 Human CAS Aaw71167 Peptide u Aag70315 Human CNN Abg74903 Human TFR Aau69193 Human Ace Aay07411 HSV-1 TK
2.1 504 2 AAW64669 7 2.1 504 2 AAW64669 7 2.1 504 2 AAW70496 7 2.1 504 2 AAW70496 7 2.1 504 2 AAW70303 7 2.1 504 2 AAW70303 7 2.1 504 2 AAW70303 7 2.1 504 3 AAW70301 7 2.1 504 3 AAW70301 7 2.1 504 4 AAB0311 7 2.1 504 4 AAB0311 7 2.1 504 4 AAB0311 7 2.1 504 6 ABC7240 7 2.1 504 6 ABC7240 7 2.1 504 6 ABC7240 7 2.1 504 6 ABC7240 7 2.1 504 6 ABC7240 7 2.1 504 7 AAB8525 7 2.1 504 7 AAB8525 7 2.1 504 7 AAB8525 7 2.1 504 7 AAB8525 7 2.1 504 7 AAB8521 7 2.1 504 7 AAB8525 7 2.1 504 7 AAB8525 7 2.1 504 7 AAB8525 7 2.1 504 7 AAB8525 7 2.1 504 7 AAB8525 7 2.1 504 7 AAB8525 7 2.1 504 7 AAB8525 7 2.1 504 7 AAB8525 7 2.1 504 7 AAB8525 7 2.1 504 7 AAB8525 7 2.1 504 8 AAB87204 7 2.1 504 8 AAB87204 7 2.1 655 7 AAR87206 7 2.1 658 4 AAB71312 7 2.1 685 4 AAB71312 7 2.1 685 5 AAR17312 7 2.1 685 5 AAB17312 7 2.1 685 5 AAB17312 7 2.1 686 5 AAR17312 7 2.1 686 5 AAB87659 7 2.1 1053 6 ABB9665 7 2.1 1053 6 ABB9665 7 2.1 1053 6 ABB9665 7 2.1 1053 6 ABB9662	2.1 1185 2 2.1 1239 2 2.1 1539 2 2.1 1539 2 2.1 1745 4 2.1 1745 5 2.1 1745 5 2.1 1762 7 2.1 1762 7 2.1 1766 7 2.1 1766 7 2.1 1766 7 2.1 1766 8 2.1 1766 8 2.1 1766 8 2.1 1766 8 1.8 8 4 1.8 8 10 7 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11 6 1.8 11
10000000000000000000000000000000000000	149 150 151 152 153 154 155 160 160 163 164 166 167 170

Abp07511 Human ORF Abm43857 Propionib Asg11542 Arabidops Abp01202 Human ORF Abp25762 Streptoco Amm94423 Human rep		N. gon S. taphy S. taphy S. taphy Human Human Human Novel Novel Arabió Arabió Human Protei Human Propic Human Propic Human	Abpl0463 Human ORF Abp63917 Human ORF Abj10267 Human lun Aau66107 Propionib Abu51733 Helicobac Abm62626 Propionib Aab00168 Brain spe
ABP07511 ABM43857 AAG11542 ABP01202 ABP25762 ABP25762 AM94433	AAMO6643 AAMO6643 ABG61724 ABG61724 ABC05514 AAC13551 AAC16880 AAC16880 AAC16880 AAC16880 AAC16880 AAC16881 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AAC1688 AA	ABP77808 ABP1968 ABU01159 ABM15018 AAO05131 AAO05132 AAO13185 ABG56374 AAG56374 AAG60382 AAU28073 AAU28073 AAU28073 AAU28073 AAU28073 AAU28073 AAU28073 AAU3435 AAU5044 AAU5044 ABP31226 ABP32134 AAO10631	ABP10463 ABP63917 ABJ10267 AAU66107 ABU51733 ABM62626 AAB00168
		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
8888888			444444 6 8.8.8.8.8.8.8.8.8.8.8.8.8.8.8.
245 246 247 248 250 250	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	227 22 22 22 22 22 22 22 22 22 22 22 22	2955 2995 2996 2999 300

## ALIGNMENTS

```
Human, calcium binding protein, cancer; inflammation, CBP, reproductive disorder; autoimmune disorder; developmental disorder;
                                                                                             Human calcium binding protein hCBP.
                      AAY94247 standard; protein; 337 AA.
                                                                       (first entry)
                                                                       10-AUG-2000
                                               AAY94247;
          RESULT 1
```

```
The present sequence is the human calcium binding protein hCBP. It was obtained by screening a coronary artery smooth muscle cDNA library, from which five overlapping nucleic acids were isolated, sequenced and expressed to give the protein. The protein and the gene encoding it are useful for the diagnosis and treatment of the following types of disorder: cancers (such as adenocarcinomas), reproductive disorders (such as infertility, ovulatory defects, endometriosis, disruptions of the coestrus and menstrual cycles, polycystic ovary syndrome and ovarian hyperstamlation), autoimmune disorders (such as benign prostatic cypperplasia and prostatitis), developmental disorders (such as Cushing's syndrome, muscular dystrophy and gonadal dysgenesis), hereditary cucupathies, seizure disorders, immune disorders (such as AIDS, collecses, diabetes, Graves' disease, multiple sclerosis, psoriasis, crhumatoid arthritis, golaroderma, Sjogren's syndrome and ulcerative colitis), and viral, bacterial, fungal, parasitic, protozoal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AHPHILFMLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 NFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AHPHILFMLLKGYEAPQIALRCGIMLRECIRHBPLAKIILFSNOFRDFFKYVELSTFDIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 NFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPK 300
                                                                                                                                                                                                                                                                                                                                                                                     Human hCBP protein, and the nucleic acid encoding it, useful for e.g. diagnosis, prevention and treatment of cancers, immune, developmental or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKMPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKMPLFSKSHKNPAEIVKILKDNLAILEKODKKTDKASBEVSKSLQAMKEILCGTNEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٥;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 337; DB 3; Length 337; Best Local Similarity 100.0%; Pred. No. 0; Msmatches 337; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 LIEFLSSFOKERTDDEOFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 LIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                   Gorgone GA;
seizure disorder; immune disorder; infection.
                                                                                                                                                                                                                                                                                   Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 1; 72pp; English.
                                                                                                                                                            99WO-US027027.
                                                                                                                                                                                                     98US-00190965.
                                                                                                                                                                                                                                         (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                           reproductive disorders.
                                                                                                                                                                                                                                                                                 Guegler KJ,
                                                                                                                                                                                                                                                                                                                       2000-387793/33.
                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA27332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 337 AA;
                                                                              WO200029580-A1
                                                                                                                                                                                                     13-NOV-1998;
                                        Homo sapiens.
                                                                                                                                                            12-NOV-1999;
                                                                                                                    25-MAY-2000.
                                                                                                                                                                                                                                                                                   Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
```

ö;

9

240

```
301 LIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhou
                                           RESULT 3
                                                             AAM39078
                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the protein sequence for human Acute Neuronal Induced Calcium Binding Protein (ANIC-BP). ANIC-BP coding sequence and protein are useful for treating stroke, acute head trauma, multiple sclerosis and spinal cord injury. ANIC-BP coding sequence and protein are also useful as vaccines for inducing an immunological response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKOVTQIFNNILERQIGTRSPTVEYIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKKNQPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human acute neuronal induced calcium binding polypeptide, and polynucleotides encoding them useful for diagnosing or treating stroke, acute head trauma, multiple sclerosis and spinal cord injury.
                                                                                                                                                                Human; cerebroprotective; neuroprotective; vulnerary; vaccine; gene therapy; Acute Neuronal Induced Calcium Binding Protein; ANIC-BP; stroke; acute head trauma; multiple sclerosis; spinal cord injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQ1FNNILRRQIGTRSPTVEYIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKKOMPLFSKSHKNPABIVKILKDNLAILEKQDKKTDKASBEVSKSLQAMKEILCGTNEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKMPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                  Human Acute Neuronal Induced Calcium Binding Protein, ANIC-BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 337; D
100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 41-42; 45pp; English.
                                        AAB82090 standard; protein; 337 AA.
                                                                                                                                                                                                                                                                                                                                                     99EP-00118848,
                                                                                                                                                                                                                                                                                                                      18-SEP-2000; 2000WO-EP009132
                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 Den Daas I, Duecker K;
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-308142/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAF86462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 337 AA;
                                                                                                                                                                                                                                                          WO200123552-A1.
                                                                                                                                                                                                                                                                                                                                                   24-SEP-1999;
                                                                                                                                                                                                                             Homo sapiens
                                                                                                  26-JUN-2001
                                                                                                                                                                                                                                                                                       05-APR-2001.
                                                                       AAB82090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
           RESULT 2
                           AAB82090
```

g

5 d ò

g ò

à

g

∂ g à

```
The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM18642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral solerosis, and Shybrager Syndrome. Other uses include the utilisation of the activities such as Immune system suppression, Activity, chemotactic/chemokinetic activity, haemostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang D;
Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ren F, Wa
Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 337; DB 4; Length 337; 100.0%; Pred. No. 0; Nismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Α,,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; SEQ ID NO 2223; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goodrich R, Drmanac RT;
   Æ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     part of the printed specification
                                                                                                                                                                        Human polypeptide SEQ ID NO 2223.
AAM39078 standard; protein; 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00653450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-DEC-2000; 2000WO-US034263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-00488725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-00552317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-00662191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-NOV-2000; 2000US-00727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEO INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAI58234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-SEP-2000;
19-OCT-2000;
                                                                                                               22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                              leukaemia.
                                                         AAM39078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o,
```

ó

```
Wang D;
, Zhao QA;
                                         PPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYIS 120
                                                        PPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYIS 120
                                                                                       AHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIA 180
                                                                                                      SDAFATFKOLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRH 240
                                                                                                                                                    SDAFATFKDLITRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRH 240
                                                                                                                                                                                 NPAIMTKYISKPENIKLAMMILLRDKSPNIQFEAFHVFKVFVASPHKTQPIVBILLKNQPK 300
                                                                                                                                                                                                         241 NFAIMTKYISKPENLKLMMNLLRDKSPNIQFBAFHVFKVFVASPHKTQPIVEILLKNQPK 300
9
            Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; heemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ren F, Wa
Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qian XB,
Yang Y,
                                                                                                                                                                                                                                 LIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                      LIEFLSSFOKERTDDEOFADEKNYLIKOIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y,
AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ndi V, Chen R, Ma
rman T, Xu C, Xue
Drwanac RT;
                                                                                                                                                                                                                                                                                                                    Ą
                                                                                                                                                                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO 5795.
                                                                                                                                                                                                                                                                                                                AAM40864 standard; protein; 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00653450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-DEC-2000; 2000WO-US034263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-00727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C, Asundi V,
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang Z, Weh
Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-442253/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAI60020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                               22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT,
Wang J, V
                                         61
                                                                 61
                                                                                       121
                                                                                                                                                                                                                                                                                                                                         AAM40864;
                                                                                                               121
                                                                                                                                     181
                                                                                                                                                            181
                                                                                                                                                                                                                                301
                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                    g
                                        ò
                                                        Db
                                                                                     à
                                                                                                       g
                                                                                                                                                     g
                                                                                                                                                                                                                                                 셤
                                                                                                                                    Š
                                                                                                                                                                                ö
                                                                                                                                                                                                        d
                                                                                                                                                                                                                               δ
```

```
The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymuclectides are useful in gene therapy. A composition containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous and central nervous system diseases, such as closalised neuropathies and central nervous system diseases, such as localised neuropathies and central nervous system diseases, such as allocations as disease, amyotrophic alteral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity chemotactic/chemokinetic activity haemostatic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form by art of the printed specification.
                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                            170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290
                                                                                                                                                                                                                                                                                                                                                                                                                                                           230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIGELILDREHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 LLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPI
                                                                                                                                                                                                                                                                                                                                                                                         111 TRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFK
                                                                                                                                                                                                                                                                                                                                                                                                                     TRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 YVELSTFDIASDAFATFKOLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEILLKNOPKLIEFLSSFOKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEILLKNOPKLIEFLSSFOKERTDDEOFADEKNYLIKOIRDLKKTAP 228
                                                                                                                                                                                                                                                                                                                           Length 237;
                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saito K, Ya
                                                                                                                                                                                                                                                                                                                         67.4%; Score 227; DB 4; Le 100.0%; Pred. No. 7.2e-214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashi K, S
A, Nagai K,
Example 2; SEQ ID NO 5795; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                   100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein sequence SEQ ID NO:14408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB94139 standard; protein; 289 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai T, Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-00248036.
99JP-00300253.
2000JP-00118776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000EP-00116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000JP-00183767
2000JP-00241899
                                                                                                                                                                                                                                                                                                                                                         Matches 227; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                           Sequence 237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-AUG-1999;
11-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB94139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŝ
                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB94139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
 유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
```

us-10-025-730-1.oligo.rag

```
The present invention describes primer sets for synthesising 5602 full-
length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dr primer and an oligonucleotide comprisentary to the
complementary strand of a polyuncleotide which comprises one of the 5602
nucleotide sequences defined in the specification, where the
oligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises at least 15 nucleotides and the combination of
the 5'-end sequence(3'-end sequence) where the
coligonucleotide which comprises at least 15 nucleotides and the combination of
the 5'-end sequence(3'-end sequence in selected from those defined in the
specification. The primer sets can be used in antisense therapy and in
gene therapy. The primers are useful for synthesising polynucleotides,
centerially without any specialised methods. Athelists encoded by
the full-length cDNAs. The primers are also useful for the
detection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
CDNAs easily without any specialised methods. Athelists to AAH13623 represent
coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 MKEILCGTNEKEPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 FKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 LKLLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 IGTRSPIVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDF 168
Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGTRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLVKIILFSNQFRDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKEILCGINEKEPPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKYVELSTFDIASDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKLLGELILDRHNFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIVEILLKNOPKLIEFLSSFOKERTDDEOFADEKNYLIKOIRDLKKTAP 289
                                                                                                                                                                                                                                                 Claim 8; SEQ ID NO 14408; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.8%; Score 188; DB 4; Length 289; 99.7%; Pred. No. 1.5e-175; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                    CDNAs.
```

```
ö
                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; calcium binding protein; cancer; inflammation; MO25; CBP; reproductive disorder; autoimmune disorder; developmental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seizure disorder; immune disorder; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse calcium binding protein MO25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY94248 standard; protein; 341 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY94248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus ap.
```

g

셤  $\delta$ g  $\stackrel{>}{\circ}$  q ò 셤

à

SXXXXXXXXXXXXXXXX

```
The present sequence is the mouse calcium binding protein MODS. It was used in a sequence alignment to identify human calcium binding protein C used in a sequence alignment to identify human calcium binding protein characters. The hCBP protein and the gene encoding it are useful for the as adenocarcinomas, reproductive disorders (such as infertility, covulatory defects, endometriosis, disruptions of the oestrus and mentrual cycles, polycystic ovary syndrome and ovarian prostatic ovary syndrome and ovarian hyperstimulation), autoimmune disorders (such as benign prostatic syndrome, muscular dystrophy and gonadal dysgenesis), hereditary neuropathies, seizure disorders, immune disorders (such as ALDS, allergies, anaemia, asthma, atherosclerosis, cholecystitis, Crohn's disease, diabetes, Graves' disease, multiple sclerosis, psoriasis, cheumatoid arthritis, scleroderma, Sjogren's syndrome and ulcerative colitis), and viral, bacterial, fungal, parasitic, protozoal and helminthic infections
                                                                                                                                                                                                                                   Human hCBP protein, and the nucleic acid encoding it, useful for e.g. diagnosis, prevention and treatment of cancers, immune, developmental or reproductive disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, acute neuronal induced calcium-binding protein; ANIC-BP;
Mo25 homologue; HymA homologue; drug screening; stroke;
acute head trauma; multiple sclerosis; spinal cord injury; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ANIC-BP (acute neuronal induced calcium-binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.8%; Score 23; DB 3; Length 341; 000.0%; Pred. No. 1:1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                           Gorgone GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                       Disclosure; Page 66-67; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 IMTKYISKPENLKLMMNLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cerebroprotective; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB48970 standard; protein; 341 AA.
                                                                                                                                                                           Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 IMTKYISKPENLKLMMNLLRDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUN-2000; 2000WO-EP005457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99EP-00112024.
                                                                         99WO-US027027.
                                                                                                           98US-00190965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similaricy
hes 23; Conservative
                                                                                                                                         (INCY-) INCYTE PHARM INC
                                                                                                                                                                           Guegler KJ,
                                                                                                                                                                                                        WPI; 2000-387793/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200078947-A1.
             WO200029580-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUN-1999;
                                                                                                           13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                            12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-DEC-2000.
                                            25-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB48970;
                                                                                                                                                                           rang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB48970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
```

```
The invention relates to human acute neuronal induced calcium-binding protein (ANIC-BP) and to nucleic acid encoding it. The invention also relates to expression systems and recombinant host cells comprising ANIC-BP DNA, the recombinant production of ANIC-BP, antibodies specific for ANIC-BP, fusion proteins comprising ANIC-BP, antibodies specific for region, and methods of screening ANIC-BP and an immunoglobulin FC region, and methods of screening ANIC-BP and an immunoglobulin FC and ANIC-BP proteins and nucleotides are useful for treating stroke and acute head trauma, multiple sclerosis and spinal cord injury. ANIC-BP proteins are useful in screening assays, for identifying membrane bound or soluble are useful in screening assays, for identifying membrane bound or soluble diagnostic reagents, as tools for tissue expression studies, for diagnostic reagents studies, as genetic vaccines, and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and in the surface and an interpretation surface and an interpretation surface and an interpretation surface and an interpretation surface and an interpretation surface and an interpretation surface and an interpretation surface and an interpretation surface and an interpretation surface and an interpretation surface and an interpretation surface and an interpretation surface and an interpretation surface and an interpretation surface and an interpretation surface and an interpretation and an int
                                                                                                                                                                                                          Novel acute neuronal induced calcium binding protein, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spice variant; human; stroke; head trauma; Parkinson's disease;
Alzheimer's disease; multiple sclerosis; spinal cord injury;
cerebroprotective; antiparkinsonian; nootropic; neuroprotective; therapy;
                                                                                                                                                                                                                                     head trauma, stroke, multiple sclerosis and spinal cord injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human acute neuronal induced calcium binding protein ANIC-BP-1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acute neuronal induced calcium binding protein; ANIC-BP-1B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                           Von Melchner L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.8%; Score 23; DB 4; Le 100.0%; Pred. No. 1.1e-13; Live 0; Mismatches 0;
                                                                           Fischer V, Seyfried C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 IMTKYISKPENLKLMMNLLRDKS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 IMTKYISKPENLKLMMNLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB20387 standard; protein; 350 AA
                                                                                                                                                                                                                                                                                      Claim 2; Page 37; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99EP-00119113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-2000; 2000WO-EP009475
                        (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                            2001-102721/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis; vaccine
                                                                                                                                                       N-PSDB; AAC91772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 341 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                           Daas I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                     acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
```

Duecker K, Den Daas I;

WPI; 2001-266306/27.

N-PSDB; AAF30688.

ö

```
The present sequence is that of a novel human acute neuronal induced calcium binding protein-like protein splice variant, ANIC-NP-1B. The protein shows homology to other members of the calcium binding protein family, including ANIC-BP, a protein discovered by mRNA differential display that is upregulated in a rat model of head trauma. ANIC-BP and ANIC-BP-1B differ in their C-terminal portions. The variant protein could serve as a novel drug target. The invention provides ANIC-BP-1B colymucleotides (see AAR30688) and polypeptides, expression vectors, host cells and antibodies, as well as methods for producing the protein and correcting or preventing disorders associated with expression of the protein by inhibiting or activating the action of ANIC-BP-1B. Diseases that may be treated include stroke and acute head trauma, Parkinson's disease, Alzheimer's disease, multiple sclerosis and spinal cord injury. The polynucleotides and polypeptides can also be used in diagnostic assays and in vaccines, and to identify agonists and antagonists useful for treating conditions associated with ANIC-BP-1B imbalance
Novel human acute neuronal induced calcium-binding protein like protein splice variant, useful for treating stroke, acute head trauma, Parkinson's disease, Alzheimer's disease multiple sclerosis, spinal cord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel acute neuronal induced calcium binding protein type I ligand polypeptides, useful in the treatment of stroke, head trauma, multiple sclerosis, Parkinson's disease, Alzheimer's disease and spinal cord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, acute neuronal induced calcium binding protein type 1 ligand; ANIC-BP-1; human disease; Etroke; head trauma; multiple sclerosis; Parkinson's disease; Alzheimar's disease; spinal cord injury; vaccine; gene therapy; fusion protein; Gal4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%; Score 23; DB 4; Length 350; 00.0%; Pred. No. 1.1e-13; ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 IMTKYISKPENLKLMMNLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 IMTKYISKPENLKLMMNLLRDKS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gal4-human ANIC-BP-1 fusion protein.
                                                                                                  Claim 2; Page 44-45; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE10858 standard; protein; 496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAR-2001; 2001WO-EP003149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2000; 2000EP-00106110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Den Daas I, Duecker K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-607519/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200170771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE10858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 injury.
                                                               injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE10856
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
The invention relates to human acute neuronal induced calcium binding protein type 1 (ANIC-BP-1) ligand polypeptides and polynucleotides. Sequences of the invention are useful for treating human diseases including stroke, head trauma, multiple sclerosis, Parkinson's disease, Alzheimer's disease and spinal cord injury. They are also useful as vaccines. ANIC-BP-1 ligands are useful for identifying membrane bound soluble receptors. Polynucleotides of the invention are useful as diagnostic reagents, for chromosome localization studies, and as valuable tools for tissue expression studies. They are also useful in gene therapy. The present sequence is Ga14-human ANIC-BP-1 fusion protein comprising the Ga14 protein and a C-terminally linked human ANIC-BP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, acute neuronal induced calcium binding protein type 1 ligand, ANIC-BP-1; human diesase; stroke, head trauma; multiple sclerosis; Parkinson's disease; Alzheimer's disease; spinal cord injury; vaccine; gene therapy; fusion protein; LexA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel acute neuronal induced calcium binding protein type I ligand polypeptides, useful in the treatment of stroke, head trauma, multiple sclerosis, Parkinson's disease, Alzheimer's disease and spinal cord
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                     Length 496;
                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                  6.8%; Score 23; DB 4; Le
100.0%; Pred. No. 1.5e-13;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203. .552
/note= "Human ANIC-BP-1 protein"
Disclosure; Page 42-44; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. 202
/note= "LexA protein"
                                                                                                                                                                                                                                                                                                                                   244 IMTKYISKPENLKLMMNLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                400 IMTKYISKPENLKIMMNLLRDKS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LexA-human ANIC-BP-1 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duecker K, Hock B;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE10859 standard; protein; 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2000; 2000EP-00106110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAR-2001; 2001WO-EP003149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MERE ) MERCK PATENT GMBH.
                                                                                                                                                                                                                                                                                    Local Similarity 100.
es 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-607519/69.
                                                                                                                                                                                                                                     Sequence 496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200170771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Den Daas I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE10859;
                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ношо
                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                AAE10859
                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
```

The invention relates to human acute neuronal induced calcium binding

Disclosure; Page 44-46; 46pp; English.

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The
protein type 1 (ANIC-BP-1) ligand polypeptides and polynuclectides. Sequences of the invention are useful for treating human diseases including stroke, head trauma, multiple sclerosis. Parkinson's disease, Alzheimer's disease and spinal cord injury. They are also useful as vaccines. ANIC-BP-1 ligands are useful for identifying membrane bound soluble receptors. Polynucleotides of the invention are useful as diagnostic reagents, for chromosome localization studies, and as valuable tools for tissue expression studies. They are also useful in gene therapy. The present sequence is Lexa-human ANIC-BP-1 fusion protein comprising the LexA protein and a C-terminally linked human ANIC-BP-1
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                        ·,
                                                                                                                                                                                                                                                                                             6.8%; Score 23; DB 4; Length 552;
100.0%; Pred. No. 1.7e-13;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 54203; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #23835.
                                                                                                                                                                                                                                                                                                                                                                                    244 IMTKYISKPENLKLMMNLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                         456 IMTKYISKPENLKLMMNLLRDKS 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG23844 standard; protein; 354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100..
Best 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS88031
                                                                                                                                                                                                                                                            Sequence 552 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG23844;
                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG23844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8888888888888%8
                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
The present sequence is the Drosophila calcium binding protein DMO25. It was used in a sequence alignment to identify human calcium binding protein holds. The hOBP protein and the gene encoding it are useful for the diagnosis and treatment of the following types of disorder: cancers (such as adenocarcinomas), reproductive disorders (such as infertility, ovulatory defects, endometriosis, disruptions of the oestrus and menticular oycles, polycystic ovary syndrome and ovarian hyperstimulation), autoimmune disorders (such as benign prostatic hyperplasia and prostatitis), developmental disorders (such as Cushing's syndrome, muscular dystrophy and gonadal dysquensis), hereditary neuropathies, seizure disorders, immune disorders (such as AIDS, allergies, anaemia, asthma, atherosclerosis, choiceystitis, Crohn's disease, diabetes, Graves' disease, multiple sclerosis, psoriasis, colutis), and viral, bacterial, fungal, parasitic, protozoal and helminthic infections
                                                                                                                                                                                                                                                                             ô
polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fit.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human hCBP protein, and the nucleic acid encoding it, useful for e.g. diagnosis, prevention and treatment of cancers, immune, developmental or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; calcium binding protein; cancer; inflammation; DMO25; CBP; reproductive disorder; autoimmune disorder; developmental disorder; seizure disorder; immune disorder; infection.
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                             ..
                                                                                                                                                                                                                                  5.0%; Score 17; DB 4; Length 354; 100.0%; Pred. No. 8.4e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gorgone GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila calcium binding protein DMO25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 67-68; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY94249 standard; protein; 339 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corley NC,
                                                                                                                                                                                                                                                                                                                                                    233 SENYVTKRÖSLKLIGEL 249
                                                                                                                                                                                                                                                                                                                 219 SENYVTKRQSLKLLGEL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US027027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00190965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                      Query Match 5.0 Best Local Similarity 100. Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reproductive disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-387793/33.
                                                                                                                                                                                                 Sequence 354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200029580-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY94249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                               g
      δ
```

```
ö
                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL18176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 7968; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.5%; Score 15; DB 4; Length 339; 100.0%; Pred. No. 7.3e-06;
                                       Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indele
                                                                  0; Indels
                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 7968.
                                      DB 3; Le
7.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Prec. ....
                                               100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myers EW;
                                       Score 15;
Pred. No.
                                                                                                                                                                                                    ABB60392 standard; protein; 339 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000; 2000US-0191637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 LRRQIGTRSPTVEYI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRRQIGTRSPTVEYI 119
                                                                                                105 LRRQIGTRSPTVEYI 119
                                                                                                                              103 LRROIGTRSPTVEYI 117
                                    4.5%;
                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                     Local Similarity 100.
ses 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABL04495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 339 AA;
             Sequence 339 AA;
                                                                                                                                                                                                                                                                                                                                                                                              WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                       pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interactions.
                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105
                                                                                                                                                                                                                                   ABB60392;
                                         Query Match
                                                                   Matches
                                                                                                                                                                         RESULT 13
                                                                                                                                                                                        ABB60392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                 ਨੇ
X S
                                                                                                   ð
```

RESULT 14

AAY94250

Homo sapiens.

```
The present sequence is the C. elegans yeast-like CBP. It was used in a sequence alignment to identify human calcium binding protein hCBP. The hCBP protein and the gene encoding it are useful for the diagnosis and treatment of the following types of disorder: cancers (such as adenocarcinomas), reproductive disorders (such as infertility, ovulatory defeotes, endometriosis, disruptions of the osetrus and menstrual cycles, polycystic ovary syndrome and ovarian hyperstimulation), autoimmune disorders (such as benign prostatic hyperplasia and prostatitis), developmental disorders (such as Cushing's syndrome, muscular dystrophy and goorders (such as Allos, allergies, anaemia, asthma, and gonadal dysgenesis), hereditary neuropathies, seizure disorders, immune disorders (such as Allos, allergies), anaemia, asthma, atheresses, multiple sclerosis, psoriasis, rheumatoid arthritis, calsease, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, Sjogren's syndrome and ulcerative colitis), and viral, bacterial, fungal, parasitic, protozoal and helminthic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human hCBP protein, and the nucleic acid encoding it, useful for e.g. diagnosis, prevention and treatment of cancers, immune, developmental or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                          Calcium binding protein; cancer; inflammation; yeast-like CBP; CBP; reproductive disorder; autoimmune disorder; developmental disorder; seizure disorder; immune disorder; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.2%; Score 14; DB 3; Length 377;
100.0%; Pred. No. 7.8e-05;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                      C. elegans yeast-like calcium binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gorgone GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #23834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 68-69; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG23843 standard; protein; 383 AA.
AAY94250 standard; protein; 377 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US027027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-00190965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 LRRQIGTRSPTVEY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 LRROIGTRSPTVEY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.(
Matches 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reproductive disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guegler KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-387793/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200029580-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-2002
                                                                                                                                       10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG23843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT,
                                                               AAY94250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG23843
```

```
The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGN primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food pupplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders in diagnostics, forensics, gene mapping, identification of mutations in diagnostics and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and to acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this electronic format directly from MIPO at the printed specification, but was obtained in electronic format directly from MIPO at (II) and (II) accompany of the printed specification, but was obtained in electronic format directly from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , DB 4; here, o. 0.0072; o; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 54202; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #25363.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG25372 standard; protein; 639 AA.
                                                                                                                                    30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                             31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                  Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 TEAVAQLAQELY 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 TEAVAQLAQELY 74
                                                                                                                                                                                                                                                                                                                        2001-639362/73
                                                                                                                                                                                                                                                                                Drmanac RT, Liu C,
                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS88030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 383 AA;
                                                       WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                              11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG25372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 16
SXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
```

ö

ð g

```
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAY-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2-JUN-1
\Sigma
                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, ollgomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed ectivity of is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biddiversing amino acid sequences. AEG00010-AEG30377 represent novel human diagnostic mino acid sequences. AEG00010-AEG30377 represent novel human diagnostic mino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MUPO at the printed specification, but was obtained in electronic format directly from MUPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.6%; Score 12; DB 4; Length 639;
100.0%; Pred. No. 0.012;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays protein fragment SEQ ID NO: 51164.
                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 55731; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG41153 standard; protein; 139 AA.
                                                                                                                                                  Tang YT;
                                                                                    31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                            30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 TEAVAQLAQELY 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 TEAVAQLAQELY 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zea mays subsp. mays.
                                                                                                                                                                          WPI; 2001-639362/73.
N-PSDB; AAS89559.
                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 639 AA;
             WO200175067-A2
                                                                                                                                                                                                                                                       biodiversity.
                                   11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG41153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG41153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
ð
```

```
99US-0123180P.
99US-0123548P.
99US-0125788P.
                                                                                                                                                                                                                                                                   99US-0134218P.
99US-0134219P.
99US-0134221P.
99US-0134370P.
                                                                                                                                                                                                                                                                                                                                     990S-0135353P.
990S-0135629P.
990S-013692P.
990S-013632P.
990S-0137222P.
                                                                                                                                                                                                                                                                                                                                                                                                          99US-0137502P.
99US-0137724P.
99US-0138094P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0139452P.
99US-0139453P.
99US-0139492P.
99US-0139454P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0139455P.
99US-0139456P.
99US-0139457P.
99US-0139458P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0139459P.
99US-013946UP.
99US-0139462P.
99US-0139462P.
99US-0139750P.
                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0138540P.
99US-0138847P.
99US-0139119P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0139817P.
99US-0139899P.
99US-0140353P.
                                                                                                                                                                                                                                                                                                                    99US-0134941P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0141287P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0140354P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0140695P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0140991P
                  2000EP-00301439
                 25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-1999;
                                                                                                                              16-APR-1999
                                                                                                                                                          23-APR-1999;
                                                                                                                                                                                                 30-APR-1999;
                                                                                                                                                                                                                     05-MAY-1999
                                                                                                                                                                                                                             06-MAY-1999
                                                                                                                                                                                                                                                 07-MAY-1999
                                                                                                                                                                                                                                                                     14-MAY-1999
                                                                                                                                                                                                                                                                                                  14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                     27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                    03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .6-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUN-1999
06-SEP-2000
                                                                                                                                                                                                                                       06-MAY-1999
                                                                                                                                                                                                                                                                                       14-MAY-1999
                                                                                                                                                                                                                                                                                                           L8-MAY-1999
                                                                                                                                                                                                                                                                                                                      19-MAY-1999
                                                                                                                                                                                                                                                                                                                               20-MAY-1999
                                                                                                                                                                                                                                                                                                                                          21-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                            04-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                          0-0100-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    .0-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8-JUN-1999
```

```
PR 01-701-1399; 90TS-0142154P.

PR 02-701-1399; 90TS-0142290P.

PR 06-701-1399; 90TS-0142290P.

PR 12-701-1399; 90TS-0142290P.

PR 13-701-1399; 90TS-014237P.

PR 13-701-1399; 90TS-014324P.

PR 13-701-1399; 90TS-014324P.

PR 13-701-1399; 90TS-014324P.

PR 13-701-1399; 90TS-0144085P.

PR 13-701-1399; 90TS-0144085P.

PR 13-701-1399; 90TS-0144085P.

PR 13-701-1399; 90TS-0144332P.

PR 23-701-1399; 90TS-0144332P.

PR 21-701-1399; 90TS-0144332P.

PR 21-701-1399; 90TS-0144332P.

PR 21-701-1399; 90TS-0144332P.

PR 22-701-1399; 90TS-0144332P.

PR 22-701-1399; 90TS-0144332P.

PR 22-701-1399; 90TS-0144332P.

PR 22-701-1399; 90TS-0144332P.

PR 22-701-1399; 90TS-0144332P.

PR 22-701-1399; 90TS-0144332P.

PR 22-701-1399; 90TS-0144332P.

PR 22-701-1399; 90TS-0144332P.

PR 22-701-1399; 90TS-0144332P.

PR 22-701-1399; 90TS-0144332P.

PR 22-701-1399; 90TS-0144332P.

PR 22-701-1399; 90TS-0145218P.

PR 22-701-1399; 90TS-0145218P.

PR 22-701-1399; 90TS-0145318P.

PR 22-701-1399; 90TS-0145318P.

PR 22-701-1399; 90TS-0145318P.

PR 22-701-1399; 90TS-0145318P.

PR 22-701-1399; 90TS-0145318P.

PR 22-701-1399; 90TS-0145318P.

PR 22-701-1399; 90TS-0147321P.

PR 22-701-1399; 90TS-0147321P.

PR 22-701-1399; 90TS-0147321P.

PR 22-701-1399; 90TS-0147321P.

PR 22-701-1399; 90TS-0147321P.

PR 22-701-1399; 90TS-0147321P.

PR 22-701-1399; 90TS-0147321P.

PR 22-701-1399; 90TS-0149322P.

PR 22-701-1399; 90TS-0149322P.

PR 22-701-1399; 90TS-0149322P.

PR 22-701-1399; 90TS-0149322P.

PR 22-701-1399; 90TS-0149322P.

PR 22-701-1399; 90TS-0149322P.

PR 22-701-1399; 90TS-0149322P.

PR 22-701-1399; 90TS-0149322P.

PR 22-701-1399; 90TS-0149322P.

PR 22-701-1399; 90TS-0149322P.

PR 22-701-1399; 90TS-0149322P.

PR 22-701-1399; 90TS-0149322P.

PR 22-701-1399; 90TS-0149322P.

PR 22-701-1399; 90TS-0149323P.

PR 22-701-1399; 90TS-0149323P.

PR 22-701-1399; 90TS-0149323P.

PR 22-701-1399; 90TS-0149323P.

PR 22-701-1399; 90TS-0149323P.

PR 22-701-1399; 90TS-0149323P.

PR 22-701-1399; 90TS-0149323P.

PR 22-701-1399; 90TS-0149323P.

PR 22-701-1399; 90TS-0149323P.

PR
```

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays protein fragment SEQ ID NO: 51163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.4%; Score 8; DB 3
100.0%; Pred. No. 23;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG41152 standard; protein; 148 AA
99US-0154139P.
99US-0155459P.
99US-0155659P.
99US-0156589P.
99US-0156589P.
99US-0156589P.
99US-01571117P.
99US-01571213P.
99US-01571213P.
99US-0159234P.
99US-0159234P.
99US-0159234P.
99US-0159234P.
99US-0159234P.
99US-0159234P.
99US-0159234P.
99US-0159331P.
99US-0160741P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
99US-016074P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-1999; 99US-0121825P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 MLRECIRH 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays subsp. mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MLRECIRH 8
                                                                           28-SEP-1999

29-SEP-1999

20-OCT-1999

06-OCT-1999

06-OCT-1999

13-OCT-1999

13-OCT-1999

13-OCT-1999

14-OCT-1999

14-OCT-1999

14-OCT-1999

14-OCT-1999

14-OCT-1999

14-OCT-1999

12-OCT-1999

12-OCT-1999

12-OCT-1999

12-OCT-1999

12-OCT-1999

13-OCT-1999

14-OCT-1999

15-OCT-1999

15-OCT-1999

15-OCT-1999

16-OCT-1999

17-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000.
                    22-SEP-1999;
23-SEP-1999;
24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG41152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG41152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

99015-0143624P 99015-0144005P 99015-0144005P 99015-0144325P 99015-01443312P 99015-01443312P 99015-01443312P 99015-01443312P 99015-01443312P 99015-01443312P 99015-01443312P 99015-01443312P 99015-01443312P 99015-01443312P 99015-01443312P 99015-01443312P 99015-01443312P 99015-01443312P 99015-01443312P 99015-01443312P 99015-01443312P 99015-01443312P 99015-01443312P 99015-0145931P 99015-0145931P 99015-0145931P 99015-0145931P 99015-0149323P 99015-0149323P 99015-0149323P 99015-0149323P 99015-0149323P 99015-0149323P 99015-0149323P 99015-01499323P 99015-01499323P 99015-01499323P 99015-0151339P 99015-0151339P 99015-0151339P 99015-0151339P 99015-0151339P 99015-0151339P 99015-0151339P 99015-0151339P 99015-0151339P 99015-0151339P
14-Jul-1999 16-Jul-1999 16-Jul-1999 19-Jul-1999 19-Jul-1999 19-Jul-1999 19-Jul-1999 19-Jul-1999 19-Jul-1999 19-Jul-1999 20-Jul-1999 21-Jul-1999 22-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Jul-1999 23-Ju
% % % % % % % % % % % % % % % % % % %
990YS - 0.12318 0P 990YS - 0.12318 0P 990YS - 0.12626 4P 990YS - 0.12626 4P 990YS - 0.12624 4P 990YS - 0.12624 4P 990YS - 0.12624 4P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.13064 1P 990YS - 0.1306 1P 990YS - 0.1306 1P 990YS - 0.1306 1P 990YS - 0.1306 1P 990YS - 0.1306 1P 990YS - 0.1306 1P 990YS - 0.1306 1P 990YS - 0.1306 1P 990YS - 0.1306 1P 990YS - 0.1306 1P 990YS - 0.1306 1P 990YS - 0.1306 1P 990YS - 0.1306 1P 990YS - 0.1306 1P 990YS - 0.1306 1P 990YS - 0.1306 1P 990YS - 0.1406 95 P 990YS - 0.1406 95 P 990YS - 0.1406 95 P 990YS - 0.1406 95 P 990YS - 0.1406 95 P 990YS - 0.1406 95 P 990YS - 0.1406 95 P 990YS - 0.1406 95 P 990YS - 0.1406 95 P 990YS - 0.1406 95 P 990YS - 0.1406 95 P 990YS - 0.1406 95 P 990YS - 0.1406 95 P 990YS - 0.1406 95 P 990YS - 0.1429 90 P
0.5-MAR-1999 2.5-MAR-1999 2.5-MAR-1999 0.6-APR-1999 0.6-APR-1999 119-APR-1999 119-APR-1999 129-APR-1999 129-APR-1999 129-APR-1999 130-APR-1999 130-APR-1999 140-MAY-1999 150-MAY-1999 160-MAY-1999 170-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 180-MAY-1999 18
X X X X X X X X X X X X X X X X X X X

```
9905-01342189

9905-01342189

9905-01342199

9905-013417689

9905-01351249

9905-013512318

9905-01351229

9905-01351229

9905-01351229

9905-01372289

9905-01372289

9905-01372289

9905-01372289

9905-01394589

9905-01394589

9905-01394589

9905-01394589

9905-01394589

9905-01394589

9905-01394589

9905-01394589

9905-01394589

9905-01394589

9905-01394589

9905-01394589

9905-01394589

9905-01394589

9905-01394589

9905-01394589

9905-01394589

9905-01394589

9905-01406918

9905-01406918

9905-0142839

9905-0142839

9905-0142839

9905-01428328

9905-01428328
                               990S-0130S10P
990S-0130831P
990S-0132048P
990S-0132407P
990S-0132484P
990S-0132486P
990S-0132486P
990S-0132486P
990S-0132486P
                                                                         04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
                                                                                                                                                                                                                       28-MAY-1999;
01-JUN-1999;
03-JUN-1999;
04-JUN-1999;
07-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1999;
08-JUL-1999;
09-JUL-1999;
12-JUL-1999;
13-JUL-1999;
14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                   18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                      18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                               18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-1999;
21-JUN-1999;
22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-JUN-1999;
24-JUN-1999;
28-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                              8-JUN-1999
                                                                                                                                                                                                                                                                                                            6-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-1999
01-JUL-1999
                                                                                                                                                                                               24-MAY-19
25-MAY-19
27-MAY-19
                                                                                                                                                                                                                                                                          10-JUN-1
                                                                                                                                                                                                                                                                                           14-JUN-1
16-JUN-1
                                                                                                                                                                                                                                                                                                                    17-JUN-1
 ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                           Length 148;
                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays protein fragment SEQ ID NO: 51162.
                                                                                                                                                                                                                                                                                           2.4%; Score 8; DB 3
100.0%; Pred. No. 25;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       AAG41151 standard; protein; 154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0121825P.
99US-0123180P.
99US-0125784P.
99US-0126264P.
99US-0126748EP.
99US-012674EP.
99US-0157753P.
99US-0158865P.
99US-015823P.
99US-015823P.
99US-015923P.
99US-015923P.
99US-015923P.
99US-015923P.
99US-015933P.
99US-015933P.
99US-015933P.
99US-015933P.
99US-015933P.
99US-015933P.
99US-01698P.
99US-01608P.
99US-01608P.
99US-01608P.
99US-01608P.
99US-01608P.
99US-01608P.
99US-01608P.
99US-016184P.
99US-01608P.
99US-016184P.
99US-016184P.
99US-016184P.
99US-016184P.
99US-016184P.
99US-016184P.
99US-016184P.
99US-016184P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                                                                                                                                                                                                                                                       18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100...
8; Conservative
                                                                                                                                                                                                                                                                                                                           145 MLRECIRH 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays subsp. mays.
                                                                                                                                                                                                                                                                                                                                            MLRECIRH 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
05-0CT-1999;
06-0CT-1999;
06-0CT-1999;
12-0CT-1999;
13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
12-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
23-0CT-1999;
24-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                        AAG41151;
                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                       RESULT 19
```

g ò

```
9905-0144334P.
9905-0144334P.
9905-0144334P.
9905-0144632P.
9905-01446314P.
9905-01446314P.
9905-0145086P.
9905-0145086P.
9905-0145087P.
9905-0145087P.
9905-0145087P.
9905-0145087P.
9905-0145087P.
9905-0145087P.
9905-0145088P.
9905-0145088P.
9905-0145088P.
9905-014508P.
9905-0147308P.
9905-0147308P.
9905-0147308P.
9905-0147308P.
9905-0147308P.
9905-0147308P.
9905-0147308P.
9905-0147308P.
9905-0147308P.
9905-0147308P.
                                                                                                                                                                                                                                                                                                                    99US-0149722P
99US-0149733P
99US-0149902P
99US-0149902P
99US-0150566P
99US-0150566P
99US-015066P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9905-0155486P
9905-0155659P
9905-0156458P
9908-0157117P
9908-015713P
9908-015753P
9908-015865P
9908-015823P
9908-015823P
9908-015823P
                                                                                                                                                                                                                                                                                                                                                                                 99US-0151066P.
99US-0151080P.
99US-0151303P.
99US-015138P.
99US-0152363P.
99US-0153070P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0153758P.
99US-0154018P.
99US-0154039P.
99US-0154779P.
                                                                                                                                                                                                                                                                                      99US-0148684P.
99US-0149368P.
99US-0149175P.
99US-0149426P.
                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-1999;
13-SEP-1999;
15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-1999;
13-OCT-1999;
13-OCT-1999;
                     20 - ULL - 1999;
20 - ULL - 1999;
20 - ULL - 1999;
21 - ULL - 1999;
21 - ULL - 1999;
22 - ULL - 1999;
22 - ULL - 1999;
22 - ULL - 1999;
                                                                                                                                                                                                                                                                                                                                                                                 27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
                                                                                                         23-JUL-1999;
23-JUL-1999;
26-JUL-1999;
27-JUL-1999;
                                                                                                                                                      28-JUL-1999;
02-AUG-1999;
02-AUG-1999;
02-AUG-1999;
                                                                                                                                                                                                            05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
                                                                                                                                                                                                                                                                11-AUG-1999;
12-AUG-1999;
13-AUG-1999;
13-AUG-1999;
                                                                                                                                                                                                                                                                                                             18-AUG-1999;
20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                   23-AUG-1999;
25-AUG-1999;
26-AUG-1999;
27-AUG-1999;
                                                                                                                                                                                             04-AUG-1999;
04-AUG-1999;
                                                                                                                                                                                                                                  06-AUG-1999
                                                                                                                                                                                                                                                                                                                                             23-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                        07-SEP-1999
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 5505; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                     Length 154;
                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 5505.
                                                                                                                                                                                                                                                   2.4%; Score 8; DB 3;
100.0%; Pred. No. 26;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myers EW;
                                                                                                                                                                                                                                                                                                                                                        ABB59571 standard; protein; 464 AA
     9905-0159329P.
9905-0159310P.
9905-015963P.
9905-015964P.
9905-015964P.
9905-016076P.
9905-016076P.
9905-016070P.
9905-0160814P.
9905-0160814P.
9905-0160814P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PWD,
                                                                                                                                              99US-0161404P.
99US-0161405P.
99US-0161406P.
99US-0161359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                    99US-0161360P.
99US-0161361P.
                                                                                                                                                                                                                99US-0161992P.
                                                                                                                                                                                                                                  99US-0162142P
                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŗ
                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                       145 MLRECIRH 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                          16 MLRECIRH 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-656860/75.
                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABL03674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interactions.
                        14-0CT-1999)
14-0CT-1999
18-0CT-1999
18-0CT-1999
21-0CT-1999
21-0CT-1999
21-0CT-1999
21-0CT-1999
21-0CT-1999
21-0CT-1999
                                                                                                                                             25-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                                                   22-OCT-1999;
22-OCT-1999;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001.
       14-OCT-1999;
14-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                           ABB59571;
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                     RESULT 20
                                                                                                                                                                                                                                                                                                                                               ABB5957
                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                         à
```

Pred. No. 1.4e+02;

100.08;

Best Local Similarity

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30512).

ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, SEQ ID NO 993; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                              Length 464;
                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 993.
                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                            2.4%; Score 8; DB 4
100.0%; Pred. No. 72;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB58067 standard; protein; 923 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z
                                                                                                                                                                                                                                                          Local Similarity 100.
Les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                      166 ADLQLIDE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                   84 ADLQLIDF 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABL02170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 923 AA;
                                                                                                                                                                                                           Sequence 464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB58067;
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  55555555555<del>X</del>&
                                                                                                                                                                                                                                                                                                                     ð
```

2.4%; Score 8; DB 4; Length 923;

Query Match

```
The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PKDs primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cartivity of (II) as useful in gene therapy techniques to restore normal activity of (II) or to tract disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II) are useful for treating disorders of sites expressing (II) are useful for treating disorders of sites expressing (II) and its binding partners are useful in medical imaging controlly abbrarant protein expression or biological activity. The plypeptide and polymucleotide sequences have applications in disorders or produce other types of data and products dependent on DNA and and can to produce other types of data and products dependent on DNA and anno acid sequences. ABG00010-ABG30077 represent novel human diagnostic mino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                   Human, chromosome mapping; gene mapping; gene therapy, forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 4 ilarity 100.0%; Pred. No. 76; Conservative 0; Mismatches
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 33894; 103pp; English.
                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein #3526.
                                                                                                                                                                                     ABG03535 standard; protein; 44 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                     (first entry)
  8; Conservative
                                                                             449 SSGLLVTL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
Les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                         75 SSGLLVTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS67722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo gapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biodiversity.
                                                                                                                                                                                                                                                                     13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2001.
                                                                                                                                                                                                                              ABG03535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
  Matches
                                                                                                                                                                                                                          à
                                                                             셤
```

du ò

```
990S-0139492P.
990S-0139444P.
990S-0139456P.
990S-0139456P.
990S-0139456P.
990S-0139460P.
990S-0139460P.
990S-0139460P.
990S-0139460P.
990S-014033P.
990S-014033P.
990S-014033P.
990S-014033P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-01453BP.
990S-01453BP.
990S-01453BP.
990S-01453BP.
990S-01453BP.
990S-01453BP.
990S-01453BP.
990S-01453BP.
990S-01453BP.
990S-01453BP.
990S-01453BP.
990S-01453BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0148319P.
99US-0148341P.
99US-0148565P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-1999)
02-AUG-1999)
02-AUG-1999)
03-AUG-1999)
04-AUG-1999)
06-AUG-1999)
06-AUG-1999)
06-AUG-1999)
06-AUG-1999)
06-AUG-1999)
09-AUG-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-AUG-1999;
11-AUG-1999;
12-AUG-1999;
13-AUG-1999;
                                                                                                                                                                                                                                                                               19-701-1999
19-701-1999
19-701-1999
19-701-1999
19-701-1999
20-701-1999
20-701-1999
21-701-1999
                                                                                                                                                                                                                                                                                                                                                                                22-JUL-1999;
22-JUL-1999;
22-JUL-1999;
23-JUL-1999;
                                                                                                                                                                                                                                 13-JUL-1999;
14-JUL-1999;
15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                        21-JUL-1999;
21-JUL-1999;
22-JUL-1999;
                                                                         18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                        29-JUN-1999;
30-JUN-1999;
01-JUL-1999;
01-JUL-1999;
                                                                                                 18-JUN-1999;
                                                                                                                                                                                                                                                         16-JUL-1999;
16-JUL-1999;
                                                         18-JUN-1999;
                                                                                                                         23-JUN-1999;
                                                                                                                                  23-JUN-1999;
                                                                                                                                        24-JUN-1999;
  Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter, termination sequence.
                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 70973
                                                                AAG55362 standard; protein; 46 AA.
                                                                                                                                                                                                                                99US-0121825P.
99US-0125788P.
99US-0125788P.
99US-0125788P.
99US-0126784P.
99US-0126784P.
99US-0126744P.
99US-0128234P.
99US-0128714P.
99US-0138041P.
99US-0138041P.
99US-0132484P.
99US-0132484P.
99US-0132484P.
99US-0132484P.
99US-0132484P.
99US-0132484P.
99US-013248P.
99US-013248P.
99US-013248P.
99US-013248P.
99US-013248P.
99US-013248P.
99US-0134728P.
99US-0134728P.
99US-0134728P.
99US-0134728P.
99US-0134728P.
99US-0134728P.
99US-0134728P.
99US-013468P.
99US-013468P.
99US-013468P.
99US-013468P.
99US-013468P.
99US-013468P.
99US-013468P.
99US-013468P.
99US-0137724P.
99US-0137724P.
                                                                                                                                                                                                                  25-FEB-2000; 2000EP-00301439
                                                                                                 18-OCT-2000 (first entry)
                                                                                                                                                                 Arabidopsis thaliana
          NLAILEK 30
                         NLAILEK 35
                                                                                                                                                                                                                                25-FEB-1999;

05-MAR-1999;

23-MAR-1999;

25-MAR-1999;

25-MAR-1999;

10-APR-1999;

10-APR-1999;

10-APR-1999;

10-APR-1999;

10-APR-1999;

10-APR-1999;

10-APR-1999;

10-APR-1999;

10-APR-1999;

10-MAY-1999;

10-MAY-1999;

11-MAY-1999;

11-MAY-1999;

11-MAY-1999;

11-MAY-1999;

11-MAY-1999;

11-MAY-1999;

11-MAY-1999;

11-MAY-1999;

11-MAY-1999;

11-MAY-1999;

12-MAY-1999;

12-MAY-1999;

13-MAY-1999;

14-MAY-1999;

15-MAY-1999;

16-MAY-1999;

16-MAY-1999;

17-MAY-1999;

18-MAY-1999;

19-MAY-1999;

19-MAY-1999;

10-UNI-1999;

10-UNI-1999;

10-UNI-1999;

10-UNI-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUN-1999;
16-JUN-1999;
16-JUN-1999;
                                                                                                                                                                                  EP1033405-A2
                                                                                                                                                                                                  06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUN-1999
                                                                                 AAG55362;
                        29
           24
                                                 RESULT 23
```

(first entry)

```
Escherichia coli polypeptide SEQ ID NO 1453
              ABB53042 standard; protein; 51 AA
                                                                             11-FEB-2002
                                              ABB53042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 25
   ABB53042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP05605
                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 3; Length 46;
100.0%; Pred. No. 79;
iive 0; Mismatches 0; Indels
            99US-0149368P.
99US-0149175P.
99US-0149426P.
                                                         99US-0149722P.
99US-0149723P.
99US-0149929P.
99US-0149902P.
                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0157753P.
99US-0157865P.
99US-0158029P.
99US-0158232P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0159584P.
99US-0160741P.
99US-0160767P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0160815P.
99US-0160980P.
99US-0160981P.
99US-0160989P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0161992P.
99US-0161993P.
99US-0162142P.
                                                                                                                                                                                                                                            99US-0151930P.
99US-0152363P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0159330P.
                                                                                                                                                                  99US-0151065P.
                                                                                                                                                                                                                                                                                                         99US-0154018P.
                                                                                                                                                                                                                                                                                                                                                                                                 99US-0156458P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0160768P.
                                                                                                                        99US-0149930P
                                                                                                                                                     99US-0150884P
                                                                                                                                                                                                99US-0151080P
                                                                                                                                                                                                               99US-0151303P
                                                                                                                                                                                                                               99US-0151438P
                                                                                                                                                                                                                                                                            99US-0153070P
                                                                                                                                                                                                                                                                                            99US-0153758P
                                                                                                                                                                                                                                                                                                                                       99US-0154779P
                                                                                                                                                                                                                                                                                                                                                      99US-0155139P
                                                                                                                                                                                                                                                                                                                                                                      99US-0155486P
                                                                                                                                                                                                                                                                                                                                                                                    99US-0155659P
                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0157117P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0158369P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0159293P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0159294P
99US-0159295P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0159329P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0159637P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0160814P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0161404P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0161405P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0161359P
99US-0161360P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0161361P
99US-0161920P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
18-OCT-1999;
21-OCT-1999;
           16-AUG-1999;
17-AUG-1999;
18-AUG-1999;
20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                      16-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                    22-SEP-1999;
23-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-1999;
29-SEP-1999;
                                                                                                                      23-AUG-1999
25-AUG-1999
                                                                                                                                                                                                  27-AUG-1999
                                                                                                                                                                                                               30-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-1999
25-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Loc
Matches
$\frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\pi} \frac{\pi}{\p
```

```
The invention relates to a library of DNA fragments of Escherichia colistrains comprising polynucleotides (ABA88577-ABA881929 and ABA89533) and encoded proteins (ABB5249-ABB52994-ABB53094) of nature B2/D+A-. The polynucleotides have potential antiflammatory, antibacterial and immunosuppressive activity as part of pharmaceutical compositions used to treat, palliate or prevent extra-intestinal E colinfections. The polypeptides are useful for determining the phylogenic group of a given E. coli strain. These polypeptides can detect and treat an undesired development of E. coli, particularly an extra-intestinal infection that include systemic and non-diarrhoeal infections such as septicaemia, pyelonephritis and meningitis this is particularly as advantageous as bacterial resistence is increasing with the more frequent use of broad spectrum antibiotics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A library of DNA fragments of Escherichia coli strains for the phylogenic determination of a given strain comprises polynucleotides of nature B2/D +
                            immunosuppressive; extra-intestinal infection; phylogeny; meningitis; systemic infection; non-diarrhoeal infection; septicaemia; pyelonephritis; antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tinsley C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 4; Length 51;
100.0%; Pred. No. 87;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bingen E, Bonacorsi S, Clermont O, Nassif X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ORFX protein sequence SEQ ID NO:11192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP05605 standard; protein; 83 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Fig 6; 646pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  10-MAR-2000; 2000FR-00003145.
02-FEB-2001; 2001FR-00001449.
                                                                                                                                                                                                                                                                                                                                        12-MAR-2001; 2001WO-EP003445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 EILLKNQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-550253/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EILLKNQ 19
                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 51 AA;
                                                                                                                                                                                                               WO200166572-A2.
                                                                                                                                                                                                                                                                        13-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP05605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AXAXEXEX
Example
```

ö

. 0

Gaps

ö

Indels

Conservative

LLVTLIA 84

78 7

ਨੇ

LLVTLIA 8

25-JUN-2002 (first entry)

```
degenerative disorder; ostecarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
                                                                                                                                                                                                                                                                                      Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 11192; 1037pp; English.
                                                                                                                                                      29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                         30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                 Shimkets RA, Leach MD;
                                                                                                                                                                                                            (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                      WPI; 2002-106308/14.
N-PSDB; ABN21357.
                                                                 myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 83 AA;
                                                                                                           WO200192523-A2.
                                                                                      Homo sapiens.
                                                                                                                                 06-DEC-2001
```

The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 on the specification). ARM12722 concode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating a pathology associated with an ORFX-associated disorder. ORFX proteins are useful for treating a syndrome associated with ORFX-associated disorder. ORFX polymucleotide squarcome associated with ORFX-associated disorder. ORFX polymucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of ancer, hyperprolliferative disorders, intrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders related to organ transplantation, cardiovascular disease, disorders related to organ transplantation, cardiovascular diseases, disorders infectious contains and disorders. Infectious disease, various immune deficiencies and disorders, infectious architis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also consetul for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodonal disease, and for gut consetul for treating burns, incisions, ulcers, for treating observation and treatment of lung or liver fibrosis, coperation or regeneration and treatment of lung or liver fibrosis, coperation, put was obtained in electronic form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/bublished_pot_esquences

```
Query Match
2.1%; Score 7; DB 5; Ler
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                           20 ILKDNLA 26
                                                                                                                                       71 ILKDNLA 77
                                                                                              ð
```

ABP08677 standard; protein; 97 AA.

ABP08677;

ö

Gaps

. 0

0; Indels Length 83;

```
The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1) in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABPD0010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide squences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, hemographic osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertenaion, hypothyroidism, cholesterol ester storder and control ester at the control ester and control ester and control ester and control ester at the control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control ester and control es
                                                                                                                                                 Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperporliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hyperension; hyperthyoidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arthritis, autoimmune thyroiditis, myasthemia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcres, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 5; Length 97; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 17336; 1037pp; English.
                                                                                          Human ORFX protein sequence SEQ 1D NO:17336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSKSLOA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 VSKSLQA 48
                                                                                                                                                                                                                                                                                                                                                                        nyasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABN24429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200192523-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
\%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              엄
```

```
2000US - 0246478P

2000US - 0246533P

2000US - 0246524P

2000US - 0246524P

2000US - 0246534P

2000US - 0246534P

2000US - 0246534P

2000US - 0246534P

2000US - 024661P

2000US - 024661P

2000US - 024661P

2000US - 024661P

2000US - 024920P

2000US - 024920P

2000US - 024921P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P

2000US - 0249214P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0249297P.
2000US-0249299P.
2000US-0249300P.
2000US-0250160P.
2000US-0231968P.
2000US-0232397P.
2000US-0232399P.
2000US-02324010P.
2000US-023364P.
2000US-023364P.
2000US-0233654P.
2000US-023423P.
2000US-023423P.
2000US-023423P.
2000US-023423P.
2000US-023423P.
2000US-023423P.
2000US-023423P.
2000US-023434P.
2000US-023464P.
2000US-023463P.
2000US-023438P.
2000US-023438P.
2000US-023438P.
2000US-023438P.
2000US-023438P.
2000US-023438P.
2000US-023636P.
2000US-023636P.
2000US-0237037P.
2000US-0237037P.
2000US-0237037P.
2000US-0237037P.
2000US-0237037P.
2000US-0237037P.
2000US-0237037P.
2000US-0237037P.
2000US-0237037P.
2000US-0237037P.
2000US-0237037P.
2000US-0237037P.
2000US-0237037P.
2000US-0237037P.
2000US-0237037P.
2000US-0237037P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0246475P.
2000US-0246476P.
2000US-0246477P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0241826P.
2000US-0244617P.
2000US-0246474P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0241809P
                                                                                                                                                                                                                                                              25-SEP-2000; 25-SEP-2000; 26-SEP-2000; 27-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CGT-2000;
20-CG
                                                                                                                                                               14-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SEP-2000; 21-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -NOV-2000;
-NOV-2000;
-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-OCT-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-NOV-2000;
    Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis.
                                                                                                                                                                                                                 Human immune/haematopoietic antigen SEQ ID NO:14388
                                                                          AAM86795 standard; protein; 98 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JAN-2000; 2000US-0179065P.

24-FEB-2000; 2000US-018652BP.
22-FEB-2000; 2000US-018652BP.
22-MAR-2000; 2000US-0186350P.
16-MAR-2000; 2000US-0186350P.
16-MAY-2000; 2000US-0198074P.
19-MAY-2000; 2000US-0198074P.
19-MAY-2000; 2000US-0198074P.
28-JUN-2000; 2000US-020515P.
30-JUN-2000; 2000US-0215486P.
30-JUN-2000; 2000US-0215486P.
11-JUL-2000; 2000US-0215486P.
11-JUL-2000; 2000US-0216647P.
07-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
14-JUL-2000; 2000US-022514P.
14-JUC-2000; 2000US-0225214P.
14-JUC-2000; 2000US-0225214P.
14-JUC-2000; 2000US-0225264P.
14-JUC-2000; 2000US-0225264P.
14-JUC-2000; 2000US-0225264P.
14-JUC-2000; 2000US-0225264P.
14-JUC-2000; 2000US-0225264P.
14-JUC-2000; 2000US-0225264P.
14-JUC-2000; 2000US-0225264P.
14-JUC-2000; 2000US-0225264P.
14-JUC-2000; 2000US-0225269P.
14-JUC-2000; 2000US-0225269P.
14-JUC-2000; 2000US-0225269P.
14-JUC-2000; 2000US-0225269P.
14-JUC-2000; 2000US-0225269P.
14-JUC-2000; 2000US-0225269P.
14-JUC-2000; 2000US-0225269P.
14-JUC-2000; 2000US-0225575P.
14-JUC-2000; 2000US-0225759P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-2000; 2000US-0227182P.
30-AUG-2000; 2000US-0227182P.
30-AUG-2000; 2000US-022987P.
01-SEP-2000; 2000US-0229343P.
01-SEP-2000; 2000US-0229344P.
01-SEP-2000; 2000US-0229344P.
05-SEP-2000; 2000US-0229509P.
05-SEP-2000; 2000US-0229509P.
06-SEP-2000; 2000US-0239509P.
06-SEP-2000; 2000US-0231242P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0231414P.
08-SEP-2000; 2000US-0231414P.
08-SEP-2000; 2000US-0231414P.
08-SEP-2000; 2000US-0231414P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0226681P.
2000US-0226868P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JAN-2001; 2001WO-US001354
                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
12-AUG-2000; 2
22-AUG-2000; 2
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                    07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                       AAM86795;
                           RESULT 27
AAM86795
```

```
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) admino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and traatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting the diagnose and treat immune/haemacopoietic-related diseases, especially concern and cancer metastases of haematopoietic-derived cells. AAK64703
                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, secreted protein; gene therapy; vaccine; treatment; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; SEQ ID NO 14388; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 7; DB 4; Length 98; 100.0%; Pred. No. 1.6e+02; cive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein, SEQ ID NO: 430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG89310 standard; protein; 99 AA.
                                                                                                                                                                                                                                                                             Barash SC, Ruben SM;
               05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-025198BP.
05-DEC-2000; 2000US-0256719P.
06-DEC-2000; 2000US-0251479P.
08-DEC-2000; 2000US-0251866P.
                                                                                                                          08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
                                                                                                                                                                                 11-DEC-2000; 2000US-0254097P.
                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 IRHEPLA 156
                                                                                                                                                                                                                                                                                                                    WPI; 2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 IRHEPLA 14
                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAK59576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200142451-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-2001.
                                                                                                                                                                                                                                                                               Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG89310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG89310
```

Gaps ; 0

```
The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides considered and be accepted by the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET conserved that affect the actifying mutations or deletions in a patient's genome that affect the actifying mutations or deletions in a patient's concent that affect the actifying mutations or deletions in a patient's patients own production of GENSET polypeptides. Conversely, antisense concleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in amples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide of expression and activity. The present sequence is a GENSET polypeptide of
                                                                                                                                                                                                                           Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant; gastrointestinal; gene therapy; GENSET; heavy metal toxicity; cancer inflammatory disease; immune disorder; neuromuscular; toxicity; central nervous system; cardiovascular; gastrointestinal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 4; Length 99; 100.0%; Pred. No. 1.6e+02; ative 0; Mismatches 0; Indels
                                                                                                                                  Dumas Milne Edwards J, Bougueleret L, Jobert S;
                                                                                                                                                                                                                                                                                                           Claim 21; Page 898; 921pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP76204 standard; protein; 99 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human GENSET protein SEQ ID 530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-APR-2001; 2001WO-IB000914.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2001; 2001WO-IB000914.
07-DEC-2000; 2000WO-IB001938.
                                  08-DEC-1999; 99US-0169629P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                      WPI; 2001-367870/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 KEPPTEA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 KEPPTEA
                                                                                                                                                                                           N-PSDB; AAH64913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 99 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200283898-A1
                                                                                           (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP76204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP76204
```

0;

Giordano J;

```
New GENSET polynucleotides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the
                                                                  Dumas Milne Edwards J, Jobert S,
                                                                                                                                                                                                                                                                                                                                                                                   Claim 14; Page 565; 735pp; English.
                                                                     Tanaka H,
                                                                                                                            WPI; 2003-075548/07
(GEST ) GENSET.
                                                                     Bejanin S,
                                                                                                                                                                                                                                                                                                                    toxicity
```

The present invention relates to novel GENSET polynucleotides (AB236404-AB23691). The polynucleotides and belasistin encoding polypeptides (ABP75963-ABP76368). The polynucleotides and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity 2.1%; Score 7; DB 6; Length 99; 100.0%; Pred. No. 1.6e+02; rive 0; Mismatches 0; Indels Sequence 99 AA;

7; Conservative Query Match Best Local Similarity 59 Matches

KEPPTEA 65 87 KEPPTEA 93 à

ABP76061 standard; protein; 99 AA. (first entry) 21-FEB-2003 RESULT 30
ABP76061
XX
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76
AC ABP76

Cytostatic; antiinflammatory; nootropic; neuroprotective; cardiant; gastrointestinal; gene therapy; GRNBET; heavy metal toxicity; cancer; inflammatory disease; immune disorder; neuromuscular; toxicity; central nervous system; cardiovascular; gastrointestinal. Human GENSET protein SEQ ID 268.

Homo sapiens

WO200283898-A1.

24-OCT-2002.

18-APR-2001; 2001WO-IB000914.

18-APR-2001; 2001WO-IB000914

(GEST ) GENSET

New GENSET polynucleotides and polypeptides, useful for treating heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, CNS, cardiovascular or gastrointestinal effects of the Giordano Jobert S, Dumas Milne Edwards J, Bejanin S, Tanaka H, WPI; 2003-075548/07

Claim 14; Page 444; 735pp; English.

toxicity

The present invention relates to novel GENSET polynucleotides (ABZ36404-ABZ3691) encoding polypeptides (ABP75963-ABP76368). The polynucleotides

```
.
0
and polypeptides are useful in screening and diagnostic assays for abnormal GENSET expression and/or biological activity. They are also useful for screening of compounds for treating or preventing GENSET-related disorders, such as heavy metal toxicity, cancer, inflammatory diseases, immune disorders, and the neuromuscular, central nervous system (CNS), cardiovascular or gastrointestinal effects of the toxicity
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                            Length 99;
                                                                                                                                                                               2.1%; Score 7; DB 6; Ler
100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                            59 KEPPTEA 65
                                                                                                                                                                                                                                                                                              KEPPTEA 93
                                                                                                                                                                                               Local Similarity
nes 7; Conserv
                                                                                                                                            Sequence 99 AA;
                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                         Matches
        8888888%
                                                                                                                                                                                                                                                                ò
```

AAO09956 standard; protein; 107 AA. Human polypeptide SEQ ID NO 23848. 06-NOV-2001 AA009956; AA009956 

ö

Gaps

; 0

0; Indels

RESULT 31

Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation

Homo sapiens.

WO200164835-A2

26-FEB-2001; 2001WO-US004927.

28-FEB-2000; 2000US-00515126. 18-MAY-2000; 2000US-00577409.

(HYSE-) HYSEQ INC

Liu C, Drmanac RT; Tang YT,

WPI; 2001-514838/56. N-PSDB; AA189887 Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.

Claim 20; SEQ ID NO 23848; 1399pp + Sequence Listing; English

The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to growing to cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymorphides are useful in gene therapy, vaccines or peptide therapy. The polymothes have various cytokine-like activities, e.g. atem cell growth factor activity, haematopoises regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 107 AA;

Query Match

2.1%; Score 7; DB 4; Length 107;

```
ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased example, N and P may be used to treat disorders associated with decreased that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                  Gaps
                                                                                                                                                                                                                                                                                                                cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 7; DB 4; Length 113; 100.0%; Pred. No. 1.8e+02; ive 0; Mismatches 0; Indels
                Indels
                                                                                                                                                                                                                                                                             Human colon cancer antigen protein SEQ ID NO:5203.
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA;
                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 6889; 9803pp; English.
                                                                                                                                                                       AAG74439 standard; protein; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-2000; 2000WO-US026524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0157137P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0163280P.
100.08;
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100...
7, Conservative
                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barash SC,
                                                 272 EAFHVFK 278
                                                                                                                                                                                                                                                                                                                                colorectal carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-235357/24.
                                                                                  36 EAFHVFK 42
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAH33870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  WO200122920-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-1999;
                                                                                                                                                                                                                                                                                                                colon
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-NOV-1999;
                                                                                                                                                                                                                                         03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruben SM,
                                                                                                                                                                                                          AAG74439;
                                                                                                                                                                                                                                                                                                                Human;
                  Matches
                                                                                                                                   RESULT 32
                                                                                                                                                                         ð
```

```
Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                        Antibacterial, vaccine, gene therapy, infection, sepsis, diagnosis, enzymatic assay, antibiotic target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel genes and encoded proteins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 6; Length 115;
100.0%; Pred. No. 1.9e+02;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 24324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 2368; 49pp; English.
                                                                                                          Staphylococcus aureus protein #1184.
                                                                                                                                                                                                                                                                                                                                                                                Scarselli M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB65844 standard; protein; 139 AA.
              ABM71944 standard; protein; 115 AA.
                                                                                                                                                                                                                                                                                      27-MAR-2002; 2002WO-IB002637.
                                                                                                                                                                                                                                                                                                                  27-MAR-2001; 2001GB-0007661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002 (first entry)
                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S. aureus, e.g. sepsis.
                                                                                                                                                                                      Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                  Masignani V, Mora M,
                                                                                                                                                                                                                                                                                                                                                                                                               2003-120786/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDNLAIL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 KDNLAIL 28
                                                                                                                                                                                                                                                                                                                                                  (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ACF73504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical.
                                                                                                                                                                                                                      WO200294868-A2.
                                                                            20-NOV-2003
                                                                                                                                                                                                                                                   28-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB65844;
                                            ABM71944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
ABM71944
                             ð
```

ò

Dp ò

```
ð
                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                The invention relates to an isolated mucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell.cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                              Disclosure; SEQ ID NO 24324; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 7; DB 4; Length 139;
100.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #16949.
                                                                                                                       Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU31422 standard; protein; 141 AA.
                                                                                                                       Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2002; 2002WO-US009107.
                                                23-MAR-2001; 2001WO-US009231.
                                                                   23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klebsiella pneumoniae.
                                                                                                                      Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 7; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                              249 ISKPENL 255
                                                                                                                                          WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                11 ISKPENL 17
                                                                                                (PEKE ) PE CORP NY.
                                                                                                                                                    N-PSDB; ABL09947
                                                                                                                                                                                                                                                                                                                                                 Sequence 139 AA;
         WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200277183-A2.
                                                                                                                                                                                              interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU31422;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
The invertion relates to an isolated mucleic acid comprising any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid controlled expression is inhibited by the antisense encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated of polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody apable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular continues mucleic acid; (4) an antibody apable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular proliferation or the activity of agene in an operon required for collidar proliferation or the activity of agene in an operon required for collidar proliferation or the biological pathway required for proliferation, or that inhibits proliferation of an identifying a gene required for callular proliferation of the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or the biological pathway in which a proliferation-required gene or which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the extent or organism or screening the target of a compound that inhibits the continue of an organism. The antisense nucleic acids are useful for strains; or (13) identifying proteins or screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, C. the target prokaryotic essential genes. Note: The sequence data for this court of the partice of the particle of the particle of the particle of the particle of the particle of the particle of the particle of the particle of the particle of the particle of the particle of the particle of the p
                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              differentiation; immune stimulating; vaccine; suppression; gene therapy; bematopotasis regulation; tissue growth; activin; inhibin; cadherin; chemotactic; chemokinetic; hemostatic; thrombolytic; anti-inflammatory; tumour invasion suppressor; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein clone gg894_13 alternate reading frame protein.
   Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; nutrition; cytokine; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 6; Length 141;
100.0%; Pred. No. 2.3e+02;
ive 0; Mismatches 0; Indels
   Ohlsen KL,
Forsyth RA,
   Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID NO 59346; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY29337 standard; protein; 176 AA.
   Malone C,
                                 Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 AEIVKIL 113
                                                                                                        2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 AEIVKIL 21
                                                                                                                                     N-PSDB; ACA35292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 141 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
   Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY2933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XSXEXEXEXEX
```

ö

```
protein polymucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or supporating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, haematopoiesis regulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activity, chemotactic/chemokinetic activity, and thrombolytic activity, receptor/ligand activity, and thrombolytic activity, receptor/ligand activity, and thrombolytic activity. The polynucleotides are also stated to be useful for inhibition activity. The polynucleotides are also stated to be useful for
                                                                                                                                                                                                   Merberg D;
rk HF, Fechtel K;
                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a human secreted protein. Human secreted
                                                                                                                                                                                                                                                                                                               New polynucleotides encoding secreted human proteins derived from, e.g. fetal brain potentially used as immunostimulators.
                                                                                                                                                                                                     vallie ER, Collins-Racie LA, Merber
Steininger RJ, Wong GG, Clark HF,
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 134; 139pp; English.
                                                                                                                                                                                                     Lavallie ER,
                                                                         99WO-US001404.
                                                                                                          98US-0072134P.
99US-00235609.
                                                                                                                                                                (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                        Agostino MJ,
                                                                                                                                                                                                       Mccoy JM,
                                                                                                                                                                                                                                                         WPI; 1999-458682/38.
                                                                                                                                                                                                                                                                              N-PSDB; AAX90444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 176 AA;
 WO9937674-A1
                                                                       21-JAN-1999;
                                                                                                          22-JAN-1998;
20-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy
                                    29-JUL-1999.
                                                                                                                                                                                                     Jacobs K,
Treacy M,
```

2.1%; Score 7; DB 2; Length 176; 100.0%; Pred. No. 2.8e+02; Live 0; Mismatches 0; Indels 7; Conservative Best Local Similarity LLGELIL 104 231 LLGELIL 237 98 Query Match Matches ò

ö

Gaps . 0

> AAU39088 standard; protein; 176 AA. 16-JAN-2002 AAU39088; RESULT 37 AAU39088

Human secreted protein gg894_1 #2. (first entry)

ö

Human; secreted protein; antiinflammatory; immunosuppressive; nootropic; neuroprotective; antiarthritic; antimicrobial; vulnerary; cytostatic; antidabetic; vircide; antiinfertility; anticonvulsant; vasotropic; antiparkinsonian; immunostimilant; dermatological; antirheumatic; antitumor; antiulcer; osteopathic; tranquiliser; cerebroprotective; orbytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodeficiency; SCID; tumour; autoimmune disorder; multiple sclerosis; rheumatoid arthritis; graft-versus.host disease; mysloid deficiency; wound healing; ulcer; periodontal disease; osteoporosis; osteoporthritis; Alzheimer's disease; parkinson's disease; Huntington's disease; infection; candiac disease; tricke; sepsis; inflammatory bowel disease; contraceptive; immunogen; food supplement;

ABB55797 standard; protein; 176 AA.

Homo sapiens.

Human, clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy; immune disorder; bacterial infection; fungal infection; cancer; tumour; autoimmune disorder; systemic lupus erythematosus; wound; ulcer; inhibin;

Human polypeptide SEQ ID NO 280.

(first entry)

14-FEB-2002

ABB55797;

```
The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of various immune deficiencies and disorders e.g. severe combined immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis, systemic lupus crythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation. The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (GVHD), in the induction of tumour immunity, myeloid or lymphoid cell deficiencies, wound healing and tissue repair, in the treatment of burns, incisions and ulcers, as well as in treatment of periodontal disease, osteoporosis or osteoarthritis, mediated by inflammatory processes, diseases of the peripheral nervous system, Alzheimer's,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkinson's disease, Huntington's disease, amy orthoghic lateral sclerosis, and Shy-Drager syndrome, infections, infarction of cardiac and central nervous system vessel e.g. stroke, sepsis, inflammatory bowel disease, ulcers, bone regeneration. The protein, having activin- or inhibin-related activities is useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. The proteins and nucleic acids are also useful as food supplements. The present sequence represents a secreted protein of the invention
                                                                                                                                                                                                                                                            Clark H;
                                                                                                                                                                                                                                                                                                                                                                                         Secreted human proteins, useful as vaccine for treating various diseases such as autoimmune disorders (e.g. multiple sclerosis), and nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                        Evans C;
Wong GG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 4; Length 176;
100.0%; Pred. No. 2.8e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                   Mccoy JM, Lavallie E, Collins-Racie LA, Agostino MJ, Steininger RJ, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Page 617-618; 619pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  system disorders (e.g. stroke).
                                                                                                                          30-MAR-2000; 2000US-00539330, 04-DEC-2000; 2000US-00729674.
                                                                                 22-MAR-2001; 2001WO-US009369.
                                                                                                                                                                                          (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100. es 7; Conservative
                                                                                                                                                                                                                                                                              Merberg D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 LLGELIL 237
                                                                                                                                                                                                                                                                                                                          WPI; 2001-639363/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 LLGELIL 104
                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS59272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 176 AA;
WO200175068-A2.
                                        11-0CT-2001
                                                                                                                                                                                                                                                                              Fechtel K,
                                                                                                                                                                                                                                   Jacobs K,
Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB55797
ଟ
```

osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; activin; haemophilia; cardiac infarction; stroke; sepsis; arthritis; vulnerary; ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic; crohn's disease; cytostatic; anti-inflammatory; immunomodulacr; neuroprotective; haemostatic; thrombolytic; anti-inflammatory.

Homo sapiens.

US2001039335-A1.

08-NOV-2001

2000US-00729674 04-DEC-2000;

97US-0067454P. 97US-0068379P. 98US-0070346P. 97US-0126425P 04-DEC-1997

98US-0070755P. 98US-0071304P. 98US-0072134P. 98US-0070643P 98US-0075038P. 23-NOV-1998; 30-MAR-2000; 02-JAN-1998 07-JAN-1998 08-JAN-1998 13-JAN-1998 30-JAN-1998

COLLINS-RACIE L A. ď MCCOY J M. LAVALLIE E JACOBS K. (JACO/) (COLLA) LAVA/)

2000US-00539330

EVANS C. MERBERG D. TREACY M. (EVAN/) (MERB/) (TREA/)

AGOSTINO M J. STEININGER R J SPAULDING V. WONG G G. CLARK H. (AGOS/) (SPAU/)
(WONG/) (CLAR/) (FECH/)

FECHTEL K.

Collins-Racie LA, Evans C; Steininger RJ, Spaulding , Lavallie ER, 1, Agostino MJ, Fechtel K; D, Treacy M, Clark H, Fe Mccoy JM, Jacobs K, Merberg D Wong GG,

WPI; 2002-040725/05.

New secreted proteins and encoding polynucleotides, useful in gene therapies, particularly for preventing or treating autoimmune disorders, cancer, graft-versus-host disease, wound, osteoporosis, stroke or inflammations.

Disclosure, Page 343-344; 349pp; English.

The invention relates to isolated polymucleotides (ABA90876-ABA90968 and ABA9080) and encoded proteins (ABB55698-ABB55800), especially polymucleotides SEQ ID NO 1 (ABA90876) and SEQ ID NO 19 (ABA90885) and polymucleotides SEQ ID NO 10 (ABB55707) contained in proteins SEQ ID NO 2 (ABB55698) and SEQ ID NO 20 (ABB55707) contained in clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 ace deposited with the American Type Culture Collection (AFCO) with accession number 98599. The polymucleotides and encoded polypeptides have cytostatic, anti-inflammatory, immunomodulator, vulnerary, neuroprotective, activity, inhibin, chemotactic, haemostatic, thrombolytic and anti-inflammatory activity and actinia as cytokine modulators and anti-inflammatory activity and actinia as cytokine modulators and anti-inflammatory activity and actinia as cytokine modulators and collections, particularly for preventing, treating or ameliorating any of the following diseases: immune deficiency and disorders; e.g. bacterial cor funcial inflammatosus or graft-versus-host disease; myeloid or lymphoid cell deficiencies; wound, burns, indisions and ulcers, osteoporosis or contentral and peripheral nervous system diseases and

neuropathies, e.g. Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis or Shy-Drager syndrome; haemophilia, cardiac infarction or stroke; inflammations, shock, sepsis or systemic inflammatory response syndrome, ischaemia-reperfusion injury, endotoxin lethality, arthritis, inflammatory bowel disease or Crohn's disease; or tumours or cancers, pemphigus vulgaris or pemphigus foliaceus Gaps ; 2.1%; Score 7; DB 5; Length 176; 100.0%; Pred. No. 2.8e+02; Ve 0; Mismatches 0; Indels 100.08; Local Similarity 100. nes 7; Conservative 231 LLGELIL 237 LLGELIL 104 Sequence 176 AA; 86 Query Match Matches 88888888 ₽ 셤

RESULT 39 AAU31106

AAU31106 standard; protein; 192 AA. AAU31106; 

(first entry) 18-DEC-2001

Novel human secreted protein #1597.

Human, vaccination; gene therapy, nutritional supplement, stem cell proliferation; haematopoiesis, nerve tissue regeneration, immune suppression; immune stimulation; anti-inflammatory; leukaemia. Human;

Homo sapiens.

WO200179449-A2.

25-OCT-2001.

16-APR-2001; 2001WO-US008656.

18-APR-2000; 2000US-00552929. 26-JAN-2001; 2001US-00770160.

(HYSE-) HYSEQ INC.

Drmanac RT; Liu C, Tang YT,

WPI; 2001-611725/70.

range of human polypeptides, useful in genetic Nucleic acids encoding a range o vaccination, testing and therapy

Claim 20; Page 403-404; 765pp; English.

the first the following the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptides. The polypeptides are also useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying a density and an antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins as nutritional supplements. They may be used to increase tem cell proliferation; to regulate haematopoiesis, and in bone, cartilage, tendon an unitation; as anti-inflammatory agents; and in treatment of leukaemias. ANU29510-AAU33304 represent the amino acid sequences of novel human can be used to increase of novel human can be used to increase of novel human can be used as nutritional supplements. invention relates to novel human secreted polypeptides. The

Sequence 192 AA;

```
9905-01391199

9905-0139452P

9905-0139452P

9905-0139454P

9905-0139454P

9905-0139454P

9905-0139454P

9905-0139453P

9905-0139453P

9905-0139460P

9905-0139460P

9905-0139460P

9905-0139460P

9905-0139460P

9905-0139460P

9905-0139460P

9905-0139460P

9905-0139460P

9905-0139460P

9905-0139460P

9905-0139460P

9905-0140334P

9905-0140334P

9905-0140334P

9905-014124P

9905-014334P

9905-0144335P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0147303P.
99US-0147416P.
99US-0147493P.
99US-0147935P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1999;
09-AUG-1999;
09-AUG-1999;
                                                                             18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                          18-JUN-1999;
21-JUN-1999;
22-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-AUG-1999;
04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
                             17-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-1999;
02-AUG-1999;
03-AUG-1999;
                                                                                                                                                                                                                                                                                       666
                                                                                                                                                           3-JUN-1999;
       14-JUN-1999
                                                              8-JUN-1999
                                                                     8-JUN-1999
                                                                                                                                                                  24-JUN-1999
                                                                                                                                                                                 29-NUL-1999
                                                      8-JUN-1999
                                                                                                           18-JUN-1999
                                                                                                                                                  23-JUN-1999
                                                                                                                                                                          28-JUN-1999
                                                                                                                                                                                                                                666
ô
                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                     Gaps
                      ٠;
    2.1%; Score 7; DB 4; Length 192;
100.0%; Pred. No. 3e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 1364.
                                                                                         AAG05091 standard; protein; 197 AA
                                                                                                                                                                                                                                                           990S-0123180P.
990S-0123548P.
990S-0126264P.
990S-0126264P.
990S-0127462P.
990S-0128234P.
                                                                                                                                                                                                                                                                                                                 990S-0128714P

990S-0129845P

990S-0130449P

990S-0130891P

990S-0132048P

990S-013248P

990S-0132484P

990S-0132486P

990S-0132486P

990S-0132486P

990S-0132481P

990S-0134219P

990S-0134219P

990S-0134219P

990S-0134219P

990S-0134219P

990S-0134219P

990S-0134219P

990S-0134219P

990S-0134219P

990S-0134219P

990S-0134219P

990S-0134219P

990S-0134218P

990S-0134218P

990S-0134218P

990S-0134218P

990S-0134218P

990S-0134218P

990S-0134218P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0137222P.
99US-0137528P.
99US-0137502P.
99US-0137724P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0138094P.
                                                                                                                                                                                                                                      2000EP-00301439
                                                                                                                                                                                                                                                     99US-0121825P.
                                                                                                                        17-OCT-2000 (first entry)
   Query Match
Best Local Similarity 1000.
Matches 7; Conservative
                                                                                                                                                                                      Arabidopsis thaliana.
                                                  167 ADLQLID 173
                                   84 ADLQLID 90
                                                                                                                                                                                                      EP1033405-A2
                                                                                                                                                                                                                                    25-FEB-2000;
                                                                                                                                                                                                                                                                                                                 08-APR-1999;
16-APR-1999;
19-APR-1999;
21-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1999;
08-JUN-1999;
10-JUN-1999;
                                                                                                                                                                                                                     06-SEP-2000.
                                                                                                                                                                                                                                                    25-FEB-1999;
05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-1999
                                                                                                                                                                                                                                                                           23-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                              06-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -JUN-1999
                                                                                                         AAG05091;
                                                                           RESULT 40
                                                                                   AAG05091
                                                 D.
                                                                                           ð
```

```
990S-0149923P
990S-0149930P
990S-015066P
990S-0151066P
990S-0151060P
990S-0151060P
990S-0151080P
990S-0151303P
990S-0151303P
990S-015303P
990S-015303P
990S-015303P
990S-015566P
990S-015568P
990S-015568P
990S-015568P
990S-015563P
990S-015563P
990S-015563P
990S-015563P
990S-015563P
990S-015563P
990S-015563P
990S-015563P
990S-0159633P
990S-0159638P
990S-0159638P
990S-0159638P
990S-0159638P
990S-0159638P
990S-0159638P
990S-015963P
990S-016963P
990S-016963P
990S-016963P
990S-016963P
990S-016963P
990S-016963P
990S-016963P
990S-016963P
990S-016963P
990S-016963P
990S-016963P
                  99US-0148565P.
99US-0148684P.
99US-0149368P.
                                      99US-0149175P.
99US-0149426P.
99US-0149722P.
                                                                                                                                                                                                                                                                                                                                                                                                          99US-0161361P.
99US-0161361P.
99US-0161992P.
       99US-0148319P.
                                                                                                                                                                                                                                                                                                                                                                                                      99US-0161360P
                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0161993P
99US-0162142P
                                                                                                                                                                                                                                              12-0CT-1999;
13-0CT-1999;
13-0CT-1999;
13-0CT-1999;
                                                                                                                                                                                                                                                                        14-0CT-1999;
14-0CT-1999;
                                            18-AUG-1999;
20-AUG-1999;
                                                                                          26-AUG-1999
                                                                                                                                                                                     23-SEP-1999
                                                                                                                                                                                                         29-SEP-1999
                                                                                                                                                                                                                                                                                                                            21-OCT-1999
21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                             22-0CT-1999,
22-0CT-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                      29-0CT-1999
                                                                                                                                                                                                                                                                                                         18-OCT-1999
```

```
Gaps
                                                        ..
Query Match 2.1%; Score 7; DB 3; Length 197; Best Local Similarity 100.0%; Pred. No. 3.1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                          3.1e+02;
les 0; Indels
```

ô

antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 5. Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; Wehrman T; Ren F, Xue AJ, Zhao QA, Wang J, Wehrma Wang D, Ma Y, Asundi V, Wang Z, Weng G; Human novel polypeptide sequence, SEQ ID NO:1581. ADC31499 standard; protein; 199 AA. Drmanac RT; 24-SEP-2002; 2002WO-US030474. 24-SEP-2001; 2001US-0324631P. 18-DEC-2003 (first entry) WPI; 2003-371981/35. Tang TY, Zhang J, Zhou P, Ghosh M, V 42 TFKDLLT 48 (HYSE-) HYSEQ INC. Haley-Vicente D, N-PSDB; ADC30528 WO2003029271-A2. Homo sapiens. 10-APR-2003. ADC31499; RESULT 41 ADC31499 

New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer

Claim 20; SEQ ID NO 1581; 1185pp; English.

The invention relates to 971 novel human CDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to mucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a mucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; an antibody polymucleotides or polypeptide of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of peventing, treating or ameliorating a medical condition; kits comprising polymucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention and identification of compounds that modulate the expression or activity of the polymucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention are useful in diagnostics, draw screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disorders wounds burner also patestory. disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or AAG30715 standard; protein; 213 AA.

AAG30715

AAG30715;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dirofilaria immitis mature venom allergen antigen 5-like protein VA5 (AAW11481), or PDIVA205, is capable of eliciting an immune response (cellular and/or humoral) in animals. It is encoded by a cDNA molecule nDiVA615 (AAT51379). VA5-like proteins (see also AAW11480-86) can be used in vaccines to prevent helminth infection
primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence atta for this partent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venom allergen antigen 5-like gene; VA5; helminth; parasite; nDiVA615; PDiVA205; vaccine; heartworm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding helminth venom allergen antigen 5-like protein pref. from Dirofilaria immitis or Onchocerca volvulus, useful esp. in vaccines to prevent helminth infection.
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    D. immitis mature venom allergen antigen 5-like protein PDiVA205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                             0;
                                                                                                                                                            2.1%; Score 7; DB 7; Length 199;
100.0%; Pred. No. 3.1e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 2; Length 205;
100.0%; Pred. No. 3.2e+02;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 19; Page 91-92; 124pp; English.
                                                                                                                                                                                                                                                                                                                                      AAW11481 standard; protein; 205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-00450944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-US007709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                           Local Similarity 100.
Les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tripp CA, Wisnewski N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 RDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dirofilaria immitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-020935/02.
N-PSDB; AAT51379.
                                                                                                                                                                                                                           73 LYSSGLL 79
                                                                                                                                                                                                                                                       57 LYSSGLL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HESK-) HESKA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 205 AA;
                                                                                                                              Sequence 199 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9637218-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                      22-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                     AAW11481;
                                                                                                                                                              Query Match
                                                                                                                                                                              Best Loc
Matches
                                                                                                                                                                                                                                                                                                        RESULT 42
    888888888888
                                                                                                                                                                                                                                                      Dp
                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
```

RDLKKTA 99

93

RESULT 43

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                         Arabidopsis thaliana protein fragment SEQ ID NO: 36771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0139457P.
99US-0139458P.
99US-0139459P.
                                                                                                                                                                                                                                                                                                                                                                                                                99US-0135124P.
99US-0135353P.
                                                                                                                                           25-FEB-2000; 2000EP-00301439.
                                                                                                                                                                      99US-0123180P.
                                                                                                                                                                                       99US-0125788P
                                                                                                                                                                                                                99US-0127462P.
                                                                                                                                                                                                                         99US-0128234P.
                                                                                                                                                                                                                                  99US-0128714P.
                                                                                                                                                                                                                                          99US-0129845P
                                                                                                                                                                                                                                                   99US-0130077P.
                                                                                                                                                                                                                                                           99US-0130449P.
                                                                                                                                                                                                                                                                   99US-0130510P
                                                                                                                                                                                                                                                                         99US-0130891P
                                                                                                                                                                                                                                                                                    99US-0131449P.
                                                                                                                                                                                                                                                                                           99US-0132048P.
                                                                                                                                                                                                                                                                                                    99US-0132407P
                                                                                                                                                                                                                                                                                                            99US-0132484P.
                                                                                                                                                                                                                                                                                                                     99US-0132485P,
                                                                                                                                                                                                                                                                                                                             99US-0132486P
                                                                                                                                                                                                                                                                                                                                     99US-0132487P
                                                                                                                                                                                                                                                                                                                                              99US-0132863P
                                                                                                                                                                                                                                                                                                                                                      99US-0134256P.
                                                                                                                                                                                                                                                                                                                                                             99US-0134218P,
                                                                                                                                                                                                                                                                                                                                                                       99US-0134219P
                                                                                                                                                                                                                                                                                                                                                                                99US-0134221P
                                                                                                                                                                                                                                                                                                                                                                                       99US-0134370P
                                                                                                                                                                                                                                                                                                                                                                                               99US-0134768P
                                                                                                                                                                                                                                                                                                                                                                                                         99US-0134941P.
                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0135629P.
                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0136021P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0136392P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0136782P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0137222P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0137528P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0137502P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0137724P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0138094P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0138847P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0139452P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0139492P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0139455P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0138540P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0139456P
                         (first entry)
                                                                                                                                                                                               99US-01
                                                                                                                                                                                                        99US-01
                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                           EP1033405-A2
                                                                                                                                                                                                                                                                                                                                            07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                       19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
                         17-0CT-2000
                                                                                                                            06-SEP-2000,
                                                                                                                                                                      05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                01-APR-1999;
                                                                                                                                                                                                                         06-APR-1999;
                                                                                                                                                                                                                                 08-APR-1999;
                                                                                                                                                                                                                                          16-APR-1999;
                                                                                                                                                                                                                                                  19-APR-1999;
                                                                                                                                                                                                                                                                          23-APR-1999;
                                                                                                                                                                                                                                                                                    28-APR-1999;
                                                                                                                                                                                                                                                                                          30-APR-1999;
                                                                                                                                                                                                                                                                                                                   05-MAY-1999;
                                                                                                                                                                                                                                                                                                                             06-MAY-1999
                                                                                                                                                                                                                                                                                                                                    06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                      14-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                               8-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JUN-1999;
                                                                                                                                                                                                                                                           21-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1999
```

```
RR 18-70N-1999; 990S-0139462P
RR 18-70N-1999; 990S-0139462P
RR 18-70N-1999; 990S-0139462P
RR 18-70N-1999; 990S-0139462P
RR 21-70N-1999; 990S-0139750P
RR 22-70N-1999; 990S-0139817P
RR 22-70N-1999; 990S-0140354P
RR 22-70N-1999; 990S-0140354P
RR 12-70N-1999; 990S-0140354P
RR 12-70N-1999; 990S-014032P
RR 12-70N-1999; 990S-014032P
RR 12-70N-1999; 990S-014032P
RR 12-70N-1999; 990S-014032P
RR 12-70N-1999; 990S-014032P
RR 12-70N-1999; 990S-014032P
RR 12-70N-1999; 990S-014032P
RR 12-70N-1999; 990S-014032P
RR 12-70N-1999; 990S-014032P
RR 12-70N-1999; 990S-014032P
RR 22-70N-1999; 990S-014032P
RR 22-70N-1999; 990S-014032P
RR 22-70N-1999; 990S-014032P
RR 22-70N-1999; 990S-014032P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014433P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-70N-1999; 990S-014432P
RR 22-7
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 2.1%; Score 7; DB 3; Length 213; Local Similarity 100.0%; Pred. No. 3.3e+02; Les 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG23888 standard; protein; 213 AA
9905-0149902P-9905-0149902P-9905-0150884P-9905-0151066P-9905-0151066P-9905-0151066P-9905-0151080P-9905-0151080P-9905-0151080P-9905-0151080P-9905-0151080P-9905-015108P-9905-015413P-9905-015418P-9905-015513P-9905-015513P-9905-015513P-9905-015513P-9905-015929P-9905-015929P-9905-015929P-9905-015929P-9905-015929P-9905-015932P-9905-015923P-9905-015923P-9905-015932P-9905-015932P-9905-015932P-9905-015932P-9905-015932P-9905-015932P-9905-015932P-9905-015932P-9905-015932P-9905-015932P-9905-016098P-9905-016098P-9905-016098P-9905-0161405P-9905-016135P-9905-016135P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905-0161932P-9905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAFHVFK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||||||
EAFHVFK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-0CT-1999
14-0CT-1999
14-0CT-1999
14-0CT-1999
18-0CT-1999
21-0CT-1999;
21-0CT-1999;
                                                                                                                                                                                                          15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
23-SEP-1999;
                                                                                                                                                                                                                                                                                                                        29-SEP-1999;
04-OCT-1999;
05-OCT-1999;
06-OCT-1999;
07-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-OCT-1999;
13-OCT-1999;
14-OCT-1999;
                                                                                                                                                                                                                                                                                           24-SEP-1999,
28-SEP-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-1999)
                                                                                                                                                                             10-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Si
Matches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG23888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 44
AAG23888
ID AAG23
XX
AC AAG23
XX
DT 17-0C
XX
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

ö

us-10-025-730-1.oligo.rag

```
9905-0140353P

9905-0140354P

9905-0140354P

9905-0140354P

9905-0141842P

9905-014287P

9905-0142892P

9905-0142892P

9905-0142892P

9905-0142892P

9905-0144884P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0145088P

9905-0145088P

9905-0145088P

9905-0145088P

9905-0145088P

9905-014518P

9905-014518P

9905-014518P

9905-014538P

9905-014538P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0145318P

9905-0147318P

9905-0147318P

9905-0147318P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0149722P.
99US-0149723P.
99US-0149929P.
99US-0149902P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0149930P.
99US-0150566P.
99US-0150884P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0151065P.
99US-0151066P.
99US-0151080P.
99US-0139899P
                                                                                                                                                                                                                                                                                                                                                                     02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
22 - JUN - 1999;
23 - JUN - 1999;
23 - JUN - 1999;
24 - JUN - 1999;
26 - JUN - 1999;
30 - JUN - 1999;
01 - JUL - 1999;
01 - JUL - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-1999;
09-AUG-1999;
10-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-AUG-1999;
12-AUG-1999;
13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-AUG-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-AUG-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1999
27-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1999;
                                                                                                                                                       19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                        06-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                06-AUG-1999
                                                                                                                                        .6-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                        02-AUG-1999
 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
Arabidopsis thaliana protein fragment SEQ ID NO: 27359.
                                                                                                               99US-0121825P.
99US-012180P.
99US-0125788P.
99US-0125788P.
99US-012824P.
99US-012824P.
99US-0128244P.
99US-013081P.
99US-013081P.
99US-0131081P.
99US-0131081P.
99US-0131081P.
99US-0131081P.
99US-0131081P.
99US-0131081P.
99US-0131081P.
99US-0131081P.
99US-0131081P.
99US-0131081P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
99US-013108P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0139750P.
99US-0139763P.
99US-0139817P.
                                                                                                25-FEB-2000; 2000EP-00301439.
                                                Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-00N-1999;
16-00N-1999;
16-00N-1999;
17-00N-1999;
18-00N-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 - 70N - 1999)
18 - 70N - 1999)
18 - 70N - 1999)
18 - 70N - 1999)
18 - 70N - 1999)
18 - 70N - 1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JUN-1999;
18-JUN-1999;
21-JUN-1999;
                                                                                                              25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
                                                                                                                                                                                                                                                               05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
                                                                EP1033405-A2
                                                                                                                                                                                                               23-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                14-MAY-1999;
18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                        24-MAY-1999;
25-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1999
08-JUN-1999
                                                                                06-SEP-2000.
                                                                                                                                                       29-MAR-1999
                                                                                                                                                                                        16-APR-1999
                                                                                                                                                                                                19-APR-1999
                                                                                                                                                                                                         21-APR-1999
                                                                                                                                                                                                                                                        04-MAY-1999
                                                                                                                                                                                                                                                                                                                666
                                                                                                                                                                                                                                                                                                                                                        20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                               28-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                         04-JUN-1999
```

```
25-FEB-2000;
                                                                                                                                             23-MAR-1999;
25-MAR-1999;
09-MAR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
                    EP1033405-A2
                                                                                                     25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-7UV-1999
30-7UV-1999
                                                06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-1999
        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.1%; Score 7; DB 3; Length 213; Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 56818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG45275 standard; protein; 213 AA
 990S-0151339P

990S-0151338P

990S-0153379P

990S-0153070P

990S-0154039P

990S-0154039P

990S-0154039P

990S-0155466P

990S-0155466P

990S-0155239P

990S-015539P

990S-015539P

990S-015539P

990S-0159239P

990S-0159239P

990S-0159239P

990S-0159238P

990S-0159238P

990S-0159238P

990S-0159238P

990S-0169614P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0160960P

990S-0161350P

990S-0161350P

990S-0161350P

990S-0161350P

990S-0161350P

990S-0161350P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAFHVFK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 EAFHVFK 154
30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
10-SEP-1999;
11-SEP-1999;
15-SEP-1999;
16-SEP-1999;
22-SEP-1999;
23-SEP-1999;
23-SEP-1999;
24-SEP-1999;
                                                                                                                                                                                 29-SEP-1999

04-OCT-1999

06-OCT-1999

07-OCT-1999

13-OCT-1999

13-OCT-1999

13-OCT-1999

14-OCT-1999

14-OCT-1999

14-OCT-1999

14-OCT-1999

14-OCT-1999

14-OCT-1999

12-OCT-1999

12-OCT-1999

13-OCT-1999

13-OCT-1999

14-OCT-1999

15-OCT-1999

16-OCT-1999

17-OCT-1999

17-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OCT-1999

18-OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                                                                                                       28-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG45275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 45
    g
```

```
990S-0121825P.
990S-0123180P.
990S-0125788P.
990S-012664P.
990S-012664P.
990S-01267462P.
990S-0128244P.
990S-0128244P.
990S-0130891P.
990S-0132448P.
990S-0132448P.
990S-0132448P.
990S-0132448P.
990S-0132448P.
990S-0132448P.
990S-0132448P.
990S-0132448P.
990S-0132448P.
990S-0132448P.
990S-0132448P.
990S-0132488P.
990S-0132488P.
990S-013424P.
990S-0134484P.
990S-0134484P.
990S-0134484P.
990S-0134484P.
990S-0134484P.
990S-0134484P.
990S-0134484P.
990S-0134484P.
990S-0134484P.
990S-0134484P.
990S-0134488P.
990S-01344854P.
990S-01344854P.
990S-0139458P.
990S-0139458P.
990S-0139458P.
990S-0139458P.
990S-0139466P.
990S-0139466P.
990S-0139466P.
990S-0139463P.
990S-0139463P.
990S-0139463P.
990S-0139463P.
2000EP-00301439
```

```
990S-0141842P

990S-0142134P

990S-0142300P

990S-0142803P

990S-0142872P

990S-0143314P

990S-0144331A

990S-0144331A

990S-0144331A

990S-0144331A

990S-0144331B

990S-0144331B

990S-0144332P

990S-0144331B

990S-0144331B

990S-0144331B

990S-0144331B

990S-0144331B

990S-0144331B

990S-0144331B

990S-0144331B

990S-0145086B

990S-014508B

990S-014508B

990S-014508B

990S-014508B

990S-014508B

990S-014508B

990S-014508B

990S-014508B

990S-014508B

990S-014508B

990S-014508B

990S-014638B

990S-014638B

990S-014638B

990S-014638B

990S-014638B

990S-014638B

990S-014638B

990S-014638B

990S-014638B

990S-014638B

990S-014931B

990S-014931B

990S-014931B

990S-014931B

990S-014931B

990S-014931B

990S-014931B

990S-014931B

990S-014931B

990S-014931B

990S-014931B

990S-014933B

990S-014933B

990S-015133B

990S-015133B
                                                      13 - 70L - 1999

14 - 70L - 1999

15 - 70L - 1999

16 - 70L - 1999

16 - 70L - 1999

19 - 70L - 1999

19 - 70L - 1999

19 - 70L - 1999

19 - 70L - 1999

19 - 70L - 1999

19 - 70L - 1999
                                                                                                                                              20-JUL-1999;
20-JUL-1999;
20-JUL-1999;
21-JUL-1999;
21-JUL-1999;
22-JUL-1999;
                                                                                                                                                                                                                                                                                     28 - UL - 1999

02 - AUG - 1999

02 - AUG - 1999

03 - AUG - 1999

04 - AUG - 1999

05 - AUG - 1999

06 - AUG - 1999

06 - AUG - 1999

07 - AUG - 1999

08 - AUG - 1999

09 - AUG - 1999

10 - AUG - 1999

10 - AUG - 1999

10 - AUG - 1999

10 - AUG - 1999
                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1999
16-AUG-1999
18-AUG-1999
20-AUG-1999
20-AUG-1999
23-AUG-1999
23-AUG-1999
23-AUG-1999
25-AUG-1999
25-AUG-1999
25-AUG-1999
26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-SEP-1999;
13-SEP-1999;
15-SEP-1999;
                                                                                                                               19-JUL-1999;
                                                                                                                                                                                                              22-JUL-1999
22-JUL-1999
                                                                                                                                                                                                                               23-JUL-1999
                                                                                                                                                                                                                                                       26-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                       11-AUG-1999
```

```
Human, mental disorder; thyroid disease; renal failure; anorexia; inflammatory condition; Crohn's disease; rheumatoid arthritis; HIV; autoimmune disorder; schizophrenia; migraine; stroke; dementia; obesity; depression; Parkinson's disease; Alzheimer's disease; viral infection; Huntington's disease; human immunodeficiency virus; type 2 diabetes; anorexia; hypotension; hypertension; thrombosis; myocardial infarction; atherosclerosis; cancer; sexual dysfunction; G protein-coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 3; Length 213; 100.0%; Pred. No. 3.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G protein-coupled receptor, nGPCR-2105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU25691 standard; protein; 215 AA.
         9905-0154799
9905-015439P
9905-0155458P
9905-015458P
9905-0157131P
9905-0157131P
9905-015723P
9905-015723P
9905-0159294P
9905-0159294P
9905-0159294P
9905-0159294P
9905-0159294P
9905-0159294P
9905-0159294P
9905-0159294P
9905-0159294P
9905-0159294P
9905-016931P
9905-0169414P
9905-0160981P
9905-0160981P
9905-0160981P
9905-0160981P
9905-0160981P
9905-0160981P
9905-0160981P
9905-0160981P
9905-0160981P
9905-0160981P
9905-0161950P
9905-0161950P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 EAFHVFK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 EAFHVFK 154
         20.58P-1999;
22.58P-1999;
24.58P-1999;
26.58P-1999;
26.58P-1999;
04.0CT-1999;
06.0CT-1999;
06.0CT-1999;
07.0CT-1999;
13.0CT-1999;
14.0CT-1999;
14.0CT-1999;
14.0CT-1999;
14.0CT-1999;
14.0CT-1999;
14.0CT-1999;
14.0CT-1999;
12.0CT-1999;
13.0CT-1999;
14.0CT-1999;
14.0CT-1999;
14.0CT-1999;
16.0CT-1999;
17.0CT-1999;
18.0CT-1999;
18.0CT-1999;
18.0CT-1999;
18.0CT-1999;
                                                                                                                                                                                                                                                              21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU25691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nGPCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU25691
à
```

ö

WO200162924-A2

Homo sapiens.

```
Tripp CA, Wisnewski N;
    19-MAR-2003.
                                                                                                              Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW11479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ξē
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW11479
    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                         The invention relates to novel isolated human G protein-coupled receptors (nGPCR-x). The nGPCR-x can be used for screening compounds which can be used to treat mental disorders, thyroid disease, renal failure, inflammatory conditions such as Crohn's disease, rheumatoid arthritis, autoimmune disorders, schizophrenia, migraine, stroke, dementia, disease, n. Parkinson's disease, Alzheimer's disease, and Huntington's disease. They may also be used for treating viral infections such as human immunodeficiency virus (HIV), type 2 diabetes, obesity, anorexia, atherosclerosis, cancer, and sexual dysfunction. AAUJS6172 and represent the amino acid sequences of novel human G protein-coupled receptors, nGPCR-2031 to nGPCR-2140 respectively, as described in the
                                                                                                                                                                                                                                                              Novel nucleic acid and encoded nGPCR-x, used to screen for compounds for use in the treatment of mental disorders, such as Alzheimer's disease, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic, Anti-inflammatory, Osteopathic, Neuroprotective, Nootropic, Gene Therapy, human, secretory protein, membrane proteins, cancer, inflammatory disease, osteoporosis, neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 4; Length 215; 100.0%; Pred. No. 3.4e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                            Lind P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA54954 standard; protein; 217 AA.
                                                                                                                                                                                                                                                                                                         Claim 31; Page 82; 263pp; English.
                                                                                                                                                                                                          Vogeli G, Wood LS, Parodi LA,
                                                 24-FEB-2000; 2000US-0184602P.
24-FEB-2000; 2000US-0184604P.
24-FEB-2000; 2000US-0184608P.
24-FEB-2000; 2000US-018469P.
24-FEB-2000; 2000US-0184712P.
24-FEB-2000; 2000US-0184712P.
24-FEB-2000; 2000US-0184712P.
24-FEB-2000; 2000US-0184716P.
24-FEB-2000; 2000US-0184716P.
24-FEB-2000; 2000US-0184715P.
24-FEB-2000; 2000US-0184715P.
24-FEB-2000; 2000US-0184725P.
                                                                                                                                                                                   (PHAA ) PHARMACIA & UPJOHN CO
                               23-FEB-2001; 2001WO-US005989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein, SEQ ID 2522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                              WPI; 2001-570632/64.
                                                                                                                                                                                                                                                                                   Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 LAQELYS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 LAQELYS 27
                                                                                                                                                                                                                                           N-PSDB; AAS43001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ното варіеля
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP1293569-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2003
           30-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA54954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA54954
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
                                                                                                                                                                                                                                       Irie R, Tamechika I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venom allergen antigen 5-like gene; VA5; helminth; parasite; nDiVA833;
PDiVA221; vaccine; heartworm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel human secretory or membrane proteins (ADA4672-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ishii S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D. immitis venom allergen antigen 5-like protein PDiVA221.
                                                                                                                                                                                                        Otsuki T, Wakamatsu A, Sato H,
Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.1%; Score 7; DB 6; Length 217; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 14; SEQ ID NO 2522; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .16
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW11479 standard; protein; 221 AA.
                                                                                                                             (HELI-) HELIX RES INST.
(REAS-) RES ASSOC BIOTECHNOLOGY.
21-MAR-2002; 2002EP-00006586.
                                                  14-SEP-2001; 2001JP-00328381.
24-JAN-2002; 2002US-0350435P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                 Sugiyama T,
                                                                                                                                                                                                                                          Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
                                                                                                                                                                                                                                                                                                                        WPI; 2003-395539/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dirofilaria immitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 NLAILEK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HESK-) HESKA CORP
                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADA53315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 217 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9637218-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-NOV-1996
```

```
Dirofilaria immitis venom allergen antigen 5-like protein VAS (AAW11479), or PolvA221, is capable of eliciting an immune response (cellular and/or humoral) in animals. It is encoded by a CODN clone (AAT5176) isolated from a D. immitis cDN library by screening with immune dog serum. VAS-like proteins (see also AAW11480-86) can be used in vaccines to prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                    Nucleic acid encoding helminth venom allergen antigen 5-like protein -
pref. from Dirofilaria immitis or Onchocerca volvulus, useful esp. in
vaccines to prevent helminth infection.
                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 2; Length 221;
100.0%; Pred. No. 3.4e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ORFX protein sequence SEQ ID NO:5824.
                                                                                                            Claim 13; Page 89-90; 124pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                             ABP02921 standard; protein; 236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0206132P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-AUG-2000; 2000US-0228716P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAY-2001; 2001WO-US010836
                            N-PSDB; AAT51376, AAT51378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                             330 RDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                        109 RDLKKTA 115
           WPI; 1997-020935/02
                                                                                                                                                                                                             helminth infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myasthenia gravis
                                                                                                                                                                                                                                          Sequence 221 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABN18673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200192523-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP02921;
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 49
                                                                                                                                                                                                                                                                                                                                                                                                              임
                                                                                                                                                                                                                                                                                                                               à
```

The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1

Novel human polypeptides and polynuclectides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.

Disclosure; SEQ ID NO 5824; 1037pp; English.

ö

Gaps

```
in the specification). ABN15762 to ABN27252 encode the human ORFX creating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polymucleotide sequences can be used in gene therapy. ORFX sequences can be used in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polymucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders related to organ transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, disorders mellitus, systemic corrage disease, various immune deficiencies and disorders; infectious diseases, autoimmune thyroders such as multiple sclerosis, rheumatoid archaitis, autoimmune thyroders such as multiple sclerosis, rheumatoid archaitis, autoimmune inflammatory eye disease. ORFX proteins are also carburitis, autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating setephorosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, protection or regeneration tissues and conditions resulting from systemic cytokine damage. NB. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPPO at ftp.wipo.int/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ubiquitin conjugating enzyme; UBC; RATLId6; immune disorder; regulated in activated T-lymphocyte 1d6; neuronal disorder; cancer; tumour; lymphoproliferative; cancer; adenocarcinoma; leukaemia; myeloma; sarcoma, neurodegenerative; inflammatory; rheumatoid archritis; asthma; multiple sclerosis; psoriasis; neuronal; Alzheimer's disease; dementia; depression; epilepsy; acquired immuno deficiency syndrome, allergy; AIDS; anaemia; atopic dermatitis; diabetes mellitus; dermatological; myocardial infarction; renal tubular acidosis; gonadal dysgenesis; dysplasia; cataract; cytostatic; neuroprotective; nootropic; anti-HIV; anticorulsant; antiinflammatory; Cushing's syndrome; cardiant; hilly; ophthalmological; transmembrane domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 5; Length 236; 100.0%; Pred. No. 3.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yang W, Finger JN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human RATL1d6 transmembrane domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE24494 standard; protein; 245 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-2001; 2001WO-US046559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-OCT-2000; 2000US-0244688P.
30-JUL-2001; 2001US-0308706P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 YVTKRQS 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 YVTKR0S 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-479758/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200236741-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bowen MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE24494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE24494
            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
the invention relates to a novel ubiquitin conjugating enzyme (UBC)

bomologue, RATLIG6 (regulated in activated T-lymphocytes 1d6) and its

corresponding nucleic acid. The invention also relates to methods for

treating, diagnosing, preventing and screening for disorders related to

the expression of RATLIG6. UBC is useful for screening for candidate

compounds capable of binding to and/or modulating its activity. UBC is

useful for treating an immune or neuronal disorder in a mammal. The

method is useful for treating a cancer or tumour. It is useful for

suppressing the immune response in a subject requiring the suppression.

It is also useful for treating lymphopooliferative disorder. Cancer e.g.

disorder, inflammatory disorders e.g. rheumatoid arthritis, asthma,

multiple sclerosis, psoriasis, etc, ineuronal disorders e.g. Alzheimer's

disease, dementia, depression, epilepsy, etc, immune disorder or immune

related disorders such as acquired immuno deficiency syndrome (AIDS),

allergy, anaemaia, atopic dermatitis, diabetes mellitus, myocardial

infarction, etc, developmental disorders e.g. Cushing's syndrome, renal

tubular acidosis, gonadal dysgenesis, dysplasia, cataract, etc. The

present sequence is human RATLIG6 transmembrane domain
Novel ubiquitin conjugating enzyme polypeptide isolated from activated human T cell, for screening modulators useful for treating cancer, immune disorder, lymphoproliferative disorder, neurodegenerative disorder.
                                                                                                                       Claim 6; Page 61; 169pp; English.
```

Sequence 245 AA;

```
.
0
 2.1%; Score 7; DB 5; Length 245;
100.0%; Pred. No. 3.8e+02;
live 0; Mismatches 0; Indels
                              0; Indels
            Local Similarity 100.
es 7; Conservative
                                                                                      138 NLAILEK 144
                                                         24 NLAILEK 30
Query Match
                         Matches
                                                         ð
                                                                                   qq
```

ö

Gaps

AAU63772 standard; protein; 257 AA. 27-FEB-2002 AAU63772; RESULT 51 AAU63772 

Propionibacterium acnes immunogenic protein #24668. (first entry)

SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.

Propionibacterium acnes.

WO200181581-A2

01-NOV-2001

20-APR-2001; 2001WO-US012865

21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P.

(CORI-) CORIXA CORP.

Bhatia A; Wang SS, Mitcham JL, Wang St , Jen S, Carter D; L'maisonneuve J, Zhang Y, Skeiky YAW, Persing DH,

WPI; 2001-616774/71.

N-PSDB; AAS59635

Propionibacterium acnes polypeptides and nucleic acids useful for

```
Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by 2. Lacres. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. The disorders is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the cample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies of specific for P acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and climpate expression and activity of P. acnes polypeptides and confidence treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes proteins by carryme linked immunosorbent assay (BLISA). Note: The sequence data for this patent did not form part of the printed specification, but was considered in electronic format directly from WIPO at
vaccinating against and diagnosing infections, especially useful for
                                                                                     Example 1; SEQ ID NO 24967; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
                                 treating acne vulgaris.
```

Sequence 257 AA;

Gaps .. Length 257; 2.1%; Score 7; DB 4; Length 257; 100.0%; Pred. No. 4e+02; iive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100."
Matches 7; Conservative

ô

105 LRRQIGT 111 107 LRRQIGT 113 g à

RESULT 52

ABM60291 standard; protein; 257 AA. ABM60291 ID ABM

(first entry) 20-OCT-2003 ABM60291;

Propionibacterium acnes predicted ORF-encoded polypeptide #24967.

Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.

Propionibacterium acnes

WO2003033515-A1.

24-APR-2003.

11-OCT-2002; 2002WO-US032727.

1:5-OCT-2001; 2001US-00978825;

(CORI-) CORIXA CORP.

Bhatia A, Benson DR, Persing DH, Lodes MJ, Mitcham JL, Skeiky YAW, Perei Zhang Y, Wang S, Jen S, Lode Barth B, Vallieve-Douglags J; 

Jones R, Carter D;

Maisonneuve JL;

2003-381789/36. N-PSDB; ACF64564. New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

 $x \times 0$ 

```
The invention relates to an isolated polymucleotide (ACF6443-5-AUF6473) canoding a Propionibacterium acnes polymetides. The invention also relates to polypeptides encoded by the polymucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polymucleotide of the invention, antibodies against polypeptides of the invention; in immunostation, fusion proteins comprising a polypeptide of the invention; and immune response specific for a P. acnes to polymucleotides, antibodies, fusion proteins. T cell populations, or antigen-presenting cells that express the polymucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the development of P. acnes in a patient. The P. acnes polymetides to antibodies, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the correction or for invention and manner response specific for a P. acnes in a patient. The P. acnes polymeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the colympetides are useful for dagnosing, preventing or treating acne protein. The polymucleotides can almanue response specific for a P. acnes or protein. The polymucleotides can almanue response specific for a P. acnes or unclaic acid hybridisation. The vaccine composition is useful for performing a diagnostic assay. The present confidence represents a polymeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polymucleotides of the printing frame) contained within the P. acnes polymucleotides of the frame and contained within the performing diagnostic form part of the printing and contained within the performance of the printing form part of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the printing of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; noctropic; neuroprotective; anticonvulsant; osteopathic; antiparkinitc; immunosupressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antitivital; antibacterial; antibungal; antirhenmatic; antithyroid; antitivecins antianemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                              invention relates to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
2.1%; Score 7; DB 6; Length 257;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ORFX ORF1537 polypeptide sequence SEQ ID NO:3074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from WIPO at ftp.wipo.int/pub/published pct sequences
Example 1; SEQ ID NO 24967; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB41773 standard; protein; 263 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000WO-US008621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 LRRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 LRRQIGT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 257 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200058473-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB41773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB41773
```

δ

```
AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepacotropic, valnerary; antiporalatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antiporalisant; inmunosuppressant; immunostimulant; cardiant; thrombolytic; cagulant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antibacterial; antitungal; antitheumatic; antithyroid; an antibacterial; antivines an or treating pathological conditions associated with an ORFX associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol eser storage, storage, systemic lupus erythematosus, severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SCID), AlDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis, and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterioses; survival; virulence; protective antigen; vaccine; mycobacterial disease; tuberculosis; leprosy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.1%; Score 7; DB 3; Length 263; Best Local Similarity 100.0%; Pred. No. 4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M. tuberculosis and M. leprae marker protein #328.
                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 2294; 5507pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU05677 standard; protein; 275 AA.
                 31-MAR-1999; 99US-0127607P.

02-APR-1999; 99US-0127636P.

05-APR-1999; 99US-0127728P.

30-MAR-2000; 2000US-00540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-FEB-2002; 2002WO-IB001973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-APR-2003 (first entry)
                                                                                                                                                               Shimkets RA, Leach M;
                                                                                                                      (CURA-) CURAGEN CORP.
                                                                                                                                                                                                    WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 NLAILEK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 NLAILEK 30
                                                                                                                                                                                                                           N-PSDB; AAC75982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200274903-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU05677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU05677
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
```

ő

```
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                             This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and electing a polymuclectide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. Impare infection. The method reduces the number of potential new targets and protective antigens for new drugs and vaccine compositions to treat and prevent mycobacterial diseases, particularly tuberculosis and hycobacterium tuberculosis and Mycobacterium leprae identified using the method of the invention
                                                                                Identifying and selecting genes for survival or virulence of mycobacteria by a comparative genomic analysis of the sequences of Mycobacterium tuberculosis and M. leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                   Query Match 2.1%; Score 7; DB 5; Length 275; Best Local Similarity 100.0%; Pred. No. 4.2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by Prokaryotic essential gene #9706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haselbeck R,
Yamamoto R,
                                                                                                                           Claim 17; Page 515-516; 874pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU24179 standard; protein; 282 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-0CT-2001; 2001US-0342223P.
08-FEB-2002; 2002US-00072851.
22-FEB-2001; 2001US-0270123P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium acetobutylicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zamudio C,
Trawick JD,
                   (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                             20 ILKDNLA 26
                                                                                                                                                                                                                                                                                                                                                                                                 74 ILKDNLA 80
                                                             WPI; 2002-759885/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ACA28049
                                                                                                                                                                                                                                                                                                              Sequence 275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU24179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU24179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                 용
```

```
the invention fracter to an isolated muchel action where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid, (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular or proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway or proliferation; (7) identifying a compound that influences the activity of pathway in which a proliferation-required gene or its gene product lies or a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profifing a compound's activity; (11) a culture comprising strains in which the gene product is overspressed or underexpressed; (12) determining the extent or organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overspressed or underexpressed; (12) determining the extent or organism; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for cellular proliferation of a compound organism. The antisense nucleic acids required for cellular proliferation of a compound the capacity or a capacity or a capacity or capacity or capacity or capacity or capacity or capacity or capacity or conclude for rational concludes for rational concludes for rational concludes for rational concludes for rational concludes for rational concludes for rational concludes for rational concludes for c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hybridisation assay, genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                    invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 6; Length 282; 5. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 27358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 6
100.0%; Pred. No. 4.3
ive 0; Mismatches
                                                                                                                                                                                        Claim 25; SEQ ID NO 52103; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG23887 standard; protein; 290 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-2000; 2000EP-00301439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0121825P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 ROSLKLL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 ROSLKLL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 282 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG23887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG23887
```

990'8-0143624P. 990'8-0144085P. 990'8-0144085P. 990'8-0144085P. 990'8-0144331P. 990'8-0144331P. 990'8-0144331P. 990'8-0144331P. 990'8-0144331P. 990'8-0144331P. 990'8-0144331P. 990'8-0144331P. 990'8-0144331P. 990'8-0144331P. 990'8-0144331P. 990'8-0145081P. 990'8-0145081P. 990'8-0145081P. 990'8-0145081P. 990'8-0145081P. 990'8-0145081P. 990'8-0147303P. 990'8-0147303P. 990'8-0147303P. 990'8-0147303P. 990'8-0147303P. 990'8-0147303P. 990'8-0147303P. 990'8-0147303P. 990'8-0147303P. 990'8-0147303P. 990'8-0147303P. 990'8-0147303P. 990'8-0147303P. 990'8-014916P. 990'8-014916P. 990'8-014916P. 990'8-014916P. 990'8-014916P. 990'8-014916P. 990'8-014916P. 990'8-014916P. 990'8-014916P. 990'8-014916P. 990'8-014916P. 990'8-014916P. 990'8-0150'8P.	99US-0155139P. 99US-0155139P. 99US-0155486P. 99US-0156458P. 99US-0156458P.
14-JUL-1999; 16-JUL-1999; 16-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JU	22-SEP-1999; 23-SEP-1999; 24-SEP-1999; 24-SEP-1999; 29-SEP-1999; 04-OCT-1999;
\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	4
	•
99US-01231B0P. 99US-01231B0P. 99US-0125788P. 99US-0126648P. 99US-0126648P. 99US-0128234P. 99US-0128234P. 99US-0128234P. 99US-0138344P. 99US-0132486P. 99US-0132486P. 99US-0132486P. 99US-0132486P. 99US-0132486P. 99US-0132486P. 99US-0132486P. 99US-0132486P. 99US-0132486P. 99US-0132486P. 99US-0132486P. 99US-0132486P. 99US-0132486P. 99US-0132486P. 99US-013443P. 99US-013443P. 99US-013456P. 99US-013456P. 99US-013456P. 99US-013456P. 99US-013456P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P. 99US-013945P.	
09-MAR-1999; 23-MAR-1999; 22-MAR-1999; 01-APR-1999; 01-APR-1999; 06-APR-1999; 06-APR-1999; 19-APR-1999; 19-APR-1999; 23-APR-1999; 30-APR-1999; 30-APR-1999; 30-APR-1999; 30-APR-1999; 06-MAY-1999; 06-MAY-1999; 14-MAY-1999; 14-MAY-1999; 14-MAY-1999; 14-MAY-1999; 14-MAY-1999; 16-UNN-1999; 16-UNN-1999; 16-UNN-1999; 16-UNN-1999; 18-UNN-1999; 18-UNN-1999; 18-UNN-1999; 18-UNN-1999; 18-UNN-1999; 18-UNN-1999; 18-UNN-1999; 18-UNN-1999; 18-UNN-1999; 18-UNN-1999; 18-UNN-1999; 18-UNN-1999; 18-UNN-1999; 18-UNN-1999; 23-UNN-1999; 23-UNN-1999; 23-UNN-1999; 23-UNN-1999; 23-UNN-1999; 23-UNN-1999; 23-UNN-1999; 23-UNN-1999; 30-UNN-1999; 30-UNN-1999; 30-UNN-1999; 30-UNN-1999;	701 - 1999 701 - 1999 701 - 1999 701 - 1999 701 - 1999
7 K K K K K K K K K K K K K K K K K K K	

```
·,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy; cancer; tissue specificity; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosenthal A;
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                        Ub (,
4.4e+02;
hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dahl E,
                                                                                                                                                                                                                                                                                     DB 3; Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                              2.1%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                               Human prostate cancer-associated protein 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (META-) METAGEN GES GENOMFORSCHUNG MBH.
                                                                                                                                                                                                                                                                                                                                                                              AAY48312 standard; protein; 291 AA.
99US-0157753P.
99US-015786FP.
99US-0158029P.
99US-0158232P.
99US-015923P.
99US-0159294P.
99US-0159294P.
                                                                       990S-0159310P

990S-0159311P

990S-0159634P

990S-0160741P

990S-0160764P

990S-0160760P

990S-0160770P

990S-016070P

990S-0160911P

990S-0160901P

990S-016190P

990S-0161404P

990S-0161404P

990S-0161361P

990S-0161361P

990S-0161361P

990S-0161361P

990S-0161361P

990S-0161361P

990S-0161361P

990S-0161361P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98DE-01011194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98DE-01011194.
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.00
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             08-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Specht T, Hinzmann B,
                                                                                                                                                                                                                                                                                                                      272 EAFHVFK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-519629/44.
                                                                                                                                                                                                                                                                                                                                     225 EAFHVFK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ33482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE19811194-A1
                              12-0CT-1999;
13-0CT-1999;
13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-SEP-1999.
                                                                                                14-0CT-1999;
                                                                                                                                                         21-OCT-1999;
                                                                                                                                                                                           25-OCT-1999;
                                                                                                                                                                                                  25-OCT-1999;
                                                                                                                                                                                                                  26-OCT-1999;
26-OCT-1999;
                                                                                                                 21-OCT-1999,
21-OCT-1999,
                                                                                                                                  21-OCT-1999;
                                                                                                                                         21-OCT-1999;
21-OCT-1999;
                                                                                                                                                                          22-OCT-1999;
22-OCT-1999;
                                                                                                                                                                                                                                   26-OCT-1999;
                                                                                                                                                                                                                                                    28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                              AAY48312;
                                                                                                                                                                                                                                                                                                                                                              RESULT 57
                                                                                                                                                                                                                                                                                                                                                                      AAY4831
ID AA
                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                    g
```

```
This invention describes novel nucleic acid sequences (A) that are expressed at high level in normal prostatic tissue. Polypeptides (I) encoded by (A) are used: (a) for identifying agents for treatment of prostatic cancer and (b) for therapy of prostate cancer, optionally where expressed by gene therapy methods. (A) is also used to isolate fullingth genes (for gene therapy) and for recombinant production of (I), which can be used to raise specific antibodies. (A) are identified by assembly of ESTs (expressed sequence tags) before these are analyzed for the false results, as regards tissue specificity. This approach eliminates many of the false results, as regards tissue specificity, associated with known methods that use single (usually short) ESTs. AAY48304-Y48456 represent peptides encoded by the expressed sequence tags described in the method
                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
New nucleic acid expressed at high level in normal prostatic tissue and encoded polypeptides, used to treat cancer and screen for therapeutic
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                    DB 2; Length 291;
                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 56817.
                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 2
100.0%; Pred. No. 4.4
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG45274 standard; protein; 300 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          990S-0126264P.
990S-0126785P.
990S-0127462P.
990S-012874P.
990S-0128914P.
990S-0130077P.
990S-0130478P.
990S-0130478P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0132407P.
99US-0132484P.
99US-0132485P.
99US-0132486P.
                                                       Claim 22; 128; 194pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0131449P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0132048P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                       95 NLAILEK 101
                                                                                                                                                                                                                                                                                                                                                                            24 NLAILEK 30
                                                                                                                                                                                                                                                            of the invention
                                                                                                                                                                                                                                                                                         Sequence 291 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1999;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-1999
19-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG45274;
                              agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG45274
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFFXXXX
                                                                                                                                                                                                                                                                                                                                                                             ₹
```

1999; 990S-0145192P 1999; 990S-014513P 1999; 990S-0145218P 1999; 990S-0145218P 1999; 990S-0145313P 1999; 990S-0145313P 1999; 990S-0145313P 1999; 990S-0145313P 1999; 990S-0145313P 1999; 990S-0147303P 1999; 990S-0147303P 1999; 990S-0147303P 1999; 990S-0147303P 1999; 990S-0147303P 1999; 990S-0147303P 1999; 990S-0147303P 1999; 990S-0147303P 1999; 990S-014930P 1999; 990S-014930P 1999; 990S-014930P 1999; 990S-014930P 1999; 990S-014930P 1999; 990S-014930P 1999; 990S-014930P 1999; 990S-014930P 1999; 990S-0151086P 1999; 990S-015130P 1999; 990S-015130P 1999; 990S-015130P 1999; 990S-015130P 1999; 990S-015130P 1999; 990S-015130P 1999; 990S-015130P 1999; 990S-015130P 1999; 990S-015130P 1999; 990S-015133P 1999; 990S-015133P 1999; 990S-015133P 1999; 990S-015133P 1999; 990S-015133P 1999; 990S-015133P 1999; 990S-015133P 1999; 990S-015133P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P 1999; 990S-015533P	500 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
22 - JUL - 19 23 - JUL - 19 23 - JUL - 19 23 - JUL - 19 25 - JUL - 19 26 - JUL - 19 27 - JUL - 19 27 - JUL - 19 27 - JUL - 19 27 - JUL - 19 27 - JUL - 19 27 - JUL - 19 28 - JUL - 19 28 - JUL - 19 29 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31 - JUL - 19 31	18-0CT-1 21-0CT-1 21-0CT-1 21-0CT-1 21-0CT-1
***************************************	ጸዊ ዋዊ ዋዊ ዋ
990xs-0132487P 990xs-0134256P 990xs-0134218P 990xs-0134218P 990xs-0134211P 990xs-0134221P 990xs-0134221P 990xs-0134221P 990xs-0134764P 990xs-0135622P 990xs-0135622P 990xs-0135622P 990xs-0135622P 990xs-0135622P 990xs-0135622P 990xs-0135622P 990xs-0135622P 990xs-0135622P 990xs-0139452P 990xs-0139452P 990xs-0139452P 990xs-0139452P 990xs-0139452P 990xs-0139452P 990xs-0139452P 990xs-0139452P 990xs-0139452P 990xs-0139452P 990xs-0139452P 990xs-0139452P 990xs-0139452P 990xs-0140323P 990xs-0140323P 990xs-0140323P 990xs-0141842P 990xs-0141842P 990xs-0141842P 990xs-0141842P 990xs-0141842P 990xs-0141354P 990xs-0141332P 990xs-0144333P 990xs-0144333P 990xs-0144333P 990xs-0144333P 990xs-0144333P 990xs-0144333P 990xs-0144333P 990xs-0144333P 990xs-0144333P 990xs-0144333P	990S-0144814P. 990S-0145086P. 990S-0145088P. 990S-0145085P. 990S-0145089P.
06-MAY-1999 11-MAY-1999 14-MAY-1999 14-MAY-1999 14-MAY-1999 14-MAY-1999 14-MAY-1999 14-MAY-1999 14-MAY-1999 15-MAY-1999 16-MAY-1999 16-MAY-1999 16-MAY-1999 16-MAY-1999 16-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MAY-1999 18-MA	21-JUL-1999; 21-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999;
KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK	77 77 77 77 77 77 77 77 77 77 77 77 77

```
99US-0134124P.
99US-0135124P.
99US-0135124P.
99US-0135629P.
99US-013622P.
99US-013622P.
99US-0137222P.
99US-0137224P.
99US-013724P.
99US-013724P.
99US-013724P.
99US-0137563P.
99US-0139453P.
99US-0139453P.
99US-0139453P.
99US-0139453P.
99US-0139453P.
99US-0139453P.
99US-0139453P.
99US-0139453P.
99US-0139453P.
99US-0139453P.
99US-0139453P.
99US-0139453P.
99US-0139453P.
99US-014280P.
99US-014280P.
99US-014280P.
99US-014280P.
99US-014280P.
99US-014232P.
99US-014332P.
99US-0143332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
99US-0144332P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0145913P
                                                                            01-JUN-1999;
03-JUN-1999;
04-JUN-1999;
07-JUN-1999;
08-JUN-1999;
                                                                                                                                                          16-JUN-1999;
16-JUN-1999;
17-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                 18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                              10-JUN-1999;
10-JUN-1999;
14-JUN-1999;
                                                                                                                                                                                                                                                                       8-JUN-1999
                                                                                                                                                                                                                                                                                         8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                28-JUN-1999
  ö
                                                                                                                                                                                                                                                                                                                                         Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter, termination sequence.
                                                                                                                                                                      Gaps
                                                                                                                                                                       ·.
                                                                                                                                                 DB 3; Length 300;
                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 36770.
                                                                                                                                                 2.1%; Score 7; DB 3
100.0%; Pred. No. 4.6
tive 0; Mismatches
                                                                                                                                                                                                                                                             AAG30714 standard; protein; 300 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0121825P.
99US-0123180P.
99US-0125788P.
99US-0125788P.
99US-012645P.
99US-0127462P.
99US-0128234P.
99US-0128234P.
99US-0130510P.
99US-0130610P.
99US-0130648P.
99US-013048P.
99US-0132484P.
99US-0132484P.
99US-0132484P.
99US-0132486P.
99US-0132486P.
99US-0132486P.
99US-0132486P.
99US-0132486P.
99US-0160815P.
99US-0160980P.
99US-0160981P.
99US-0161404P.
99US-0161406P.
99US-0161359P.
99US-0161350P.
99US-0161350P.
99US-0161350P.
99US-0161920P.
99US-0161920P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0134221P
                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                                                                                                                                   17-OCT-2000 (first entry)
                                                                                                                                      Ouery Match
Best Local Similarity luv.
                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                                                                                                                                                                                        272 EAFHVFK 278
                                                                                                                                                                                                           235 EAFHVFK 241
21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                      EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
19-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-1999;
23-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-APR-1999;
30-APR-1999;
04-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAY 1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000
                                                                                                                                                                                                                                                                                AAG30714;
                                                                                                                                                                                                                                         RESULT 59

AAG30714

ACC AAG30

XX

ACC AAG30

XX

XX

DDT 17-OC

XX

XX

DE Arabic

XX

XX

CON APPRION

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 25-FB

PR 26-FB

PR 26-FB

PR 26-FB

PR 21-AP

PR 21-AP

PR 21-AP

PR 21-AP

PR 21-AP
  d
                                                                                                                                                                                         à
```

```
PR 26-UUL-1999; 99US-014536P.
PR 28-UUL-1999; 99US-014536P.
PR 02-AUG-1999; 99US-014536P.
PR 02-AUG-1999; 99US-014536P.
PR 04-AUG-1999; 99US-014536P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147204P.
PR 06-AUG-1999; 99US-0147204P.
PR 06-AUG-1999; 99US-014730P.
PR 10-AUG-1999; 99US-014730P.
PR 12-AUG-1999; 99US-014731P.
PR 12-AUG-1999; 99US-014731P.
PR 12-AUG-1999; 99US-014311P.
PR 12-AUG-1999; 99US-014311P.
PR 12-AUG-1999; 99US-014311P.
PR 12-AUG-1999; 99US-014431P.
PR 12-AUG-1999; 99US-014431P.
PR 12-AUG-1999; 99US-014431P.
PR 26-AUG-1999; 99US-014431P.
PR 26-AUG-1999; 99US-014431P.
PR 26-AUG-1999; 99US-014431P.
PR 26-AUG-1999; 99US-014431P.
PR 26-AUG-1999; 99US-014313P.
PR 27-AUG-1999; 99US-014313P.
PR 27-AUG-1999; 99US-014313P.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015106EP.
PR 27-AUG-1999; 99US-015074P.
PR 27-AUG-1999; 99US-015074P.
PR 27-AUG-1999; 99US-015074P.
PR 27-AUG-1999; 99US-015074P.
PR 27-AUG-1999; 99US-015074P.
PR 27-AUG-1999; 99US-015074P.
PR 27-AUG-1999; 99US-015074P.
PR 27-AUG-1999; 99US-015074P.
PR 27-AUG-1999; 99US-015074P.
PR 27-AUG-1999; 99US-015074P.
PR 27-AUG-1999; 99US-015074P.
PR 27-AUG-1999; 99US-015074P.
PR
```

```
ö
                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                  Gaps
                                                                                 ;
0
                                                                DB 3; Length 300; 4.6e+02;
                                                                                 0; Indels
                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 27357.
                                                           AAG23886 standard; protein; 300 AA.
                                                                                                                                                                                                                                                                                                                         99US-0121825P.
99US-0123180P.
99US-0125788P.
99US-0126764P.
99US-0126764P.
99US-0126748P.
99US-012824P.
99US-012824P.
99US-013081P.
99US-013081P.
99US-013081P.
99US-013081P.
99US-013081P.
99US-013081P.
99US-0132488P.
99US-0132488P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0134218P
99US-013421P
99US-013431P
99US-013476B
99US-013476B
99US-013476B
99US-013532P
99US-013532P
99US-013532P
99US-0161359P.
99US-016136DP.
99US-016136DP.
99US-0161920P.
99US-0161932P.
99US-0161932P.
                                                                                                                                                                                                                                                                                                           25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                          17-OCT-2000 (first entry)
                                                                Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                           Arabidopsis thaliana.
                                                                                                  272 EAFHVFK 278
                                                                                                           |||||||
235 EAFHVFK 241
                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
                                                                                                                                                                                                                                                                                                                         25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-1999;
19-APR-1999;
21-APR-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                           01-APR-1999;
06-APR-1999;
08-APR-1999;
                                                                                                                                                                                                                                                                           EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-1999;
27-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAY-1999;
20-MAY-1999;
                                                                                                                                                                                                                                                                                            06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAY-1999
                                                                                                                                                                           AAG23886;
                                                                                                                                           RESULT 60
                                                                                                                                                   AAG23886
 \dot{\delta}
                                                                                                                ద
```

* # # # # # # # # # # # # # # # # # # #	: K K K K K K K K K K K K K K K K K K K	X X X X X X X X X X X X X X X X X X X
222 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 228 P. 22	7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 7535 - 75	3335P 6322P 6322P 6322P 6322P 6324P 6344P 6344P 6351P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 6313P 63
990S-01376 990S-01377 990S-01377 990S-01377 990S-01377 990S-0139 990S-0139 990S-0139 990S-0139 990S-0139 990S-0139 990S-0139	990S-0139763P 990S-0139817P 990S-0140353P 990S-0140354P 990S-0140635P 990S-0140637P 990S-0141287P 990S-0141287P 990S-014287P 990S-014287P 990S-014287P 990S-014287P 990S-014287P 990S-014330P 990S-014325P 990S-014468P 990S-014325P 990S-014468P 990S-014468P 990S-014468P 990S-014468P 990S-014488P 990S-014488P 990S-014488P 990S-014488P 990S-014488P 990S-014488P 990S-014488P 990S-014488P 990S-014488P	990S-0144 990S-0144 990S-0144 990S-0145 990S-0145 990S-0145 990S-0145 990S-0145 990S-0145 990S-0145 990S-0145 990S-0145 990S-0145 990S-0145 990S-0146
	1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999; 1-013-1999;	
28 - MAY 01 - JUN 03 - JUN 04 - JUN 07 - JUN 08 - JUN 10 - JUN 10 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11 - JUN 11	23 - 000 23 - 000 23 - 000 23 - 000 23 - 000 24 - 000 25 - 000 25 - 000 26 - 000 26 - 000 27 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28 - 000 28	19-040 20-0401 20-0401 21-0401 21-0401 22-0401 22-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0401 23-0
# # # # # # # # # # # # # # # # # # #	*	X X X X X X X X X X X X X X X X X X X

9905-0147192P.
9905-0147192P.
9905-0147416P.
9905-0147411P.
9905-0147313P.
9905-01483119P.
9905-01483119P.
9905-01483119P.
9905-01483119P.
9905-01483119P.
9905-0148312P.
9905-0149328P.
9905-0149328P.
9905-0149328P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015133P.
9905-015969P.
9905-015969P.
9905-015969P.
9905-01696P.
9905-01696P.
9905-01696P.
9905-01698P.
9905-01698P.
9905-01698P.
9905-01698P.
9905-01698P.
9905-01698P.

04-AUG-1999; 05-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 11-AUG-1999; 11-AUG-1999; 12-AUG-1999; 12-AUG-1999; 12-AUG-1999; 12-AUG-1999; 13-AUG-1999; 13-AUG-1999; 13-AUG-1999; 13-AUG-1999; 13-AUG-1999; 13-AUG-1999; 14-AUG-1999; 14-AUG-1999; 15-EEP-1999; 16-SEP-1999; 16-SEP-1999; 17-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AU

RESULT 61

ð DP

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                      Arabidopsis thaliana protein fragment SEQ ID NO: 36769.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0135124P.
99US-0135353P.
99US-0135629P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0136782P.
99US-0137222P.
99US-0137528P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0138847P.
99US-0139119P.
99US-0139452P.
                                                                                                                                                                                                                                                                                                 99US-0127462P.
99US-0128234P.
99US-0128714P.
                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0132048P.
99US-0132407P.
99US-0132484P.
                                                                                                                                                                                                                                                                                                                                       99US-0129845P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0132485P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0132487P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0134218P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0134221P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0134768P.
99US-0134941P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0136021P.
99US-0136392P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0137502P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0138094P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0139454P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0139455P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0139456P.
                                                                                                                                                                                                                                                                                                                                                                                           99US-0130891P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0134256P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0139453P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0139492P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0139457P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0139463P
                                                                                                                                                                                              2000EP-00301439
                                                                                                                                                                                                                                                                                       99US-0126785P
                                                                                                                                                                                                                                                                                                                                                                  99US-0130449P
                                                                                                                                                                                                                                                                                                                                                                                99US-0130510P
             17-OCT-2000 (first entry)
                                                                                           termination sequence.
                                                                                                                  Arabidopsis thaliana
                                                                                                                                            EP1033405-A2.
                                                                                                                                                                                              25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-MAY-1999;
07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-1999;
                                                                                                                                                                      06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUN-1
14-JUN-1
16-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUN-1
18-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -UNIX-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUN-
  ö
                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by S. aureus, e.g. sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                        Gaps
                                                                                                                                                                                                                                                               gene therapy; infection; sepsis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6; Length 302; 0. 4.6e+02;
             DB 3; Length 300; 4.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 2.1%; Score 7; DB 6 Local Similarity 100.0%; Pred. No. 4.6 es 7; Conservative 0; Mismatches
             2.1%; Score 7; DB 3
100.0%; Pred. No. 4.6
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1646; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG30713 standard; protein; 305 AA.
                                                                                                                                                                                                                                     Staphylococcus aureus protein #823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scarselli M;
                                                                                                                                                          ABM71583 standard; protein; 302 AA.
                                                                                                                                                                                                                                                                           enzymatic assay; antibiotic target
                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2002; 2002WO-IB002637
                                                                                                                                                                                                                                                                                                                                                                                                          27-MAR-2001; 2001GB-00007661
                                                                                                                                                                                                           20-NOV-2003 (first entry)
Ouery Match
Best Local Similarity 1000
7; Conservative
                                                                                                                                                                                                                                                             Antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Masignani V, Mora M,
                                                                                                                                                                                                                                                                                                   Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLLQSEN 221
                                                                 EAFHVFK 278
                                                                                        235 EAFHVFK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-120786/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 KLLOSEN 72
                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ACF73143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 302 AA;
                                                                                                                                                                                                                                                                                                                            WO200294868-A2.
                                                                                                                                                                                                                                                                                                                                                      28-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG30713;
                                                                 272
                                                                                                                                                                                  ABM71583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
```

Matches

ò

RESULT 62 AAG30713 ID AAG3 XX AC AAG3

```
PR 18—UWN 1999; 9908—0139750 PR 21—UWN 1999; 9908—0139750 PR 22—UWN 1999; 9908—0139717 PR 22—UWN 1999; 9908—0139717 PR 22—UWN 1999; 9908—0139717 PR 22—UWN 1999; 9908—01400534 PR 24—UWN 1999; 9908—01400534 PR 24—UWN 1999; 9908—01400534 PR 24—UWN 1999; 9908—01400534 PR 24—UWN 1999; 9908—014200 PR 24—UWN 1999; 9908—014200 PR 24—UWN 1999; 9908—014200 PR 24—UWN 1999; 9908—014200 PR 24—UWN 1999; 9908—014200 PR 24—UWN 1999; 9908—014200 PR 24—UWN 1999; 9908—014200 PR 24—UWN 1999; 9908—014200 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1999; 9908—014400 PR 24—UWN 1990; 9908—014400 PR 24—UWN 1990; 9908—014400 PR 24—UWN 1990; 9
```

```
HTRM; human transcriptional regulatory molecule; arteriosclerosis; AIDS; arteriosclerosis; cirrhosis; cancer; leukaemia; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.1%; Score 7; DB 3; Length 305; Best Local Similarity 100.0%; Pred. No. 4.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTRM clone 3340290 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY73387 standard; protein; 308 AA
      9905-0151066P-
9905-0151030P-
9905-0151030P-
9905-015130P-
9905-015130P-
9905-015370P-
9905-015479P-
9905-015479P-
9905-0155139P-
9905-015713P-
9905-015713P-
9905-015713P-
9905-015823P-
9905-015823P-
9905-015823P-
9905-015923P-
9905-015923P-
9905-015923P-
9905-015923P-
9905-015923P-
9905-015923P-
9905-015923P-
9905-016076P-
9905-016074P-
9905-016074P-
9905-016074P-
9905-016074P-
9905-016074P-
9905-016074P-
9905-016074P-
9905-016074P-
9905-016074P-
9905-016077P-
9905-016077P-
9905-016077P-
9905-016077P-
9905-016077P-
9905-016077P-
9905-016077P-
9905-016077P-
9905-016077P-
9905-016077P-
9905-016077P-
9905-016077P-
9905-016077P-
9905-016077P-
9905-016077P-
9905-016077P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 EAFHVFK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 EAFHVFK 278
                                                                                                                                                         29-SEP-11999
04-OCT-11999
06-OCT-11999
06-OCT-11999
13-OCT-11999
13-OCT-11999
14-OCT-11999
14-OCT-11999
14-OCT-11999
14-OCT-11999
14-OCT-11999
14-OCT-11999
14-OCT-11999
12-OCT-11999
12-OCT-11999
12-OCT-11999
12-OCT-11999
12-OCT-11999
12-OCT-11999
12-OCT-11999
13-OCT-11999
14-OCT-11999
15-OCT-11999
15-OCT-11999
16-OCT-11999
16-OCT-11999
17-OCT-11999
18-OCT-11999
18-OCT-11999
18-OCT-11999
18-OCT-11999
18-OCT-11999
18-OCT-11999
18-OCT-11999
18-OCT-11999
18-OCT-11999
18-OCT-11999
18-OCT-11999
                                                                                                          20-SEP-1999;
22-SEP-1999;
23-SEP-1999;
                                                                   10-SEP-1999;
13-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY73387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 63
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
```

ö

Mon Apr 12 10:49:26 2004

```
protein sequences. The HTRM protein and nucleotide sequences are useful for preventing or treating disorders associated with decreased expression or activity of HTRM which include cell proliferative disorders such as attentiosclerosis and cirrhosis, cancers including adenocarcinoma and leukaemia; immune disorders such as AIDS, Addison's disease, diabetes mellitus, rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus, and myasthenia gravis; infections and trauma. Antagonists of the HTRM polypeptides are useful for treating or preventing disorders associated with increased expression or activity of HTRMs. HTRM polypeptides, their immunogenic fragments or oligopeptides are useful for cereming techniques.

CC of the HTRM polypeptides for compounds in drug screening techniques.

CC of mRNA and regulating gene function by modulating the transcription of mRNA and regulating gene function by modulating the activity of HTRM. Vectors expressing HTRM or agonists can also be used to prevent or treat disorder associated with decreased HTRM expression. Antibodies which graceing disporders associated with the expression of HTRM. Nucleotide sequences concoding HTRM may be useful to generate hybridization probes useful in aspears that detect the expression of HTRM. Nucleotide sequences among the maturally occurring genomic sequence and to detect of individuals. Using diagnostic assays, cancer can be detected prior or permitted by appearance of clinical symptoms and thereby progression of cancer can be researched by appearance of clinical symptoms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptides useful for diagnosis, prevention and treatment of cancer and
Addison's disease; multiple sclerosis; rheumatoid arthritis; infection; trauma; myasthenia gravis; adenocarcinoma; immune disorder; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY73325-Y73389 are human transcriptional regulator molecule (HTRM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ٥.
                                                                                                                                                                                                                                                                                                                                 Tang YT;
Lu DAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 3; Length 308; 100.0%; Pred. No. 4.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prevented by aggressive treatment or preventive measures
                                                                                                                                                                                                                                                                                                                                 , Reddy R,
Azimzai Y,
                                                                                                                                                                                                                                                                                                                               Lal P, Yue H,
, Baughn MR, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 144-145; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG05090 standard; protein; 320 AA.
                                                                                                                                                                           99WO-US009935.
                                                                                                                                                                                                               98US-0084254P.
                                                                                                                                                                                                                                  98US-0095827P.
                                                                                                                                                                                                                                                    98US-0102745P.
                                                                                                                                                                                                                                                                                                                             Bandman O, La
Patterson C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                         (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 NLAILEK 150
                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-052941/04.
N-PSDB; AAZ52472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 308 AA;
                                                                                             WO9957144-A2.
                                                         Homo sapiens
                                                                                                                                                                         04-MAY-1999;
                                                                                                                                                                                                             05-MAY-1998;
07-AUG-1998;
                                                                                                                                                                                                                                                    02-OCT-1998;
                                                                                                                                                                                                                                                                                                                           Hillman JL,
Gerstin EH,
                                                                                                                                    11-NOV-11999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG05090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 64
AAG05090
ID AAG050
XX
AC AAG050
XX
DT 17-0C1
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  New
  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ω
```

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
Arabidopsis thaliana protein fragment SEQ ID NO: 1363.
                                                                                                                                                                                                                                                                                 990S-0134370P
990S-013476BP
990S-0135124P
990S-013533P
990S-013532P
990S-0136392P
990S-0136392P
990S-0136782P
990S-0137528P
990S-0137528P
                                                                                                                                                                                                                                                             99US-0134218P.
99US-0134219P.
99US-0134221P.
                                                                                                                                                                                        99US-0130891P.
99US-0131449P.
99US-0132048P.
                                                                                                                                                                                                             99US-0132407P.
99US-0132484P.
99US-0132485P.
                                                                                                                                                                                                                                 99US-0132486P.
99US-0132487P.
99US-0132863P.
99US-0134256P.
                                                                                                                                                                                                                                                                                                                                                                                  99US-0138540P.
99US-0138847P.
99US-0139119P.
99US-0139452P.
                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0139456P.
99US-0139457P.
99US-0139458P.
                                                                                  25-FEB-2000; 2000EP-00301439.
                                                                                                                                  99US-0126785P
                                                                                                                                                      99US-0128714P
                                                                                                                                                                                  99US-0130510P
                                                                                                                                                                                                                                                                                                                                                                                                              99US-0139453P
                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0139492P
                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0139455P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0139750P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0139817P
                                         Arabidopsis thaliana.
                                                      EP1033405-A2
                                                                    06-SEP-2000
                                                                                                                                                                                                                                                                                                                                   27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUN-1999
                                                                                                                                                                                                                                                                                                19-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                         16-JUN-91
```

. 0

Gaps

```
9905-0140353P

9905-0140353P

9905-0140623P

9905-0140823P

9905-0141842P

9905-0142054P

9905-0142054P

9905-0142054P

9905-0142054P

9905-0142054P

9905-0142054P

9905-0142054P

9905-0142054P

9905-014332P

9905-0144332P

9905-0144332P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144338P

9905-014524P

9905-014538P

9905-014538P

9905-014538P

9905-014538P

9905-014538P

9905-014538P

9905-014538P

9905-014433P

9905-014433P

9905-014433P

9905-014433P

9905-014433P

9905-014433P

9905-014433P

9905-014433P

9905-014433P

9905-014433P

9905-014433P

9905-014433P

9905-014433P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0151065P.
99US-0151066P.
99US-0151080P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0150566P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0149902P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0149930P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-1999;
09-AUG-1999;
10-AUG-1999;
11-AUG-1999;
11-AUG-1999;
13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
16-AUG-1999;
16-AUG-1999;
11-AUG-1999;
22 - TUN - 1999;
23 - TUN - 1999;
24 - TUN - 1999;
26 - TUN - 1999;
30 - TUN - 1999;
30 - TUN - 1999;
01 - TUL - 1999;
06 - TUL - 1999;
06 - TUL - 1999;
06 - TUL - 1999;
07 - TUL - 1999;
07 - TUL - 1999;
08 - TUL - 1999;
13 - TUL - 1999;
14 - TUL - 1999;
15 - TUL - 1999;
16 - TUL - 1999;
17 - TUL - 1999;
18 - TUL - 1999;
16 - TUL - 1999;
16 - TUL - 1999;
16 - TUL - 1999;
16 - TUL - 1999;
16 - TUL - 1999;
17 - TUL - 1999;
18 - TUL - 1999;
18 - TUL - 1999;
18 - TUL - 1999;
19 - TUL - 1999;
11 - TUL - 1999;
                                                                                                                                                                                                                      20-JUL-1999;
20-JUL-1999;
20-JUL-1999;
21-JUL-1999;
21-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
23-AUG-1999;
                                                                                                                                                                   19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1999;
04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                         28-JUL-1999;
02-AUG-1999;
02-AUG-1999;
02-AUG-1999;
                                                                                                                                                                                                                                                                  21-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-1999
```

```
Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 7; DB 3; Length 320;
100.0%; Pred. No. 4.9e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 64758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG51053 standard; protein; 326 AA
990S-0151303P.
990S-0151438P.
990S-0151438P.
990S-015363P.
990S-0153070P.
990S-015403P.
990S-015403P.
990S-015458P.
990S-015539P.
990S-015539P.
990S-0157865P.
990S-0157865P.
990S-0157865P.
990S-0159294P.
990S-0159294P.
990S-0159294P.
990S-0159294P.
990S-0159294P.
990S-0159294P.
990S-0159294P.
990S-0159294P.
990S-0169314P.
990S-0169314P.
990S-0169314P.
990S-0160944P.
990S-0160944P.
990S-0160980P.
990S-0160980P.
990S-0160980P.
990S-0160980P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0161360P.
99US-0161361P.
99US-0161920P.
99US-0161992P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0161993P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0162142P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 TFKDLLT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 TFKDLLT 171
                                         10-SEP-1999;
13-SEP-1999;
15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
                                                                                                                                                                                      07-071-1999

13-071-1999

13-071-1999

13-071-1999

14-071-1999

14-071-1999

14-071-1999

14-071-1999

14-071-1999

12-071-1999

12-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999

13-071-1999
                                                                                                                                28-SEP-1999;
29-SEP-1999;
04-OCT-1999;
                                                                                                                                                                 05-OCT-1999;
                                                                                                           23-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG51053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 65
AAGS1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

0;

```
990S-0141842P.
990S-0142154P.
990S-0142390P.
990S-0142390P.
990S-0142390P.
990S-0142977P.
990S-0142977P.
990S-0144331P.
990S-0144331P.
990S-0144334P.
990S-0144334P.
990S-0144334P.
990S-0144331P.
990S-0144334P.
990S-0144334P.
990S-0144334P.
990S-0144334P.
990S-0144334P.
990S-0144334P.
990S-0144334P.
990S-0145888P.
990S-0145888P.
990S-014588P.
990S-014588P.
990S-014588P.
990S-014588P.
990S-014588P.
990S-014588P.
990S-014588P.
990S-014588P.
990S-014588P.
990S-014588P.
990S-014588P.
990S-014588P.
990S-014588P.
990S-014733P.
990S-014733P.
990S-014733P.
990S-014733P.
990S-014932P.
990S-014932P.
990S-014932P.
990S-014932P.
990S-014932P.
990S-014932P.
990S-014932P.
990S-014932P.
990S-014932P.
990S-014932P.
990S-014932P.
990S-014932P.
990S-014932P.
990S-015188P.
990S-015188P.
01-JUL-1999;
01-JUL-1999;
06-JUL-1999;
06-JUL-1999;
13-JUL-1999;
13-JUL-1999;
14-JUL-1999;
16-JUL-1999;
16-JUL-1999;
16-JUL-1999;
19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
20-JUL-1999;
20-JUL-1999;
21-JUL-1999;
21-JUL-1999;
21-JUL-1999;
21-JUL-1999;
21-JUL-1999;
21-JUL-1999;
21-JUL-1999;
21-JUL-1999;
21-JUL-1999;
21-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AUG-1999;
02-AUG-1999;
02-AUG-1999;
03-AUG-1999;
04-AUG-1999;
05-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-AUG-1999;
06-AUG-1999;
06-AUG-1999;
09-AUG-1999;
10-AUG-1999;
11-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1999)

16-AUG-1999)

18-AUG-1999)

20-AUG-1999)

20-AUG-1999)

23-AUG-1999)

23-AUG-1999)

23-AUG-1999)

25-AUG-1999)

27-AUG-1999)

27-AUG-1999)

27-AUG-1999)

27-AUG-1999)

27-AUG-1999)

27-AUG-1999)

27-AUG-1999)

27-AUG-1999)

27-AUG-1999)

27-AUG-1999)

31-AUG-1999)

31-AUG-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-AUG-1999
13-AUG-1999
    9905-0121825P.
9905-0123180P.
9905-0125788P.
9905-0126784P.
9905-0126764P.
9905-0126748P.
9905-0126748P.
9905-012874P.
9905-0130449P.
9905-0132444P.
9905-0132448P.
9905-0132448P.
9905-0132448P.
9905-0132448P.
9905-0132448P.
9905-0132448P.
9905-0132468P.
9905-0132488P.
9905-0132488P.
9905-0132488P.
9905-0132488P.
9905-0132488P.
9905-013454P.
9905-013454P.
9905-013454P.
9905-013454P.
9905-013454P.
9905-013454P.
9905-013454P.
9905-013454P.
9905-013454P.
9905-013454P.
9905-013454P.
9905-0139455P.
9905-0139455P.
9905-0139455P.
9905-0139455P.
9905-0139455P.
9905-0139455P.
9905-0139455P.
9905-0139455P.
9905-0139453P.
9905-0139453P.
9905-0139453P.
                                                                  2000EP-00301439
                                                                                        25-FEB-1999 | 05-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23-MAR-1999 | 23
                                                                 25-FEB-2000;
              EP1033405-A2
                                       06-SEP-2000
```

 $\chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \lesssim \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{\mathcal{S}} \chi_{$ 

```
The present sequence represents a Sulfolobus solfataricus endoglucanase, specifically endo-beta-1,4-glucanase, designated CelA. The new endo-beta-1,4-glucanase is produced by Sulfolobus solfataricus ATCC 35092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a Sulfolobus solfataricus endoglucanase, specifically endo-beta-1,4-glucanase, designated CelB. The new endo-beta-1,4-glucanase is produced by Sulfolobus solfataricus ATCC 35092
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                      Query Match 2.1%; Score 7; DB 2; Length 332; Best Local Similarity 100.0%; Pred. No. 5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                              Novel endonuclease - produced by Sulfolobus solfataricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel endonuclease - produced by Sulfolobus solfataricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sulfolobus solfataricus endo-beta-1,4-glucanase CelB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sulfolobus solfataricus; endoglucanase; CelA; CelB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        AAY17866 standard; protein; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 31-32; 36pp; English.
                                                                                                                                                                      Claim 1; Page 27-28; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .21
/label= signal
                                                         99DK-00000097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22. .332
/label= CelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99DK-00000097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99DK-00000097
                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sulfolobus solfataricus.
                                                                                (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           endo-beta-1,4-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                       177 FDIASDA 183
                                                                                                                                                                                                                                                                                                                                             184 FDIASDA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-279376/24.
                                                                                                       WPI; 1999-279376/24.
N-PSDB; AAX80187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX80188
                                                                                                                                                                                                                                              Sequence 332 AA;
                                 12-JAN-1999;
                                                          12-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JAN-1999;
           12-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DK9900097-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY17866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 67
                                                                                                                                                                                                                                                                                                                                                                                                                        염
                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfolobus solfataricus endo-beta-1,4-glucanase CelA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sulfolobus solfataricus; endoglucanase; CelA; CelB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Len
o. 4.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7; I
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY17865 standard; protein; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.1%; Sco
Best Local Similarity 100.0%; Pr
Matches 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .23
/label= signal
                                                                                                                                                    990S-0159294P
990S-0159294P
990S-0159330P
990S-0159331P
990S-0159331P
990S-0159634P
990S-0160741P
990S-0160767P
990S-0160768P
990S-016070P
990S-016089P
990S-016089P
990S-016089P
990S-016089P
990S-016089P
990S-016089P
990S-016089P
990S-0160980P
      99US-0154779P.
99US-0155486P.
99US-0155486P.
99US-0156458P.
99US-0156596P.
99US-0157731P.
99US-0157753P.
99US-015785P.
                                                                                                                                                                                                                                                                                                                                                                                                                                          990S-0161361P
990S-0161920P
990S-0161992P.
990S-0161993P.
990S-0162142P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24. .332
/label= CelA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sulfolobus solfataricus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endo-beta-1,4-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272 EAFHVFK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 EAFHVFK 267
                                                                                                                                                                13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DK9900097-A.
                                                                                                                               08-OCT-1999
                                                                                                                                          12-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                               25-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                  22-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY17865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
```

6

음

ò

```
ð
                                                          ð
                                                                                 셤
                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomera, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed activity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abergant protein expression or biological activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                        0;
                          2.1%; Score 7; DB 2; Length 332;
100.0%; Pred. No. 5e+02;
Live 0; Mismatches 0; Indels
                             Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 58224; 103pp; English.
                                                                                                                                                                                                                                                                      Novel human diagnostic protein #27856.
                                                                                                                                                                                  ABG27865 standard; protein; 337 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                           (first entry)
             Ouery Match
Best Local Similarity 100...
7, Conservative
                                                                                                              184 FDIASDA 190
                                                                                   177 FDIASDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAS92052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 337 AA;
 Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                                                      WO200175067-A2.
                                                                                                                                                                                                                                           18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2001.
                                                                                                                                                                                                                ABG27865;
                                                                                                                                                       RESULT 68
S
                                                                                                                                                                                    g
```

```
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTS). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
neuroprotective; antiparkinsonian; protein therapy; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis.
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ren F;
                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 5; Length 340; 100.0%; Pred. No. 5.1e+02; tive 0; Mismatches 0; Indels
Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhao QA,
                                                       0; Indels
2.1%; Score 7; DB 4; Les 100.0%; Pred. No. 5.1e+02; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhou P, Asundi V, Zhang J,
Wehrman T, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 628; 509pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG45273 standard; protein; 343 AA.
                                                                                                                                                                                                                                                                                                             ABB97360 standard; protein; 340 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human protein SEQ ID NO: 628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-SEP-2001; 2001WO-US026015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-SEP-2000; 2000US-00659671.
                                                                                                                                                                                                                                                                                                                                                                                                                          27-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 7; Conservative
Query Match 2.1
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed sequence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 NLAILEK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-292408/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 NLAILEK 30
                                                                                                               66 VAQLAQE 72
                                                                                                                                                                 31 VAÇLAÇE 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT, Liu C,
Xue AJ, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABN32546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 340 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200222660-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                     ABB97360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 70
AAG45273
ID AAG45:
                                                                                                                                                                                                                                                         RESULT 69
                                                                                                                                                                                                                                                                                      ABB97360
```

```
9905-0139750P.
9905-0139763P.
9905-0139763P.
9905-01400553P.
9905-01400553P.
9905-0140053P.
9905-0140053P.
9905-0141242P.
9905-014224P.
9905-0142324P.
9905-0142324P.
9905-0143324P.
9905-0143324P.
9905-0144332P.
9905-0144332P.
9905-0144332P.
9905-0144332P.
9905-0144332P.
9905-0144332P.
9905-0144334P.
9905-0144334P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014503P.
9905-014633P.
9905-014633P.
9905-014633P.
9905-014633P.
9905-014633P.
9905-014633P.
9905-014633P.
9905-014633P.
9905-014633P.
9905-014633P.
9905-014633P.
9905-014935P.
9905-014935P.
9905-014932P.
9905-014932P.
                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-1999;
04-AUG-1999;
04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-AUG-1999;
09-AUG-1999;
09-AUG-1999;
10-AUG-1999;
11-AUG-1999;
13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-1999;
23-AUG-1999;
25-AUG-1999;
18-JUN-1999;
18-JUN-1999;
21-JUN-1999;
22-JUN-1999;
23-JUN-1999;
23-JUN-1999;
24-JUN-1999;
29-JUN-1999;
30-JUN-1999;
30-JUN-1999;
01-JUL-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-AUG-1999;
02-AUG-1999;
02-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-AUG-1999
20-AUG-1999
                                                                                                                                                                                                                                                                         09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                             15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-AUG-1999
     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 56816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9905-0137522P
9905-0137522P
9905-0137528P
9905-0137744P
9905-0138094P
9905-0138094P
9905-0138047P
9905-0139452P
9905-0139452P
9905-0139454P
9905-0139455P
9905-0139456P
9905-0139456P
9905-0139456P
9905-0139456P
                                                                                                                                                                                                                                                                                                         99US-0121825P.
99US-0123180P.
99US-0123180P.
99US-0126788P.
99US-0126784P.
99US-0126748P.
99US-0126748P.
99US-0136744P.
99US-0130077P.
99US-0130077P.
99US-0130077P.
99US-0130040P.
99US-0132448P.
99US-0132448F.
99US-0132448F.
99US-0132448F.
99US-0132486P.
99US-0132486P.
99US-0132486P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          990S-0134221F
990S-0134370P
99US-0134768P
99US-0135124P
99US-0135324P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0135629P.
99US-0136021P.
99US-0136392P.
                                                                                                                                                                                                                                                                           25-FEB-2000; 2000EP-00301439
                                     18-OCT-2000 (first entry)
                                                                                                                                                                          Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 - MAY - 1999

18 - MAY - 1999

20 - MAY - 1999

21 - MAY - 1999

25 - MAY - 1999

25 - MAY - 1999

26 - MAY - 1999

27 - MAY - 1999

28 - MAY - 1999

30 - JUN - 1999

30 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 - JUN - 1999

310 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUN-1999;
16-JUN-1999;
17-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                         25-FEB-1999;

05-MAR-1999;

23-MAR-1999;

25-MAR-1999;

10-APR-1999;

10-APR-1999;

10-APR-1999;

11-APR-1999;

23-APR-1999;

23-APR-1999;

23-APR-1999;

23-APR-1999;

30-APR-1999;

30-APR-1999;

30-APR-1999;

30-APR-1999;

30-APR-1999;

30-APR-1999;

30-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31-APR-1999;

31
                                                                                                                                                                                                          EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1999
                                                                                                                                                                                                                                            06-SEP-2000
     AAG45273;
```

```
New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                    The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents the amino acid sequence of an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein encoded by Prokaryotic essential gene #9177.
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6; Ler
                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 6 Local Similarity 100.0%; Pred. No. 5.2 tes 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                   Example; SEQ ID NO 4130; 328pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU23650 standard; protein; 344 AA.
                                                                                                                                (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2001, 2001US-00815242.
06-SEP-2001, 2001US-00948993.
25-0CT-2001, 2001US-03429228-
08-FEB-2002, 2002US-0072851.
06-MAR-2002, 2002US-03626999P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2002; 2002WO-US009107.
                                                                                                          98US-0088701P.
                                                                                    99US-00328352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium acetobutylicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-2003 (first entry)
                      Acinetobacter baumannii
plant biocontrol agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 PKLIEFL 305
                                                                                                                                                                           WPI; 2003-576092/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 PKLIEFL 51
                                                                                                                                                     Breton G, Bush D;
                                                                                                                                                                                                                                                                                                                                                                                baumannii protein.
                                                                                                                                                                                      N-PSDB; ADA28717.
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 343 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200277183-A2.
                                                                                     04-JUN-1999;
                                          US6562958-B1
                                                                                                          09-JUN-1998;
                                                                 13-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU23650;
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU23650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acinetobacter baumannii; bacterial disease; antibacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 3; Length 343; 00.0%; Pred. No. 5.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA32843 standard; protein; 343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acinetobacter baumannii protein #4.
        99US-0151065P.
99US-0151080P.
99US-0151080P.
99US-0151438P.
99US-0151438P.
99US-0153070P.
99US-0153070P.
99US-0153070P.
99US-0154018P.
99US-0154018P.
                                                                                                                                                                                                                                         99US-0158232P
99US-0158369P
99US-0159293P
99US-0159294P
99US-0159232P
99US-0159331P
99US-0159637P
99US-0159638P
99US-0159638P
99US-0159644P
                                                                                                                                                                                                                                                                                                                                                                                                          99US-0160815P.
99US-0160815P.
99US-0160980P.
99US-0160981P.
                                                                                                                                       990S-0155139P-
99US-0155486P-
99US-015569P-
99US-015648P-
99US-0156596P-
99US-0157117P-
99US-0157753P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0161405P.
99US-0161406P.
99US-0161359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0161992P.
99US-0161993P.
99US-0162142P.
                                                                                                                                                                                                                    99US-0157865P.
                                                                                                                                                                                                                                                                                                                                                                            99US-0160767P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0161360P.
                                                                                                                                                                                                                                                                                                                                                                                                  99US-0160770P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0161404P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 EAFHVFK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 EAFHVFK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                          05-OCT-1999;
06-OCT-1999;
07-OCT-1999;
                                                                                                                                                                                                                                          08-OCT-1999;
12-OCT-1999;
13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-2003
                                                   31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
                                                                                                                                                                                                                                                                          13-OCT-1999;
13-OCT-1999;
                                                                                                                                                                                                                                                                                                14-OCT-1999;
14-OCT-1999;
                                                                                                                                                                                                                                                                                                                                14-OCT-1999;
14-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                      18-OCT-1999;
21-OCT-1999;
                                                                                                                                         22-SEP-1999;
23-SEP-1999;
                                                                                                                                                                                               04-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-1999;
                                                                                                                    16-SEP-1999
                                                                                                                                                               24-SEP-1999
                                                                                                                                                                                                                                                                                                                       14-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                       21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                        21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-1999
26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA32843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA32843
XXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
```

ó

Gaps

; 0

```
EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1999;
                                                                                                                                                                                                                                                                       23-APR-
                                                                                                                                                                                                                                                                                                                                                              05-MAY-
                                                                                                                                                                                                                                                                                                                                                                            06-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-
                                                                                                                                                                                                                             16-APR-
    the 613 antisense sequences given in the specification where expression of the 613 antisense sequences given in the specification where expression of the 613 antisense sequences given in the specification where expression of the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense modelic acid, (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway complicated for proliferation, (14) inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of the sequence of pathway in which a proliferation required for the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound,'s activity; (11) a culture comprising strains in which the gene product is overexpressed, (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense mucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation in cells other than S. aurens, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target proxaryoric essential genes. Note: The sequence is encoded by one of the target proxaryoric essential genes. Note: The sequence is encoded by one of the target proversory programes, or the retarget proversory and drug decoders. S. typhimurium, partent did not form part of the printed specification, but was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                       The invention relates to an isolated nucleic acid comprising any one of
                                Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 6; Length 344;
100.0%; Pred. No. 5.2e+02;
cive 0; Mismatches 0; Indels
                               Haselbeck R, Ohlsen KL,
Yamamoto R, Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 1362.
                             Haselbeck R,
                                                                                                                                                                          Claim 25; SEQ ID NO 51574; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG05089 standard; protein; 345 AA.
                             Malone C,
                                           Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
1es 7; Conservative
(ELIT-) ELITRA PHARM INC.
                               Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 EIVKILK 341
                                                                        WPI; 2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 BIVKILK 22
                                                                                        N-PSDB; ACA27520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG05089;
                               Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG05089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
 à
```

```
99US-0123180P.
99US-0125348P.
99US-0126264P.
99US-0126785P.
99US-0126785P.
99US-0128744P.
99US-0130449P.
99US-0130449P.
99US-0130449P.
99US-0132449P.
99US-0132449P.
99US-0132448P.
99US-013248P.
99US-013248P.
                                                                                                                                                                                                                                                                                                     99US-0134256P
99US-0134219P
99US-0134221P
99US-0134221P
99US-0134941P
99US-013124P
99US-013124P
99US-013122P
99US-013523P
99US-013522P
99US-013722P
99US-013722P
99US-013722P
99US-013722P
99US-013722P
99US-013722P
99US-013722P
99US-013722P
99US-013722P
99US-013722P
99US-013722P
99US-013722P
99US-013722P
99US-0139452P
99US-0139452P
99US-0139452P
99US-0139452P
99US-0139452P
99US-0139452P
99US-0139453P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0140991P.
99US-0141287P.
99US-0141842P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0139462P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0139463P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0139763P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0139899P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0140354P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0140695P.
99US-0140823P.
                        2000EP-00301439
                        25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUN-1999;
14-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUN-1999;
                                                                                                                                                                                                                                                                                  06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-1999;
06-SEP-2000
                                                                                23-MAR-1999,
                                                                                                      29-MAR-1999
                                                                                                                   01-APR-1999;
                                                                                                                                                                                                              28-APR-1999
                                                                                                                                                                                                                                   30-APR-1999
                                                                                                                                                                                                                                                                                                                    1999
                                                                                                                                                                                                                                                                                                                                                                 18-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                    21-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1999 - WIN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 - JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-NUL-1999
                                                                                                                                                                                                                                                                                              07-MAY-1999
                                                                                                                                                                                                                                                                                                        11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                     -MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .6-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .8-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUN-1999
                                                                                                                                                                                                                                                                                                                                           14-MAY-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7-JUN-1
```

99US-0154779P

```
9905-0151080P.
9905-0151080P.
9905-0151330P.
9905-0151330P.
9905-0153070P.
9905-0153070P.
9905-0154018P.
9905-0142154P.
9905-0142055P.
9905-0142205P.
9905-0142202P.
9905-0142220P.
9905-0143242P.
9905-0144334P.
9905-0144334P.
9905-0144334P.
9905-0144334P.
9905-0144334P.
9905-0144334P.
9905-0144334P.
9905-0144334P.
9905-0144334P.
9905-0145218P.
9905-0145218P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145318P.
9905-0145328P.
9905-0145328P.
9905-0149328P.
9905-0149328P.
                                                                                                                                                                                                                                                                                                                                                                                                                        30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-SEP-1999;
13-SEP-1999;
15-SEP-1999;
16-SEP-1999;
                                                                                                                                                                                                                                                                                                09-AUG-1999;
10-AUG-1999;
11-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                            23-AUG-1999;
23-AUG-1999;
25-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-1999;
27-AUG-1999;
                                                                                                                                                                                                                            02-AUG-1999
                                                                                                                                                                                                                                        02-AUG-1999;
                                                                                                                                                                                                                                                                                    06-AUG-1999;
                                                                                                                                                                                                                                                                                                                   12-AUG-1999;
                                                                                                                                                                                                                                                                                                                                13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                          20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                               20-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                               26-AUG-1999
                                                                                                                                                                                                               27-JUL-1999
                                                                                                                                                                                                                                                           04-AUG-1999
                                                                                                                                                                                                                                                                                                                                                   18-AUG-1999
                                                        16-JUL-1999
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                Score 7; DB 3; Length 345; Pred. No. 5.2e+02;
                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herbicidally active polypeptide SEQ ID NO 658.
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herbicidal; plant; agriculture; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB91447 standard; protein; 368 AA.
                                                                                                                                                                                                                                                                                                                                                Query Match 2.1%; Scc
Best Local Similarity 100.0%; Pr
Matches 7; Conservative 0;
      990S-0155139P
990S-0155586P
990S-0155596P
990S-0155596P
990S-0157753P
990S-0157753P
990S-0158232P
990S-0158232P
990S-0158232P
990S-0159294P
990S-0159234P
990S-0159231P
990S-0159331P
990S-0159331P
990S-0159331P
990S-0159331P
990S-0159331P
990S-0159331P
990S-0159331P
990S-0159331P
990S-016981P
990S-016081P
990S-016081P
990S-016081P
990S-016081P
990S-016081P
990S-016081P
990S-016081P
990S-016081P
990S-016081P
990S-016081P
990S-016081P
990S-016081P
990S-016081P
990S-016081P
990S-016081P
990S-016081P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-AUG-2001; 2001WO-EP009892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-2001; 2001WO-EP009892.
                                                                                                                                                                                                                                                                                                                       99US-0161993P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                 186 TFKDLLT 192
                                                                                                                                                                                                                                                                                                                                                                                                 190 TFKÖLLT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200210210-A2.
                                                      05-0CT-1999;
06-0CT-1999;
08-0CT-1999;
12-0CT-1999;
13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
                                                                                                                                                         14-0CT-1999
18-0CT-1999
21-0CT-1999
21-0CT-1999
21-0CT-1999
21-0CT-1999
22-0CT-1999
22-0CT-1999
25-0CT-1999
25-0CT-1999
25-0CT-1999
25-0CT-1999
                                                                                                                                                                                                                                                                                    26-OCT-1999;
26-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2002.
                                                                                                                                                                                                                                                                                                                       28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB91447;
                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 74
                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB91447
à
                                                                                                                                                                                                                                                                                                                                                                                                셤
```

ö

```
The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoching them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                              Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequenc from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                               Claim 5; SEQ ID NO 658; 261pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.1%; Score 7; DB 5; Length 368; Best Local Similarity 100.0%; Pred. No. 5.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human colon cancer antigen protein SEQ ID NO:4448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 6262-6264; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG73684 standard; protein; 374 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-SEP-2000; 2000WO-US026524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0157137P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           colorectal carcinoma
                                               WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-235357/24.
N-PSDB; AAH33115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 EEVSKSL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 EEVSKSL 82
                                                                                                                                                                                                                                                                                                                                                                   Sequence 368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200122920-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-APR-2001.
               Tietjen K,
                                                                                                                                                                                                                                                                                                                                    herbicides
                                                                                                                                   organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG73684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db
```

```
and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or doletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal sertingness and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at the order of the present for SEQ ID NO:1027
                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                             2.1%; Score 7; DB 4; Length 374;
100.0%; Pred. No. 5.6e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 3035.
                                                                                                                                                                                                                                                                                                                                                                                                        AAG06308 standard; protein; 377 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0128234P.
99US-0128714P.
99US-0130077P.
99US-0130449P.
99US-013049P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0131449P.
99US-0132048P.
99US-0132407P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0132485P.
99US-0132486P.
99US-0132487P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0123180P.
99US-0123548P.
99US-0125788P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0126264P.
99US-0126785P.
99US-0127462P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0134256P.
99US-0134218P.
99US-0134219P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0132484P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0132863P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                        to 1052, 7921 and 7922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                               178 NLAILEK 184
                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                     24 NLAILEK 30
                                                                                                                                                                                                                   Sequence 374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAY-1999;
14-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG06308;
                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                         AAG06308
    ò
                                                                                                                                                                                                                                                                                                                             g
```

.. 0

Gaps

..

990S - 0145913P 990S - 0145919P 990S - 0145919P 990S - 0145919P 990S - 0145919P 990S - 0147304P 990S - 0147304P 990S - 0147304P 990S - 0147304P 990S - 0147304P 990S - 0147304P 990S - 0147304P 990S - 0149319P 990S - 0149426P 990S - 0149428P 990S - 0149428P 990S - 0149438P 990S - 0149438P 990S - 014930P 990S - 014930P 990S - 014930P 990S - 015066P 990S - 015066P 990S - 015066P 990S - 0151303P 990S - 0151303P 990S - 0151303P 990S - 0151303P 990S - 0151303P 990S - 0151303P 990S - 0151303P 990S - 0151303P 990S - 0151303P 990S - 0151303P 990S - 0151303P 990S - 0151303P 990S - 0151303P 990S - 0151303P 990S - 0151303P 990S - 0151303P 990S - 0151303P	990S - 01592935 990S - 01592945 990S - 0159295 990S - 0159330P 990S - 0159331P 990S - 0159637P 990S - 0159637P 990S - 0160741P 990S - 0160770P 990S - 0160770P 990S - 0160814P 990S - 0160980P 990S - 0160980P 990S - 0160980P 990S - 0160980P 990S - 0160980P 990S - 0160980P
27 - UUL - 1999; 27 - UUL - 1999; 28 - UUL - 1999; 28 - UUL - 1999; 28 - UUL - 1999; 39 - AUG - 1999; 30 - AUG - 1999; 30 - AUG - 1999; 30 - AUG - 1999; 30 - AUG - 1999; 31 - AUG - 1999; 32 - AUG - 1999; 33 - AUG - 1999; 34 - AUG - 1999; 35 - AUG - 1999; 36 - AUG - 1999; 37 - AUG - 1999; 38 - AUG - 1999; 39 - AUG - 1999; 30 - AUG - 1999; 31 - AUG - 1999; 32 - AUG - 1999; 33 - AUG - 1999; 34 - AUG - 1999; 35 - AUG - 1999; 36 - AUG - 1999; 37 - AUG - 1999; 38 - AUG - 1999; 39 - AUG - 1999; 30 - AUG - 1999; 31 - AUG - 1999; 32 - AUG - 1999; 33 - AUG - 1999; 34 - AUG - 1999; 35 - AUG - 1999; 36 - AUG - 1999; 37 - AUG - 1999; 38 - AUG - 1999; 39 - AUG - 1999; 30 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 32 - AUG - 1999; 33 - AUG - 1999; 34 - AUG - 1999; 35 - AUG - 1999; 36 - AUG - 1999; 37 - AUG - 1999; 38 - AUG - 1999; 39 - AUG - 1999; 30 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 32 - AUG - 1999; 33 - AUG - 1999; 34 - AUG - 1999; 36 - AUG - 1999; 37 - AUG - 1999; 38 - AUG - 1999; 39 - AUG - 1999; 30 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - AUG - 1999; 31 - A	
¥ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	
99US-0134221P 99US-0134768P 99US-0134124P 99US-0135134P 99US-0135134P 99US-0135622P 99US-013672P 99US-0137528P 99US-0137528P 99US-0137528P 99US-0137528P 99US-0137528P 99US-0137528P 99US-0137528P 99US-0137528P 99US-0137528P 99US-0137528P 99US-0137528P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0139458P 99US-0140653P 99US-0140659P 99US-0142055P 99US-0142055P 99US-0142055P 99US-0142055P 99US-0142377P 99US-0142077P 99US-0142377P 99US-0142377P 99US-0142377P 99US-0142377P 99US-0142377P 99US-0142377P 99US-0142377P 99US-0142377P	99US-0144332P 99US-0144333P 99US-0144334P 99US-0144352P 99US-0144632P 99US-0144814P 99US-0144814P 99US-014508FP 99US-014508FP 99US-014508PP 99US-014508PP 99US-014508PP 99US-014518PP 99US-014518PP 99US-014518PP 99US-014518PP
14 - MAY - 1999; 18 - MAY - 1999; 20 - MAY - 1999; 21 - MAY - 1999; 22 - MAY - 1999; 23 - MAY - 1999; 24 - MAY - 1999; 25 - MAY - 1999; 26 - MAY - 1999; 27 - MAY - 1999; 38 - JUN - 1999; 39 - JUN - 1999; 30 - JUN - 1999; 31 - JUN - 1999; 32 - JUN - 1999; 33 - JUN - 1999; 34 - JUN - 1999; 35 - JUN - 1999; 36 - JUN - 1999; 37 - JUN - 1999; 38 - JUN - 1999; 39 - JUN - 1999; 30 - JUN - 1999; 31 - JUN - 1999; 32 - JUN - 1999; 33 - JUN - 1999; 34 - JUN - 1999; 35 - JUN - 1999; 36 - JUN - 1999; 37 - JUN - 1999; 38 - JUN - 1999; 39 - JUN - 1999; 30 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 32 - JUN - 1999; 33 - JUN - 1999; 34 - JUN - 1999; 35 - JUN - 1999; 36 - JUN - 1999; 37 - JUN - 1999; 38 - JUN - 1999; 39 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - JUN - 1999; 31 - J	00000000000000000000000000000000000000
######################################	

. 0

```
The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequencifrom plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; SEQ ID NO 1435; 261pp + Sequence Listing; English.
                                                                                                                                Length 377;
                                                                                                                                                       0; Indels
                                                                                                                               DB 3; Len
                                                                                                                                                                                                                                                                                                                                                 Herbicidally active polypeptide SEQ ID NO 1435.
                                                                                                                            2.1%; Score 7; DB 3
100.0%; Pred. No. 5.7
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 5
100.0%; Pred. No. 5.7
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         Herbicidal; plant; agriculture; herbicide.
                                                                                                                                                                                                                                                                     ABB92224 standard; protein; 377 AA.
                                                99US-0161361P.
99US-0161920P.
99US-0161992P.
            99US-0161406P.
99US-0161359P.
99US-0161360P.
                                                                                      99US-0161993P.
 99US-0161405P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-AUG-2001; 2001WO-EP009892
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weidler M;
                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana.
                                                                                                                                                                                                     112 LIEFLSS 118
                                                                                                                                                                                301 LIEFLSS 307
                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             WO200210210-A2
          25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                                                                        31-MAY-2002
                                                                                                                                                     7;
 25-OCT-1999;
                                                                                                  29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-2002.
                                                                                      28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tietjen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         herbicides
                                                                                                                                                                                                                                                                                               ABB92224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organisms
                                                                                                                            Query Match
                                                                                                                                                                                                                                             RESULT 77
                                                                                                                                                                                                                                                          ABB92224
ð
                                                                                                                                                                                                     셤
```

```
.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thioredoxin-porphobilinogen synthase (T-PPS) and plant porphobilinogen synthase (PPS). Methods of determining the enzymatic activity of T-PPS or PPS or its functional fragment are provided that involves contacting delta-aminolevulinic acid with the protein or its functional fragment and measuring the amount of porphobilinogen formed from it. Compounds which can modify the enzymatic activity T-PPS or PPS can also be identified similarly, which are useful for inhibiting plant growth by inhibiting enzymatic activity of T-PPS or PPS or its functional fragment. The compounds thus identified are useful as herbicides. The present sequence represents the PPS enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides novel DNA sequences encoding enzymes such as plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                     Thioredoxin; porphobilinogen synthase; T-PPS; PPS; enzyme; herbicide; delta-aminolevulinic acid; plant growth inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel plant thioredoxin-porphobilinogen synthase or porphobilinogen synthase polypeptides, useful for identifying compounds for use as herbicides by inhibiting enzymatic activity of the polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 64757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 4; Ler Local Similarity 100.0%; Pred. No. 5.8e+02; e8 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stewart S;
                                                                                                                                                                                                                                        Plant porpobilinogen synthase (PPS),
                                AAB85255 standard; protein; 384 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 21-22; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG51052 standard; protein; 400 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sevala V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PARA-) PARADIGM GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-2000; 2000WO-US034584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0171785P.
                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            Lycopersicon esculentum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crawford JM, Rice J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-418081/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 LLRDKSP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 LLRDKSP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAH22805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200146446-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1999;
                                                                                                                                                                    07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-OCT-2000
                                                                                                AAB85255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG51052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG51052
AAB8525
                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAXEXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXEX
MAXE
```

. 0

Gaps

; 0

DB 5; Length 377; 0; Indels

112 LIEFLSS 118

LIEFLSS 307

301

à d Page 59

. 000 L.MTT 00	PR 29-JUN-1999; 99US-0140991P. PR 30-JUN-1999; 99US-0141287P.	01-JUL-1999; 01-JUL-1999;	02-JUL-1999; 06-JUL-1999;	08-JUL-1999;	13-JUL-1999; 13-JUL-1999;	15-JUL-1999;	16-JUL-1999; 16-JUL-1999;	19-JUL-1999;	19-00L-1999;	19-JUL-1999; 19-JUL-1999;	19-JUL-1999;	20-JUL-1999;	20-JUL-1999; 21-JUL-1999;	21-JUL-1999;	21-JUL-1999; 22-JUL-1999;	22-JUL-1999;	22-JUL-1999; 22-JUL-1999;	23-JUL-1999;	23-JUL-1999; 23-JUL-1999;	26-JUL-1999; 27-JHH-1999;	27-JUL-1999;	28-JUL-1999; 28-JUL-1999;	02-AUG-1999;	02-AUG-1999;	03-AUG-1999; 04-AUG-1999;	04-AUG-1999; 05-AUG-1999;	05-AUG-1999;	06-AUG-1999;	09-AUG-1999; 09-AUG-1999;	10-AUG-1999;	12-AUG-1999;	13-AUG-1999; 13-AUG-1999;	16-AUG-1999;	17-AUG-1999; 18-AUG-1999;	20-AUG-1999;	20-AUG-1999;	23-AUG-1999;	25-AUG-1999;	26-AUG-1999; 27-AUG-1999;	27-AUG-1999;	2/-AUG-1999; 30-AUG-1999;	31-AUG-1999;	07-SEP-1999;
termination sequence.		EP1033405-A2.	06-SEP-2000.	25-FEB-2000; 2000EP-00301439.	25-FEB-1999; 99US-0121825P. 05-MAR-1999; 99US-0123180P.	99US-	-8066	-SD66	-S066	-8066	-S066	-Sn66	-SD66	99US-	-SD66	99US-(	)-SD66	)-SD66	-SD66	)-SD66	99US-	-S066	)-SD66	)-SU66	-SD66	)-SD66 )-SD66	99US-0	-SD66	)-SD66	99US-(	900S-	99US-(	99US-(	9908-	)-SD66	99US-	-Sn66	99US-	-sn66	99US-(	99US-013	99US-014 99US-014	99US-014

```
9903-0125788P

9903-0126264P

9903-0128234P

9903-0128244P

9903-0128448P

9903-0130474P

9903-0130449P

9903-0130449P

9903-0130449P

9903-0130449P

9903-0130449P

9903-0130449P

9903-013049P

9903-0130449P

9903-0130449P

9903-0130449P

9903-0130449P

9903-0130449P

9903-0130449P

9903-0134484P

9903-0134484P

9903-0134484P

9903-0134484P

9903-0139454P

9903-0139454P

9903-0139454P

9903-0139454P

9903-0139454P

9903-0139454P

9903-0139454P

9903-0139454P

9903-0139454P

9903-0139454P

9903-0139454P

9903-0139454P

9903-0139454P

9903-0139453P

9903-0139453P

9903-0139453P

9903-0139453P

9903-0139453P

9903-0139453P

9903-0139453P

9903-0140334P

9903-0140334P

9903-0140334P
               2000EP-00301439
                                     99US-0121825P
                                               99US-0123180P
               25-FEB-2000;
                                                                                                                                                                                          28-APR-1999
                                                                                                                                      16-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                       27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                             03-NUT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match
2.1%; Score 7; DB 3; Length 400;
Local Similarity 100.0%; Pred. No. 6e+02;
les 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 49262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG39773 standard; protein; 422 AA
           99US-0153758P

99US-0154018P

99US-0154018P

99US-015439P

99US-0155436P

99US-0155536P

99US-0155536P

99US-0156536P

99US-015753P

99US-0158232P

99US-0158232P

99US-0158234P

99US-0159234P

99US-0159234P

99US-0159234P

99US-0159234P

99US-0159234P

99US-0159234P

99US-0159234P

99US-0159234P

99US-0159331P

99US-0159331P

99US-0159331P

99US-0169384P

99US-0169384P

99US-0169384P

99US-0169384P

99US-0169384P

99US-0169384P

99US-0169384P

99US-0169384P

99US-0169384P

99US-0160384P

99US-0160384P

99US-0160384P

99US-0160384P

99US-0160384P

99US-0160384P

99US-0160384P

99US-0160384P

99US-0160384P

99US-0160384P

99US-0160384P

99US-0160384P

99US-0160384P

99US-0161360P

99US-0161360P
  99US-0153070P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0162142P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 EAFHVFK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ÉAFHVFK 341
10-SEP-1999;
13-SEP-1999;
15-SEP-1999;
20-SEP-1999;
22-SEP-1999;
22-SEP-1999;
23-SEP-1999;
24-SEP-1999;
24-SEP-1999;
04-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
12-OCT-1999;
13-OCT-1999;
14-OCT-1999;
14-OCT-1999;
12-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                             22-OCT-1999;
22-OCT-1999;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                 25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                             25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG39773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db
```

```
9905-0144884P
9905-0144884P
9905-0145088P
9905-0145088P
9905-0145087P
9905-014518P
9905-014518P
9905-014518P
9905-014518P
9905-014518P
9905-014518P
9905-014518P
9905-014518P
9905-014518P
9905-014518P
9905-014518P
9905-014518P
9905-014638P
9905-014703P
9905-014703P
9905-014703P
9905-014703P
9905-014703P
9905-014703P
9905-014703P
9905-014703P
9905-014703P
9905-014703P
9905-01488P
9905-01493P
9905-01493P
9905-01493P
9905-01493P
9905-01493P
9905-014930P
9905-014930P
9905-014930P
9905-014930P
9905-014930P
    990S 0142920P

990S 0142942P

990S 014462E

990S 014408EP

990S 014433EP

990S 014433EP

990S 014433EP

990S 014433EP

990S 014433EP

990S 014433EP
                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0153758P.
99US-0154018P.
99US-0154039P.
99US-0154779P.
99US-0155139P.
                                                                                                                                                                                                                                                                                                                                                                                                99US-0151080P.
99US-0151303P.
99US-0151438P.
                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0152363P.
99US-0153070P.
                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0151930P
                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
23-SEP-1999;
                                                                                                                                                                                                                                                           06-AUG-1999;
06-AUG-1999;
09-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                             26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                      30-AUG-1999;
                                                                          19-JUL-1999;
                                                                                                                                                                                                                                                                                                             13-AUG-1999;
      09-JUL-1999;
                                                                                                                                                                                                                                  04-AUG-1999
                                                                                                                                                                                                                                         04-AUG-1999
                                                                                                                                                                                                                                                                                           11-AUG-1999,
12-AUG-1999
                                                                                                                                                                                                                                                                                                                                             20-AUG-1999
                                                                                                                                                                                                                                                                                                                                                          23-AUG-1999
23-AUG-1999
                                                                                                                                                                                                                                                                                                         13-AUG-1999
                                                                                                                                                                                                                                                                                                                          17-AUG-1999
```

```
Human; ubiquitin conjugating enzyme; UBC; RATLId6; immune disorder; regulated in activated T-lymphocyte 1d6; neuronal disorder; cancer; tumnour; lymphoproliferative; cancer; adenocarcinoma; leukaemia; myeloma; sarcoma; neurodegenerative; inflammatory; rheumatoid arthritis; astima; multiple sclerosis; psoriasis; neuronal; Alzheimer's disease; dementia; depression; epilepsy; acquired immuno deficiency syndrome; allergy; AIDS; anaemia; atopic dermatiis; diabetes mellitus; dermatological; myocardial infarction; renal tubular acidosis; gonadal dysgenesis; dysplasia; cataract; cytostatic; neuroprotective; nootropic; anti-HIV; antionvulsant; antinflammatory; Cushing's syndrome; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human RATL1d6 (regulated in activated T-lymphocyte 1d6) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; Score 7; DB 3; Length 422;
100.0%; Pred. No. 6.3e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE24493 standard; protein; 422 AA.
         99US-0156458P.
99US-0156596P.
99US-0157153P.
99US-0157655P.
99US-015865P.
99US-0158232P.
99US-0158232P.
99US-0159294P.
99US-0159294P.
99US-015933P.
99US-0159331P.
99US-0159331P.
                                                                                                                                                                                         990S-0159584P

990S-0160741P

990S-0160767P

990S-0160814P

990S-0160814P

990S-0160981P

990S-0160981P

990S-0160981P

990S-016196P

990S-0161406P

990S-0161359P

990S-0161361P

990S-0161361P
                                                                                                                                                                                                                                                                                                                                                                                       99US-0161992P.
99US-0161993P.
99US-0162142P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.1
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 LYSSGLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 LYSSGLL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ophthalmological.
         28-SEP-1999;
29-SEP-1999;
04-0CT-1999;
06-0CT-1999;
07-0CT-1999;
12-0CT-1999;
                                                                                                                                                                                                                21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
25-0CT-1999;
                                                                                                            13-OCT-1999;
13-OCT-1999;
14-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                     26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-2002
                                                                                                                                                                                                                                                                                                                                           26-OCT-1999
                                                                                                                                              14-OCT-1999
                                                                                                                                                                               14-OCT-1999
                                                                                                                                                                                                      21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE24493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE24493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
```

Location/Qualifiers

Key Domain

```
The invention relates to a novel ubiquitin conjugating enzyme (UBC)
homologue, RATLIG6 (regulated in activated T-lymphocytes 1d6) and its
corresponding nucleic acid. The invention also relates to methods for
treating, diagnosing, preventing and screening for disorders related to
treating, diagnosing, preventing and screening for disorders related to
the expression of RATLIG6. UBC is useful for screening for candidate
compounds capable of binding to and/or modulating its activity. UBC is
useful for treating an immune or neuronal disorder in a mammal. The
method is useful for treating a cancer or tumour. It is useful for
suppressing the immune response in a subject requiring the suppression.
It is also useful for treating lymphoproliferative disorder, cancer e.g.
disorder, inflammatory disorders e.g. rheumatoid arthritis, asthma,
multiple sclerosis, psoriasis, etc, neuronal disorders e.g. Alzheimer's
disease, dementia, depression, eplepsy, etc, immune disorder or immune
related disorders such as acquired immuno deficiency syndrome (AIDS),
allery, anaemaia, atopic dermatitis, diabetes mellitus, myocardial
infarction, etc, developmental disorders e.g. Cushing's syndrome, renal
tubular acidosis, gonadal dysgenesis, dysplasia, cataract, etc. The
present sequence is human RATLIG6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; NOVX; cytostatic; antidiabetic; neuroprotective; antiparkinsonian; anorectic; gene therapy; vaccine; cancer; neurodegenerative disorder; Parkinson's disease; metabolic disorder; diabetes; obesity;
                                                                                                                                                                                                                                                                                                                                                       Novel ubiquitin conjugating enzyme polypeptide isolated from activated human T cell, for screening modulators useful for treating cancer, immune disorder, lymphoproliferative disorder, neurodegenerative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 5; Length 422;
100.0%; Pred. No. 6.3e+02;
live 0; Mismatches 0; Indels
/note= "Transmembrane domain"
                                                                                                                                                                                                                                                       Bowen MA, Wu Y, Yang W, Finger JN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABR83334 standard; protein; 422 AA.
                                                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NOVla protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Fig 3; 169pp; English.
                                                                                                                  29-OCT-2001; 2001WO-US046559.
                                                                                                                                                                          30-JUL-2001; 2001US-0308706P.
                                                                                                                                                       30-OCT-2000; 2000US-0244688P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 NLAILEK 232
                                                                                                                                                                                                                                                                                              2002-479758/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD39359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003052061-A2.
                                   WO200236741-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABR83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 82
ABR83334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

```
ACF06233 to ACF06242 encode the human NOVX proteins given in ABR83334 to ABR83343, designated NOV1a, NOV2a, NOV3a, NOV4a, NOV4b, NOV5a and have cytostatic, NOV7a, NOV9a and NOV9a respectively. NOVX sequences can have cytostatic, antidiabetic, neuroprotective, antiparkinsonian and anorectic activities, and can be used in vaccines and gene therapy. The NOVX polypeptides can be used for preparing a composition for treating or preventing a pathology associated with the NOVX-polypeptides e.g. cancer, neurodegenerative disorders such as Parkinson's disease, or metabolic disorders such as diabetes or obesity, or for tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                             New NOVX polypeptide, useful for preparing a composition for treating or preventing e.g. cancer, neurodegenerative disorders such as Parkinson's disease, or metabolic disorders such as diabetes or obesity, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                       Catterton E;
L, Patturajan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                      DW, Boldog FL, Burgess CE, Catt
Guo X, Ji W, Kekuda R, Li L, I
Spytek KA, Vernet CAM, Voss EZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 7; DB 6; Length 422;
100.0%; Pred. No. 6.3e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by Prokaryotic essential gene #17315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU31788 standard; protein; 439 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 94; 190pp; English.
                                                                                                                                                                     1/ PMAY - 2002; 2002US-U383,144.

29-MAY-2002; 2002US-0384024P.

07-AUG-2002; 2002US-0401788P.

26-AUG-2002; 2002US-0406353P.

11-AUG-2002; 2002US-0406353P.
                                                                                                                                 17-APR-2002; 2002US-0373289P.
15-MAY-2002; 2002US-0380981P.
17-MAY-2002; 2002US-0381495P.
28-MAY-2002; 2002US-0383744P.
                                                                                    2001US-0341540P.
2001US-0342592P.
2001US-0344903P.
                                          03-DEC-2002; 2002WO-US038821.
                                                                                                                                                                                                                                                           02-DEC-2002; 2002US-00307928
                                                                                                                                                                                                                                                                                                                         Anderson DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                       SR, Gorman L,
JK, Shenoy SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                          (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                 Gorman I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 NLAILEK 232
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-533005/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ACF06233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue typing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-2003
                                                                                                                    31-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-2002,
           26-JUN-2003
                                                                                                                                                                                                                                                                                                                                                        Rieger DK,
                                                                                                                                                                                                                                                                                                                         Alsobrook
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU31788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                         Edinger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU31788
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BXBXBXBXBXGXB
```

0;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

```
The interaction relates to an isolated muciesc acid comparising any one of the 6213 antisense sequences given in the specification where expression of the 6213 antisense sequences given in the specification where expression of the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular printeration, (7) identifying a compound that inhibits proliferation; (8) identifying a gene required for cellular proliferation or the activity of the gene product or that has an activity against a biological pathway required for proliferation or the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound,'s activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the confideration of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form the print of the printed specification, but was obtained in electronic format directly from Will are proved by the printed proliferation in the propers of the printed specification, but was obtained in the compount of proved proved by the printed by the proved proved by the printed 
                                                                                                                                                                                                                                                                                                                                                                                   New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 7; DB 6
100.0%; Pred. No. 6.5
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; SEQ ID NO 59712; 1766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB52729 standard; protein; 452 AA.
                                                                                                                                                                                                                                                 Malone C,
Carr GJ,
                                                                                     06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-034223P.
06-FEB-2002; 2002US-0072851.
06-MAR-2002; 2002US-0362899P.
                       21-MAR-2002; 2002WO-US009107
                                                                  2001US-00815242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-FEB-2002 (first entry)
                                                                                                                                                                                                    (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
                                                                                                                                                                                                                                                 Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 HNFAIMT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 HNFAIMT 123
                                                                                                                                                                                                                                                                                                                 WPI; 2003-029926/02
                                                                                                                                                                                                                                                                                                                                           N-PSDB; ACA35658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 439 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB52729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                 , c,
                                                                                                                                                                                                                                                 Wang I
Wall I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB52729
ID ABB5
XX
XX
AC ABB5
XX
DT 11-F
à
```

```
B2/D+A. The polymucleotides have potential intiinflammatory, antibacterial and immunosuppressive activity as part of pharmaceutical compositions used to treat, palliate or prevent extra-intestinal E. coli infections. The polypeptides are useful for determining the phylogenic group of a given E. coli strain. These polypeptides can detect and treat an undesired development of E. coli, particularly an extra-intestinal infection that include systemic and non-diarrhoeal infections such as septicaemia, pyelonephritis and meningitis this is particularly advantageous as bacterial resistance is increasing with the more frequent use of broad spectrum antibiotics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A library of DNA fragments of Escherichia coli strains for the phylogenic determination of a given strain comprises polynucleotides of nature B2/D +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a library of DNA fragments of Escherichia coli
strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533) and
encoded proteins (ABB52459-ABB52919 and ABB52954-ABB53094) of nature
                                                Escherichia coli; B2/D+A-; antiinflammatory; antibacterial; immunosuppressive, extra-intestinal infection; phylogeny; meningitis; systemic infection; non-diarrhoeal infection; septicaemia; phylonephritis; antibiotic resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis; signal transduction; DNA replication; cell division; growth; proliferation; Candida albicans; fungicide; antifungal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                             Bingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.1%; Score 7; DB 4; Length 452; Best Local Similarity 100.0%; Pred. No. 6.7e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Candida albicans essential protein SEQ ID NO 7310.
                                                                                                                                                                                                                                                                                                                                                        (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                 Escherichia coli polypeptide SEQ ID NO 859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP73473 standard; protein; 458 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 6; Fig 6; 646pp; English.
                                                                                                                                                                                                                                                                                               10-MAR-2000; 2000FR-00003145.
02-FEB-2001; 2001FR-00001449.
                                                                                                                                                                                                                                                              12-MAR-2001; 2001WO-EP003445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 DIASDAF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 DIASDAF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-550253/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Candida albicans.
                                                                                                                                                Sscherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 452 AA;
                                                                                                                                                                                     WO200166572-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200253728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2003
                                                                                                                                                                                                                       13-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP73473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP73473
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                     Zyskind JW;
Xu HH;
```

ö

Gaps

;

DB 6; Length 439; . 6.5e+02;

11-JUL-2002

```
99US-0128714P
99US-0129845P
99US-0130449P
99US-0130449P
99US-0130510P
99US-0131449P
99US-0131449P
99US-013248P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     990S-0134941P.
990S-0135124P.
990S-0135353P.
990S-013629P.
990S-0136392P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0137222P.
99US-0137528P.
99US-0137524P.
99US-0138094P.
99US-0138540P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         990S-0138847P.
990S-0139119P.
990S-0139452P.
990S-0139492P.
990S-0139454P.
990S-0139454P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0139460P.
99US-0139461P.
99US-0139462P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0139463P.
99US-0139750P.
99US-0139763P.
                                                                                                                                                                                              99US-0126264P.
99US-0126785P.
99US-0127462P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0132485P.
99US-0132486P.
99US-0132487P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0132863P.
99US-0134256P.
99US-0134218P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0139457P.
99US-0139458P.
99US-0139459P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0140353P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0140823P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0134221P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0134370P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0139817P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0140695P
                                                                                                                                                                                                                                                 99US-0128234P
                                                                                               25-FEB-2000; 2000EP-00301439
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
                               EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                       30-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUN-1999
                                                                 06-SEP-2000
                                                                                                                                                                                                                                                 06-APR-1999
                                                                                                                                                                                                                                                                                  16-APR-1999
                                                                                                                                                                                                                                                                                                      19-APR-1999
                                                                                                                                                                                                                                                                                                                                                                       28-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-MAY-1999
                                                                                                                                                                                                                                                                                                                    21-APR-1999
                                                                                                                                                                                                                                                                                                                                       23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-1
04-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JUN-
 ^{2}
                                                                                                                                                                                                                                                                                                                                                           The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying cells in which both alleles of a gene are modified, comprising modifying cone allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by insertion of the second allele is regulated by the promoter. So that expression of the second allele is regulated by the promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that cells anying both alleles modified are useful for identifying a gene that is essential to the survival or growth of a fungus, a gene that contributes to the virulence and/or pathogenicity of a fungus, a gene that contributes to the resistance of a diploid fungus to an antifungal agent that inhibits the growth of a diploid fungus and for identifying a therapeutic agent for treatment of a mammalian disease. (M1) is useful for identifying a compound which modulates the certifyty of a gene product, preferably enzymatic activity, carbon compound catabolism, biosymthetic, transporter, transcriptional, translational, signal transduction, DNA replication and cell division compound catabolism, biosymthetic, transporter, transcriptional, cativity of an underly of a useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and cativity and a susferial candida albicans protein used in the method is the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                 Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
                                                                                                                                                                                                                                                                                                                                    Claim 44; SEQ ID NO 7310; 167pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 5; Length 458;
100.0%; Pred. No. 6.8e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 38786.
                                                                                                                                                                                  Ohlsen KL;
                                                                                                                                                                                  Bussey H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG32191 standard; protein; 482 AA.
                                                                                                                                                                                  Boone C,
                                               26-DEC-2001; 2001WO-US049486.
                                                                             29-DEC-2000; 2000US-0259128P.
20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
                                                                                                                                                (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 FADEKNY 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 FADEKNY 338
                                                                                                                                                                                  Roemer T, Jiang B,
                                                                                                                                                                                                                 WPI; 2002-566694/60.
                                                                                                                                                                                                                                   N-PSDB; ABZ32023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 458 AA;
```

17-OCT-2000

AAG32191;

RESULT 86 AAG3219

Query Match Matches

à

```
PR 30-VW-1999; 99US-0141287P.

PR 01-JUL-1999; 99US-01421842P.

PR 06-JUL-1999; 99US-01421842P.

PR 06-JUL-1999; 99US-01422003P.

PR 06-JUL-1999; 99US-014230P.

PR 19-JUL-1999; 99US-014230P.

PR 13-JUL-1999; 99US-014230P.

PR 19-JUL-1999; 99US-0144324P.

PR 19-JUL-1999; 99US-0144324P.

PR 19-JUL-1999; 99US-0144324P.

PR 19-JUL-1999; 99US-0144334P.

PR 19-JUL-1999; 99US-0144334P.

PR 20-JUL-1999; 99US-0144334P.

PR 20-JUL-1999; 99US-0144334P.

PR 20-JUL-1999; 99US-0144334P.

PR 20-JUL-1999; 99US-0144334P.

PR 21-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.

PR 22-JUL-1999; 99US-0144334P.
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glaucoma; PCR amplification; primary open wide angle glaucoma;
                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 482;
                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                 .le+02;
                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 3
100.0%; Pred. No. 7.1
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY49289 standard; protein; 490 AA.
                      990S-0155139P.
990S-0155486P.
990S-0155659P.
990S-015658P.
990S-0156596P.
                                                                              990S-0157865P

990S-015823P

990S-015923P

990S-015923P

990S-015923P

990S-015933P

990S-015933P

990S-015933P

990S-015963P

990S-016963P

990S-016074P

990S-016074P

990S-016074P

990S-016074P

990S-016074P

990S-016098P

990S-016098P

990S-016196P

990S-016196P

990S-016196P

990S-016196P

990S-016196P

990S-016196P

990S-016196P

990S-016196P

990S-016196P

990S-016196P

990S-016196P

990S-016196P

990S-016196P

990S-016196P

990S-016196P
99US-0154018P.
99US-0154039P.
99US-0154779P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US007671.
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.00
Find 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse GLCIA polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                   100 LIEFLSS 106
                                                                                                                                                                                                                                                                                                                                                                                       301 LIEFLSS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLC1A gene; mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9951779-A2.
                                      24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
                                                             04-0CT-1999;
05-0CT-1999;
06-0CT-1999;
07-0CT-1999;
                                                                                                      12-OCT-1999;
13-OCT-1999;
13-OCT-1999;
13-OCT-1999;
                                                                                                                                             14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
                                                                                                                                                                                                     21-0CT-1999
21-0CT-1999
21-0CT-1999
22-0CT-1999
22-0CT-1999
25-0CT-1999
25-0CT-1999
26-0CT-1999
26-0CT-1999
26-0CT-1999
26-0CT-1999
28-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-OCT-1999.
                                                                                                                                       14-OCT-1999
                                                                                                                                                                                                                                                                                                                                       29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY49289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY49289
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₹
```

```
This is the amino acid for cytochrome 2P450RAI of the Zebra fish. Its expression is dependent on the presence of retinoic acid (RA). The retinoid-regulated genes such as the inducible cytochrome P450RAI gene specifically metabolises a derivative of the RA. The cytochrome P450 gene
                                                                                                                                                                                                                  predisposition to glaucoma. The method comprises amplifying a GLCIA gene with a primer pair selected from the sequences shown in AA237981-Z38008. The primers are used to determine whether a subject has or has the potential to develop primary open wide angle glaucoma. The present sequence represents the mouse GLCIA polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying DNA encoding inducible or suppressible cytochrome P450 - by screening for drugs which reduce the catabolism of retinoic acid, useful
                                                                                                                               Determination of a predisposition to glaucoma by analysing mutations in
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             screening for drugs which reduce the catabolism of retinoic aci
in cancer chemotherapy and the treatment of acne and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                     The invention relates to a method for the determination of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Retinoid regulated gene; cytochrome P450 gene; enzyme; oxidative metabolism; P450RAI; retinoic acid; RA; promoter.
                                                                                                                                                                                                                                                                                                                                         Length 490;
                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                          Fingert J;
                                                                                                                                                                                                                                                                                                                                        DB 3; Len
                                                                                                                                                                                                                                                                                                                       Query Match 2.1%; Score 7; UB 3
Best Local Similarity 100.0%; Pred. No. 7.2,
                                                                                                                                                                          Disclosure; Page 122-124; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 53-55; 113pp; English.
                                                        Sheffield VC, Alward WLM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW37733 standard; protein; 492 AA.
 9BUS-00056285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97WO-CA000488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-00667546
96US-00724466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TOOH ) UNIV QUEENS KINGSTON
                           (IOWA ) UNIV IOWA RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytochrome zP450RAI protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                               260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                            130 NLLRDKS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-077193/07.
                                                                                     WPI; 2000-022956/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV09251.
                                                                                                   N-PSDB; AAZ37975
                                                                                                                                                                                                                                                                                                           Sequence 490 AA;
                                                                                                                                                the GLC1A gene.
07-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Petkovich PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9749832-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-DEC-1997
                                                       Stone EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW37733:
```

```
This protein comprises a novel zebrafish retinoid metabolising protein, designated zP450RAI. Its amino acid sequence was deduced from a cDNA clone (see AAV12203) isolated from a 6-18 hr embryo library. It includes a haem-binding motif characteristic of cytochrome P450 proteins. zP450RAI is a retinoid oxidase that has the ability to hydroxylate retinoic acid at the 4 position of the beta-ionone ring, and is inducible in epithelial calls exposed to retinoic acid. Zebrafish, human and mouse P450RAIS (see AAW4159-61) are claimed. They can be expressed in host cells and used to metabolize retinoic acid in a organism or cell, in drug screening, and contained an experiment of cancer, actinic keratosis, oral lenkoplakia, secondary tumours of the head and/or neck, non-small cell lung carcinomas, basal cell carcinomas, acute promyelocytic leukaemia, skin cancer, and premalignancy associated with actinic keratosis, acne, psoriasis and/or
                                                                                                                                                                                                                       ó
in general produces enzymes involved in the oxidative metabolism of endogenous and exogenous compounds. The cytochrome P450 nucleotide sequence can be used to induce or suppress the expression of its protein. P450RAI is highly induced by RA in cell lines and tissues. This allows for development of a drug screen using promoters and nucleotide sequences to identify drugs which are useful for reducing the catabolism of RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Retinoid metabolising protein - useful to develop products to treat, e.g. cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Retinoid metabolising protein, P450RAI; retinoid oxidase; retinoic acid; zebrafish; inhibitor; antibody; cancer; actinic keratosis; oral leukoplakia; head tumour; neck tumour; nock tumour; non-small cell lung carcinoma; basal cell carcinoma; acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis;
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                         ö
                                                                                                                                                                          2.1%; Score 7; DB 2; Length 492;
100.0%; Pred. No. 7.3e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zebrafish retinoid metabolising protein zP450RAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beckett BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 50-51; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 AAW44159 standard; protein; 492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy; diagnosis; screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-CA000440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-00724466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TOOH ) UNIV QUEENS KINGSTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-00667546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petkovich PM, White JA,
                                                                                                                                                                                                                                                                                            282 SLOAMKE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-077178/07.
                                                                                                                                                                                                                                                          45 SLQAMKE 51
                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAV12203
                                                                                                                                         Sequence 492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9749815-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Danio rerio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-DEC-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ichthyosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW44159;
                                                                                                                                                                              Query Match
                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                      RESULT 89
                                                                                                                                                                                                                                                                                                                                                                        AAW44159
  88888888888
                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                 8
```

Gaps

.. 0

```
The present invention provides a novel all-trans-RA metabolising cytochrome P450, P450RAI-2, that is predominantly expressed in the brain. This novel cytochrome P450 is useful for metabolising retinoic acid in a cell or organism, for screening for their effect of protein activity, oxidizing a retinoid, screening an agent for its effect on protein activity. The P450RAI-2 polypeptide, nucleic acid and host cells containing them are useful for treating anser, wysplasia, an autoimmune or dermatological disease. A drug which has an effect on the expression of P450RAI-2 is used to inhibit retinoic acid metabolism in the treatment concern, actinic keratosis, oral leukoplakia, a secondary head and/or neck
                                                                                                                                                                                                                                                                                                                                                                                                                         Cytochrome P450; P450RAI-2; brain; retinoic acid; cancer; dysplasia; autoimmune; dermatological; cytostatic; antiinflammatory; antiseborrheic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tumour, a non-small cell lung carcinoma, a basal cell carcinoma, skin cancer, and a premalignancy associated actinic keratosis, acne, psoriasis, ichthyosis, and/or preferably acute promyelocytic leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel P450 protein useful for metabolizing retinoic acid for treating cancer, dysplasia, an autoimmune or dermatological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a zebrafish P450RAI protein that hydroxylates retinoic acid at the 4 position of the beta-ionone ring (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 4; Length 492;
100.0%; Pred. No. 7.3e+02;
ive 0; Mismatches 0; Indels
                                                                          Length 492;
                                                                                                        0; Indels
                                                                      DB 2; Le
                                                                                                                                                                                                                                                                                                                                                                                        Zebrafish cytochrome P450 polypeptide, P450RAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ramshaw H;
                                                                    2.1%; Score 7; DB 2
100.0%; Pred. No. 7.3
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 106; Page 164-166; 174pp; English.
                                                                                                                                                                                                                                                               AAB85155 standard; protein; 492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             antipsoriatic; immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-1999; 99US-0171110P.
27-JAN-2000; 2000US-0178314P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-2000; 2000WO-CA001493.
                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                   Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White JA, Petkovich PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CYTO-) CYTOCHROMA INC.
                                                                                                                                                                         282 SLQAMKE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
-hea 7; Conserva
                                                                                                                                         45 SLQAMKE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-390242/41.
                                 Sequence 492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAH22442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200144443-A2.
                                                                                                                                                                                                                                                                                                                                    11-SEP-2003
22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Danio rerio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUN-2001.
ichthyosis
                                                                                                                                                                                                                                                                                                    AAB85155;
                                                                    Query Match
                                                                                                                                                                                                                             RESULT 90
                                                                                                                                                                                                                                                AAB85155
                                                                                                                                         à
```

```
The present invention describes a polyclonal antibody (I) to a human cytochrome P450 retinoic acid metabolising peptide (P450RAI-2) comprising a sequence (see ABP52142) of 512 amino acids. (I) has expostatic, immunosuppressive and dermatological activities, and can be used in antisense therapy. (I) can be used for inhibiting P450RAI-2 induced articolar adjustment as cancer, actinic keratosis, oral reated for a disease such as cancer, actinic keratosis, oral leucoplasia, secondary tumour of the head and/or neck, non-small cell lung carcinoma, basal cell carcinoma, acute promyelocytic leukaemia, or leucoplasia and/or ichthyosis, or an in vitro system. (I) is useful for sereaning for the expression of P450RAI-2 in a sample, where the antibody interaction of P450RAI-2 in a sample, where the antibody interaction is detected by an BIISA assay.

Substrate and the antibody interaction is detected by an BIISA assay.

This method is useful for diagnosing non small lung cell carcinoma in a patient. The present sequence represents a zebrafish protein which is from the present invention. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polyclonal antibody specific to human cytochrome P450 retinoic acid metabolizing protein, P450RAI-2, useful for inhibiting P450RAI-2 induced retinoic acid hydroxylation in a human being treated for cancer.
                                                                                                                                                                                                                                                                                           Cytochrome P450; dermatological disorder; cancer; brain disorder; cytostatic; immunosuppressive; dermatological; antisense therapy; P450RAL-2; inhibiting P450RAL-2 induced retinoic acid hydroxylation; actinic keratosis; oral leucoplasia; tumour; basal cell carcinoma; non-small cell lung carcinoma; acute promyelocytic leukaemia; acne;
                                                                                                                                                                                                                                                         Zebrafish P450RAI-2 homologous protein sequence SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ramshaw H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 164-166; 179pp; English.
                                                                                                                          ABP52146 standard; protein; 492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-2001; 2001WO-CA001805.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-2000; 2000WO-CA001493.
                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petkovich PM,
                                                                                                                                                                                                                                                                                                                                                                                            psoriasis, ichthyosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CYTO-) CYTOCHROMA INC.
                                                                                                                                                                                                        (revised)
                                 282 SLOAMKE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-583506/62.
45 SLOAMKE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABQ74193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200248334-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Danio rerio.
                                                                                                                                                                                                    29-AUG-2003
                                                                                                                                                                                                                      13-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                White JA,
                                                                                                                                                                ABP52146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      field)
                                                                                     RESULT 91
                                                                                                             ABP5214(
                           g
                                                                                                                              ö
```

ö

Gaps ö

2.1%; Score 7; DB 5; Length 492; 100.0%; Pred. No. 7.3e+02; tive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 7; Conservative

Gaps

.;

Conservative

```
23-SEP-1996 (first entry)
                                                                                                                                                                                        Region
                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New DNA fragments having promoter activity, useful in retinoid metabolism, as well as in producing retinoic acid metabolizing cytochrome P450s that are useful as targets for the treatment of certain cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to retinoid (e.g., retinoic acid (RA), vitamin A) metabolising proteins and nucleic acid sequences encoding them. RA metabolising proteins contain a haeme-binding motif which is characteristic of the group of proteins known as cytochrome P450s. The sequences of the invention are useful in retinoid metabolism and in producing retinoic acid metabolishing cytochrome P450s. They are producing retinoic as targets for the treatment of certain cancers and as prostate cancer. The invention also relates to a method of screening drugs for their effect on activity of RA inducible proteins. The present sequence is P450RAI protein from zebrafish. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                       Zebrafish, retinoid metabolism; retinoic acid; RA; haeme-binding motif, vitamin A; cytochrome P450; prostate cancer; drug screening; P450RAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 5; Length 492; 100.0%; Pred. No. 7.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Petkovich PM, White JA, Beckett BR, Jones G;
                                                                                                   AAE15325 standard; protein; 492 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 2C; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          96US-00724466.
97WO-CA000440.
                                                                                                                                                                                                                                                                                                                                                                              97US-008B2164
                                                                                                                                                                                                                                                                                                                                                                                                            96US-00667546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TOOH ) UNIV QUEENS KINGSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%
7; Conservative
                                                                                                                                                                                (first entry)
                                                                                                                                                                                                           Zebrafish P450RAI protein.
                                                                                                                                                                 (revised)
                          282 ŚLOAMKE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-033254/04.
N-PSDB; AAD24484.
45 SLQAMKE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 492 AA;
                                                                                                                                                                                                                                                                                                                  US6306624-B1
                                                                                                                                                                                                                                                                                                                                                                           25-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-1996;
                                                                                                                                                              29-AUG-2003
07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                23-OCT-2001.
                                                                                                                                                                                                                                                                                     Danio rerio
                                                                                                                                  AAE15325;
                                                                       RESULT 92
                                                                                       AAE15325
                                                                                                   ò
```

```
Trabecular meshwork induced glucocorticoid response protein - useful to treat glaucoma and diagnose glaucoma, steroid sensitivity and related
                                     Trabecular meshwork induced glucocorticoid response protein; TIGR; glaucoma; therapy; diagnosis.
                 Trabecular meshwork induced glucocorticoid response protein.
                                                                                                                                                                                                                                                                                                                                                                              231. 232
/label= Heparin_sulphate_initiation_domain
                                                                                                                                                                                                                                                                                                                                                                    label= Heparin_sulphate_initiation_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label= Heparin_sulphate_initiation_domain
                                                                                                                            label= Consensus_leucine_zipper_unit
                                                                                                                                       12. 99
|label= Consensus_leucine_zipper_unit
                                                                                                                                                        10. .113
|abel= Heparin_sulphate_binding_site
                                                                                                                                                                                      Consensus_leucine_zipper_unit
                                                                                                                                                                                                28. .135 _ _ label= Consensus_leucine_zipper_unit
                                                                                                                                                                                                                            label= Consensus_leucine_zipper_unit
                                                                                                                                                                                                                                                 Consensus_leucine_zipper_unit
                                                                                                                                                                                                                                                                    Consensus_leucine_zipper_unit
                                                                                                                                                                                                                                                                             46. 150
label= Heparin_sulphate_binding_site
                                                                                                                                                                                                                                                                                                49. 159 _______label= Consensus_leucine_zipper_unit
                                                                                                57. .60
|Tabel= N-glycosylation_site
                                                                                                                                                                                                                                                                                                                   121. .222
| label = 0-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            453. .457
/label= 0-glycosylation_site
457. .459
/label= 0-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                     .306
|abel= 0-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                 /label= 0-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= 0-glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                            label= 0-glycosylation_site
                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huang W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1A-1D; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US014024
                                                                                                                                                                                                                                    /label= r~
42
                                                                                                                                                                          .128
/label= r
                                                                                                                                                                                                                                                          142. .149
'label= Co
                                                                                                                                                                                                                                                                                                                                                                                                .272
                                                                                                                                                                                                                      .142
                                                                                                                                                                                                                                                                                                                                         . 223
                                                                                                                                                                                                                                                                                                                                                                                                                                          .325
                                                                                                                                                                                                                                                                                                                                                                                                                                                             .401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'guyen TD, Polansky JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-251761/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT30152
                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                    Homo sapiens
                                                                                                                                                        Binding-site
                                                                                                                                                                                                                                                                            Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9614411-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases.
```

Gaps ..

AAR98225 standard; protein; 497 AA.

RESULT 93

**AAR98225** 

AAR98225;

282 SLQAMKE 288

g à

45 SLOAMKE 51

```
.
0
                   A novel trabecular meshwork induced glucocorticoid response protein (AAR98225), TIGR, is highly induced by glucocorticoids in the endothelial lining of the human trabecular meshwork. Excessive levels of TIGR are indicative of glaucoma. TIGR can be obtd. by expressing TIGR-encoding CDNA (see also AAR30152-53) in a bacterial or eukaryotic host. It can be sensitivity and related diseases. Leucine zipper-contg. peptides of TIGR encome.
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glucocorticoid-induced protein; TIGR; trabecular meshwork; glaucoma.
                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 2; Length 497;
100.0%; Pred. No. 7.3e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Heparin sulfate initiation domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Heparin sulfate initiation domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Heparin sulfate initiation domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Heparin sulfate binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Heparin sulfate binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                397. .401
/note= "O-Glycosylation site"
453. .457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "O-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "O-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Leucine zipper unit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "O-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "O-Glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Leucine zipper unit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Leucine zipper unit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Leucine zipper unit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Leucine zipper unit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Leucine zipper unit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Leucine zipper unit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glucocorticoid-induced protein TIGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW61390 standard; protein; 497 AA.
                                                                                                                                                                                         are also useful diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .60
/note= ""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
92. .99
                                                                                                                                                                                                                                                                                                                                                                                                                            134 NLLRDKS 140
                                                                                                                                                                                                                                                                                                                                                                                    260 NLLRDKS 266
                                                                                                                                                                                                                                            Sequence 497 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW61390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW61390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
$8888888888$8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF THE CONTRACT OF 
                                                                                                                                                                                                                                                                                                                                                                                                                            Ωp
                                                                                                                                                                                                                                                                                                                                                                                  ð
```

```
The glucocorticoid induced protein, TIGR is produced by cells of the trabecular meshwork. By determining if the amount of TIGR present in the trabecular meshwork of an eye of a patient exceeds the amount of the protein present in the trabecular meshwork of an eye of an individual who does not have, and is not predisposed to have glaucoma, you can diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                          Diagnosis of glaucoma or steroid sensitivity - by protein detection or
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 2; Length 497;
100.0%; Pred. No. 7.3e+02;
ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 49261.
                      /note= "O-Glycosylation site"
 /note= "O-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG39772 standard; protein; 497 AA.
                                                                                                                                                                      Nguyen TD;
                                                                                                                                                                                                                                                                                                                                                                                  2.13,
100.0%; Pre
                                                                                                                                                                                                                                                           Claim 67; Fig 1; 26pp; English.
                                                                                         96US-00649432
                                                                                                              94US-00336235,
95US-00546568,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          990S-0123548P.
990S-0125788P.
99US-0126264P.
99US-0126785P.
99US-0127462P.
99US-0128234P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-2000; 2000EP-00301439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0121825P.
               .459
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                        the presence of glaucoma
                                                                                                                                               (REGC ) UNIV CALIFORNIA
                                                                                                                                                                    Polansky JR, Huang W,
                                                                                                                                                                                                                                    polymorphism analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                              260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana.
                                                                                                                                                                                         WPI; 1998-446069/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 NLLRDKS 140
                                                                                                                                                                                                     N-PSDB; AAV28331
                                                                                                                                                                                                                                                                                                                                                             Sequence 497 AA;
          Modified-site
                                                                                         17-MAY-1996;
                                                                                                             03-NOV-1994;
20-OCT-1995;
                                           US5789169-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-1999;
05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG39772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG397
₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
```

0;

19-701-1 19-701-1 20-701-1 20-701-1 20-701-1 20-701-1 21-701-1 22-701-1 22-701-1 23-701-1 23-701-1 23-701-1 23-701-1 23-701-1	27 - JUL - 1 27 - JUL - 1 27 - JUL - 1 28 - JUL - 1 28 - JUL - 1 28 - JUL - 1 20 - AUG - 1 30 - AUG - 1 30 - AUG - 1 30 - AUG - 1 30 - AUG - 1 30 - AUG - 1 30 - AUG - 1 30 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 - AUG - 1 31 -	13-AUG-11 13-AUG-11 17-AUG-11 17-AUG-11 18-AUG-12 20-AUG-12 23-AUG-12 23-AUG-12 22-AUG-19 27-AUG-19 27-AUG-19 31-AUG-19	01-SEP-19 10-SEP-19 11-SEP-19 11-SEP-19 11-SEP-19 16-SEP-19 23-SEP-19 23-SEP-19 24-SEP-19 24-SEP-19 28-SEP-19 04-OCT-19 06-OCT-19 06-OCT-19 13-OCT-19
***************************************	K K K K K K K K K K K K K K K K K K K		Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z Z
4449 4447 4447 4477 4919 4919 6019 6019 6019 6019 6019 6019 6019 6	709- 4688- 5241- 5241- 529- 529- 5229- 5229- 549- 649- 649- 649- 649- 649- 649- 649- 6	22 F. 44P. 77P. 77P. 70P. 00P. 00P. 77P. 77P. 74P.	######################################
990S-01296 99US-01306 99US-01308 99US-01308 99US-01318 99US-01324 99US-01324 99US-01324 99US-01324 99US-01324 99US-01328	990S-01343 990S-01343 990S-01351 990S-01353 990S-01356 990S-01356 990S-01367 990S-01375 990S-01375 990S-01375 990S-01385 990S-01385	990S-01394 990S-01394 990S-01394 990S-01394 990S-01394 990S-01394 990S-01394 990S-01394 990S-01394 990S-01394 990S-01394	99US-0140695P 99US-014082P 99US-0141287P 99US-0141124P 99US-0142154P 99US-01420EP 99US-01420EP 99US-014290P 99US-014292P 99US-014362P 99US-014362P 99US-014362P 99US-014408EP 99US-014408EP 99US-0144331P 99US-0144331P
	14-MAX-1999; 19-MAX-1999; 20-MAY-1999; 20-MAY-1999; 24-MAY-1999; 25-MAY-1999; 27-MAY-1999; 27-MAY-1999; 01-JUN-1999; 01-JUN-1999; 04-JUN-1999; 04-JUN-1999; 04-JUN-1999; 10-JUN-1999; 10-JUN-1999; 10-JUN-1999; 14-JUN-1999; 16-JUN-1999; 16-JUN-1999; 16-JUN-1999;		
<u> </u>	ម្តាយ ជា ជា ជា ជា ជា ជា ជា ជា ជា ជា ជា ជា ជា		X X X X X X X X X X X X X X X X X X X

PR 19-UUL-1999) PR 19-UUL-1999) PR 20-UUL-1999) PR 20-UUL-1999) PR 20-UUL-1999) PR 20-UUL-1999) PR 21-UUL-1999) PR 22-UUL-1999) PR 22-UUL-1999) PR 22-UUL-1999) PR 22-UUL-1999) PR 22-UUL-1999) PR 22-UUL-1999) PR 22-UUL-1999) PR 22-UUL-1999) PR 23-UUL-1999) PR 22-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-UUL-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999) PR 23-EEP-1999)	9US-0144333 9US-0144335 9US-0144335 9US-0144632 9US-0144632 9US-0144632 9US-0145086 9US-0145089 9US-0145089 9US-0145089 9US-0145089 9US-0145192 9US-0145192	99US-0145276P. 99US-0145913P. 99US-0145913P. 99US-0145913P. 99US-0145951P. 99US-0146386P. 99US-0146389P. 99US-0147302P. 99US-0147302P. 99US-0147302P. 99US-0147302P. 99US-0147302P. 99US-0147302P. 99US-0147303P. 99US-0147303P. 99US-0147303P. 99US-014816P. 99US-014816P. 99US-0148171P. 99US-0148319P. 99US-0148319P. 99US-0148319P. 99US-014831P. 99US-014831P. 99US-014831P. 99US-014831P. 99US-014831P. 99US-014831P. 99US-014831P.	US-0149922P US-0149922P US-0149930P US-0150864P US-01510665P US-01510666P US-0151303P US-0151303P US-0153353P US-0153353P US-0153353P US-0153353P US-0153353P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P US-0154339P
	19-JUL-199 RR 19-JUL-199 RR 20-JUL-199 RR 20-JUL-199 RR 20-JUL-199 RR 21-JUL-199 RR 21-JUL-199 RR 22-JUL-199 RR 22-JUL-199 RR 23-JUL-199 RR 23-JUL-199	26 - JUL - 1995 27 - JUL - 1995 27 - JUL - 1995 28 - JUL - 1995 28 - JUL - 1995 02 - AUG - 1995 03 - AUG - 1999 04 - AUG - 1999 05 - AUG - 1999 06 - AUG - 1999 06 - AUG - 1999 11 - AUG - 1999 11 - AUG - 1999 13 - AUG - 1999 13 - AUG - 1999 14 - AUG - 1999 15 - AUG - 1999 16 - AUG - 1999 17 - AUG - 1999 18 - AUG - 1999 18 - AUG - 1999 18 - AUG - 1999 18 - AUG - 1999 18 - AUG - 1999 18 - AUG - 1999 18 - AUG - 1999 18 - AUG - 1999 18 - AUG - 1999 18 - AUG - 1999	23AUG-1999 23AUG-1999 25AUG-1999 26AUG-1999 27AUG-1999 31AUG-1999 31AUG-1999 31AUG-1999 31AUG-1999 31AUG-1999 31AUG-1999 31AUG-1999 32SEP-1999 33AUG-1999 34SEP-1999 35AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36AUG-1999 36A

· 0

0; Gaps

```
The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and insecticides, theractions in higher eukaryotes for the development of discloses genomic DNR sequences (ABLIG176-ABL30511), expressed DNR sequences (ABLIG176-ABL30511), expressed DNR ABR72072). The sequence data for this partent did not form part of the printed specification, but was obtained in electronic form part of the from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to determining whether a subject has or is at risk of developing glaucoma, retinal degenerative disease, or a cardiovascular disease, comprises generating a transcriptional or translational profile (i.e. 'fingerprint') in the subject or in a sample obtained from the subject, based on the expression of the different myocilin (MYOC, also Known as trabecular meshwork inducible glucocorticoid responsive protein, TIGR) mRNA species or polypeptide forms, where a difference in the profile relative to that in a normal subject indicates that the subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining the presence or the risk of having glaucoma, retinal degenerative or cardiovascular diseases in a subject, comprises generating transcriptional or translational profiles based on myocilin
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; TIGR; MYOC; Myocilin; Glaucoma; blindness; trabecular meshwork inducible glucocorticoid responsive protein; retinal degenerative disease; RD; retinitis pigmentosa; macular degeneration; Usher syndrome; cardiovascular disease; congenital heart disease; myocardial ischaemia; stroke; acute endocardiis; hypertenive heart disease; arrhythmia;
                                                                                                                                                                                        2.1%; Score 7; DB 4; Length 500; 100.0%; Pred. No. 7.4e+02; ative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                 ABU07341 standard; protein; 500 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arteriosclerotic heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18; Fig 3; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                Human TIGR/Myocilin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-DEC-2001; 2001WO-US048622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2001; 2001US-0281442P.
23-JUL-2001; 2001US-0306889P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABX10137, ABX10138.
                                                                                                                                                                         Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acids and proteins.
                                                                                                                                                                                                                                                                    124 LLVTLIA 130
                                                                                                                                                                                                                                             84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-058597/05
                                                                                                                                                                                                                                         78 LLVTLIA
                                                                                                                                                              Sequence 500 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KONG/) KONG T H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200282969-A2.
                                                                                                                                                                                                                                                                                                                                                                                      27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                            ABU07341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kong TH;
                   8×666666666666888
                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, SEQ ID NO 23829; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 3; Length 497;
100.0%; Pred. No. 7.36+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 23829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB65679 standard; protein; 500 AA.
                                      990S-015931P
990S-0159637P
990S-0159638P
990S-0159684P
990S-0160741P
990S-0160767P
                                                                                                                                               99US-0160814P.
99US-0160815P.
99US-0160980P.
                                                                                                                                                                                    99US-0160981P.
99US-0160989P.
99US-0161404P.
                                                                                                                                                                                                                                                    99US-0161359P.
                                                                                                                                 99US-0160770P
                                                                                                                                                                                                                          99US-0161405P
                                                                                                                                                                                                                                                                              99US-0161361P.
                                                                                                                                                                                                                                                                                                                  99US-0161993P.
                                                                                                                                                                                                                                        99US-0161406P
                                                                                                                                                                                                                                                                                                       99US-0161992P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2000; 2000US-0191637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-2000; 2000US-00614150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                   144 LYSSGLL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                          73 LYSSGLL 79
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABL09782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200171042-A2.
                                                                                       21-0CT-1999
                                                                                                      21-0CT-1999
                                                                                                                  21-0CT-1999
                                                                                                                                                                      22-OCT-1999
                                                                                                                                                                                 -OCT-1999
                                                                                                                                                                                             22-OCT-1999
                                                                                                                                                                                                           25-OCT-1999
                                                                                                                                                                                                                                     25-OCT-1999
                                                                                                                                                                                                                                                26-0CT-1999
                                                                                                                                                                                                                                                                26-OCT-1999
                                                                                                                                                                                                                                                                          26-OCT-1999
                                                                                                                                                                                                                                                                                         28-OCT-1999
                                                                                                                                                                                                                                                                                                    28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB65679;
                                                                                                                                                                                                                       25-OCT-
                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB65679
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                dd
```

```
has or is at risk of developing the above-mentioned diseases. Also proluded are: (1) a method for establishing MYOC genetic population of profile in a population of individuals having glaucoma, retinal degenerative disease, or a cardiovascular disease, or a cardiovascular disease, comprising determining disease, or a cardiovascular disease, comprising determining MYOC genetic profile of an individual disease, comprising determining MYOC genetic profile of an individual and disease, comprising determining MYOC genetic profile of an individual and comparting the individual's MYOC genetic profile of an individual and a kit for determining whether a subject has or is likely individual; and a kit for determining whether a subject has or is likely conclete acid, or an antibody or peptide sprobe of specifically conclete acid, or an antibody or peptide sprobe capable of specifically conclete acid, or an antibody or peptide sprobe capable of specifically conclete acid, or an antibody or peptide sprobe or primer which hybridises to the MYOC binding to the novel MYOC polypeptide(s), and instructions for use. The method is useful for the prognosis and/or disagnosis of glaucoma, retinal degenerative diseases (RDD) or cardiovascular diseases (RDD) or cardiovascular diseases (RDD) or cardiovascular diseases (RDD) or cardiovascular diseases, myocardial ischaemia, stroke, acute endocarditis, disease, myocardial ischaemia, stroke, acute endocarditis, disease), and in screening assays for the identification of therapeutics mentioned diseases in a subject. The present sequence represents the human MyOC protein
              BBBBBBBBBBBBBBBBBBBBBBBBB
```

```
2.1%; Score 7; DB 6; Length 500;
100.0%; Pred. No. 7.46+02;
tive 0; Mismatches 0; Indels
                                                             Conservative
                                                                                       260 NLLRDKS 266
                                                                                                                     144 NLLRDKS 150
                           Query Match
Best Local Similarity
Sequence 500 AA;
                                                          Matches
                                                                                       ò
                                                                                                                   d
```

Gaps

·,

ADE54515 standard; protein; 502 AA. 29-JAN-2004 (first entry) ADE54515; 

Rat Protein Q9RlJ4, SEQ ID NO 318. Rattus norvegicus.

Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

WO2003016475-A2

27-FEB-2003.

14-AUG-2002; 2002WO-US025765.

14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P.

Costigan M; (GEHO ) GEN HOSPITAL CORP. Woolf C, D'urso D, (FARB ) BAYER AG.

Befort K, WPI; 2003-268312/26. New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat

Claim 48; Fig 8; 105pp; English.

```
derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the westor, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a that subjected to pain and a pray, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal the expression of a polynucleotide sequence of the capression of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the composition, a method for identifying a compound that regulates the activity of one or more of the composition, a method for pain, a method for pain, a method for producing a pharmaceutical composition, a continity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating computates the activity of one or more of the pain and a pharmaceutical composition comprising the one or more of pain and a pharmaceutical composition comprising the one or more of polypeptides or their antibodies. The polymoleotide or the compound that modulates its activity is useful for preparing a medicament for treating continies of the polymoleotide. The polymoleotide or the compound that main a server of the properties or their animal mans a man and the preparing a medicament for treating continies of the pain animal mans a server of the pain and a pharmaceutical mans animal mans and a pharmaceutical mans and a pharmaceutical mans animal man and a pharmaceutical mans and a pharmaceutical mans and a pharmaceutical mans and a pharmaceutical mans and a pharmaceutical mans and a mans and a pharmaceutical mans and a pharmaceutical mans and a pharmaceutical mans and a pharmaceutical mans and a pharmaceutical mans and a pharmaceutical mans and a pharmaceutical mans and a pharmaceutical mans and a pharmaceutical mans and a ph
  human polynucleotides or a polynucleotide which represents a fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; trabecular meshwork induced glucocorticoid response protein; human; diagnosis; glaucoma; polymorphism; steroid sensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (Chung), chronic constriction therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of TIGR nucleic acid sequences - used for, e.g. developing products for diagnosis, prognosís and treatment of glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 7; Length 502;
100.0%; Pred. No. 7.4e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW64669 standard; protein; 504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US000468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-00791154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-00938669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polansky JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 NILRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 NLLRDKS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human TIGR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-427946/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAV51391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9832850-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUL-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nguyen TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW64669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW64669
q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
```

ò

Gaps

.. 0

```
glucocorticoid response protein (TIGR) which is used in a method for diagnosing glaucoma in a patient. The method involves the detection of polymorphisms whose presence is predictive of a mutation affecting TIGR response in the patient and can be diagnostic of glaucoma or steroid sensitivity. Base substitutions and base additions upstream of and within TIGR exons can also be used to diagnose glaucoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This represents a human GLC1A protein sequence. The human GLC1A gene is associated with juvenile open angle glaucoma (30AG). The gene can be used for the development of assays for identifying molecules that modulate (agonists or antagonists) the bioactivity of a functional or mutant gene or protein. Modulators may be an antibody, protein, peptide or mutant triple helix forming nucleic acid, e.g. antisense sequence, ribozyme or a subject with glaucoma or at sisk for developing glaucoma to prevent or reduce the severity of the condition. Derivatives of GLC1A gene can be used to detect lessins of the GLC1A gene which are indicative of glaucoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated gene associated with glaucoma - used to develop products to determine whether a subject has, or is at risk of, developing glaucoma, and for treating or preventing glaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glaucoma; GLCIA; treatment; mutant; juvenile open angle glaucoma; JOAG.
                  sequence represents a novel human trabecular meshwork induced
                                                                                                                                                                       2.1%; Score 7; DB 2; Length 504;
100.0%; Pred. No. 7.4e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human glaucoma associated protein GLCIA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "encoded by NCA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 92-94; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sheffield V, Alward WLM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            AAW60670 standard; protein; 504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-US020702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-00748479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-00791347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-00822999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IOWA ) UNIV IOWA RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV37618, AAV37619.
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                    260 NLLRDKS 266
                                                                                                                                                                                                                                                                  144 NLLRDKS 150
                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-286947/25
                                                                                                                                        Sequence 504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-1997;
21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9820131-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stone EM,
                                                                                                                                                                                                                                                                                                                                                                             AAW60670
                                                                                                                                                                                                                                                                                                                  100
                This
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                              RESULT 10
X88888888888888
                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                g
```

```
Gaps
                                                                                                                                                                                        Irabecular meshwork induced glucocorticoid response*; TIGR*; human;
                                              .,
                                                                                                                                                                        Trabecular meshwork induced glucocorticoid response* protein.
                           DB 2; Length 504; 7.4e+02;
                                            Indels
                                                                                                                                                                                                                                                                                                       "consensus leucine zipper unit"
                                                                                                                                                                                                                                                                                                                         "consensus leucine zipper unit"
                                                                                                                                                                                                                                                                                                                                                                            "consensus leucine zipper unit"
                                                                                                                                                                                                                                                                                                                                           /note= "consensus leucine zipper unit"
                                                                                                                                                                                                                                                                                                                                                            "consensus leucine zipper unit"
                                                                                                                                                                                                                                                                                                                                                                                                                              "consensus leucine zipper unit"
                                                                                                                                                                                                                                                                                                                                                                                             /note= "consensus leucine zipper unit"
                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                               "heparin sulphate binding"
                                                                                                                                                                                                                                                                                       "Asn is N-glycosylated"
                         2.1%; Score 7; DB 2
100.0%; Pred. No. 7.4.
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "initiation domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "initiation domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "initiation domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "O-glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "O-glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "O-glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              464. .466 /note= "O-glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                "O-glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "0-glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "O-glycosylation"
                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                  /label= Sig_peptide
                                                                                                                                                                                                                                                                    label= Mat_protein
                                                                                                                      AAW70496 standard; protein; 504 AA.
                                                                                                                                                      11-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                     .152
                                                                                                                                                                                                                                                                                                                                                    .145
                                                                                                                                                                                                                                                                                                                                                                                      .159
                                                                                                                                                                                                                                                                                                                                                                                                      .160
                                           Conservative
                                                                                                                                                                                                                                                                                                                                 .138
                                                                                                                                                                                                                                                                                                                                                                                                                       .166
                                                                                                                                                                                                                                                                                                                                                                                                                                       .232
                                                                                                                                                                                                                                                                                                                                                                                                                                                        .233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .464
                                                                                                                                                                                                                                                                                                                 66.
                                                                                                                                                                                                                                                                                                . 92
                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                note=
                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note=
                                                                                                                                                                                                                                                                                                         'note=
                                                                           144 NLLRDKS 150
                                                           260 NLLRDKS 266
                                                                                                                                                                                                   glaucoma; diagnosis.
                                 Local Similarity
nes 7; Conserv
        Sequence 504 AA;
                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                    Binding-site
                                                                                                                                     AAW70496;
                         Query Match
                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                             Protein
                                                                                                   RESULT 101
AAW70496
                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                        Matches
                                                                                                                             X S
                                                           ò
                                                                          g
```

WO9844108-A1

or predisposition to glaucoma

```
à
                                                                                                                                                                                                                                                                                                                                          This is the amino acid sequence of a new human 55 kDa protein, designated trabecular meshwork induced glucocorticoid response* (TIGR*) protein, that is highly induced by glucocorticoids in the endothelal lining of the the buman trabecular meshwork (HTM). The sequence was deduced from an isolated cDNA clone (see AAV31484). Studies of the recombinant protein suggest (1) that the 55 kDa protein exists both in cells and in the mediuw, (2) that it undergoes oligomerisation, (3) phosphorylation, (4) glycosylation, (5) that it is susceptible to metalloprotease, (6) that it carbibits high affinity binding to extracellular matrix and HTM cells, (7) that it exhibits bind affinity binding to extracellular matrix and HTM cells, (7) that it exhibits so extracellular matrix and HTM cells, (7) that it exhibits so compared to normal patients. TIFR* cDNA, the cultures, and (8) that it exhibits high expression in the HTM of glaucomatous patients as compared to normal patients. TIFR* cDNA, the protein itself, molecules that bind it, and nucleic acid molecules that cenced it, provide improved methods and reagents for diagnosing glaucoma and related disorders, such as cardiovascular and immunological diseases that affect expression of TIGR*. A claimed method of diagnosing glaucoma involves determining if the amount of TIGR* present in the HTM exceeds the amount found in an individual not predisposed to the disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trabecular meshwork induced glucocorticoid response; TIGR; MYOC; GLClA; locus; chromosome; detection; mutant; allele; heterozygote; mutation; juvenile open-angle glaucoma; phenotype; homoallelic complementation; autosomal dominant disease; homozygote; epilepsy; mental retardation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                   New protein induced in trabecular meshwork cells by glucocorticoids useful in the diagnosis of glaucoma and related diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 7; DB 2; Length 504; 100.0%; Pred. No. 7.4e+02; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY07393 standard; protein; 504 AA.
                                                                                                                                                       Huang W;
                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1A-C; 53pp; English.
                                      97WO-US005801,
                                                                         97WO-US005391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-CA000923.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97CA-02216997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                   Nguyen TD, Polansky JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human TIGR/MYOC protein.
                                                                                                            (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 NLLRDKS 150
                                                                                                                                                                                            WPI; 1998-542701/46,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    haploinsufficiency.
                                                                                                                                                                                                               N-PSDB; AAV33484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP-1998;
                                                                         01-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9916898-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JUL-1999
08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY07393
```

ò

```
This sequence represents the protein encoded by the trabecular meshwork induced glucocorticoid response (TIGR) gene, also known as MYOC, which is mapped to the GLCIA locus on chromosome 1923-925. The invention relates to the detection of mutant and non-mutant alleles of the TIGR/MYOC gene. Juvenile open-angle glaucoma, in a heterozygotic carrier of TIGR mutations, can be treated by overexpression of mutated TIGR, which renders the phenotype of the patient normal by homoallelic complementation. This method of homoallelic complementation can be used in other autosomal dominant diseases where mutant homozygotes are phenotypically normal, e.g. a form of epilepsy and mental retardation linked to chromosome X, which only affects women. The methods can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR protein, trabecular meshwork induced glucocorticoid response, secretory protein, antibody, glaucoma; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody to trabecular meshwork protein - useful for diagnosis
                                                                                                                                  Molecular diagnosis of glaucomas associated with chromosome 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trabecular meshwork induced glucocorticoid response protein.
                                                            Anctil J;
                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 2; Length 504;
100.0%; Pred. No. 7.48+02;
live 0; Mismatches 0; Indels
                                                            Cote G,
                                                          Falardeau P,
                                                                                                                                                                                                                                                                                                                                                                used for treating haploinsufficiency
                                                                                                                                                              Disclosure, Fig 1A-J; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW73500 standard; protein; 504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nguyen ID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Col 25-28; 22pp; English.
98CA-02231720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-00336235.
95US-00546568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-00645900.
                                                          Morissette J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
Les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polansky JR, Huang W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 NLLRDKS 150
                                                                                     WPI; 1999-263703/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-069807/06.
                            (UYLA-) UNIV LAVAL.
                                                                                                     N-PSDB; AAX57606.
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 504 AA;
12-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5849879-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998
                                                          Raymond V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW73500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alaucoma.
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
```

This sequence represents the human Trabecular meshwork induced

0;

```
Human, trabecular meshwork induced glucocorticoid response protein; TIGR, glaucoma; primary open angle glaucoma; POAG; pigmentary glaucoma; low tension glaucoma; intraocular pressure; steroid; corticosteroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a human secretory protein from clone II.2. The secretory protein is designated TIGR (Trabecular Meshwork Induced Glucocorticoid Response) protein. The protein is highly induced by glucocorticoids in the endothelial lining cells of the human trabecular meshwork. The TICR polynucleotides and proteins can be used as markers for the diagnosis of glaucoma, primary open angle glaucoma (POAG), pigmentary glaucoma, and low tension glaucoma and their related diseases. They can also be used to diagnose or protect an individual's sensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated glaucoma-associated nucleic acids - which encode Trabecular
Meshwork Induced Glucocorticoid Response protein, used to develop
products for diagnosing glaucoma-related diseases.
glucocorticoid response (TIGR) protein. The TIGR protein is a secretory protein specifically bound by the antibody of the invention. The antibody, especially in labelled form, can be used in the diagnosis of glaucoma by detecting elevated levels of the protein in the trabecular meshwork of the eye. Using the antibody, glaucoma is detected more
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 Human trabecular meshwork induced glucocorticoid response protein.
                                                                                                                                                                                    ;
0
                                                                                                                                              2.1%; Score 7; DB 2; Length 504; 100.0%; Pred. No. 7.4e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                      AAW89391 standard; protein; 504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nguyen TD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-00336235.
95US-00546568.
96US-00649432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 1; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-00882238,
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W, Polansky JR,
                                                                                                                              Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                             260 NLLRDKS 266
                                                                                                                                                                                                                                           144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-095006/08
                                                                                                                Sequence 504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV81910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                     08-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5854415-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-0CT-1995
                                                                                  accurately
                                                                                                                                                                                                                                                                                                                                                     AAW89391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huang
                                                                                                                                                                                                                                                                                      RESULT 104
    8 X G G G G G G
                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                        g
```

to elevated intraocular pressure upon administration of steroids such as glucocorticoids or corticosteroids. These products can also be used for diagnosing other diseases or conditions that affect the expression or activity of the protein. The products can also be formulated for administration to patients

Sequence 504 AA;

```
o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predisposition to glaucoma. The method comprises amplifying a GLCIA gene with a primer pair selected from the sequences shown in AAZ37981-Z38008. The primers are used to determine whether a subject has or has the potential to develop primary open wide angle glaucoma. The present sequence represents the human GLCIA polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Determination of a predisposition to glaucoma by analysing mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR; trabecular meshwork inducible glucocorticoid receptor; promoter;
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A trabecular meshwork inducible glucocorticoid receptor protein.
                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                amplification; primary open wide angle glaucoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for the determination of a
   Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 7; DB 3; Length 504;
Pred. No. 7.4e+02;
                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
  DB 2; Ler
                                                                                                                                                                                                                                                                                                                                                                                                              Stone EM, Sheffield VC, Alward WLM, Fingert
2.1%; Score 7; DB 2
100.0%; Pred. No. 7.4
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 117-120; 137pp; English.
                                                                                                                                  AAY49288 standard; protein; 504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY93971 standard; protein; 504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Scor
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                           99WO-US007671.
                                                                                                                                                                                                                                                                                                                                                                 9BUS-00056285
                                                                                                                                                                                                                                                                                                                                                                                       (IOWA ) UNIV IOWA RES FOUND.
                                                                                                                                                                               07-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                         7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                       Human GLC1A polypeptide
                                                260 NLLRDKS 266
                                                                      144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-022956/02.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                Glaucoma; PCR ampl
GLC1A gene; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ37974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the GLC1A gene.
                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                           WO9951779-A2.
                                                                                                                                                                                                                                                                                                                                          07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                 07-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                          AAY49288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY93971;
                                                                                                          RESULT 105
                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                    AAY49288
                                                                                                                                   à
                                                                     д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXEXEXEX
```

```
06-SEP-2000
                                                                         25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                     04-JUN-1999
                                                                                                                                                                                                                                                                9-MAY-1999
                                                                                                                                                                                                                                                                                        24-MAY-1999
                                                                                                                                                                                                                                                                                               MAY-1999
                                                                                                                                                                                                                                                                                                                      01-JUN-1999
                                                                                                                                                                                                                                                                                                                              03-JUN-1999
                                                                                                                                                                                                                                                                                                                                                     08-JUN-1999
                                                                                                                                                                                                                                                                                                      27-MAY-19
28-MAY-19
                                                                                                                                                                                    05-MAY-1
                                                                                                                                                                                                                                 MAY-1
                                                                                                                                                                                                                                                                                                                                                           10-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-1
                                                                                                                                                     8-APR-
                                                                                                                                                                                                                                                        8-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUN-9
                                                                                                                                                                                                                                                                                                                                                                                           -NUL-9
                                                                                                                                                                                                                                                                                                                                                                                                  -KIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                        -NUC-
                                                                                                                                                                                                                                                                                                                                                                                                                         8-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                8-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUT-8.
    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                               Diagnosis, prognosis and treatment of glaucoma, based on detecting specific polymorphisms in the promoter of the trabecular meshwork inducible glucocorticoid receptor gene.
glaucoma; steroid sensitivity; progressive ocular hypertension;
                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 3; Length 504; 100.0%; Pred. No. 7.4e+02; Pretive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 64756.
                                                                                                                           Chen P, Chen H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG51051 standard; protein; 504 AA.
                                                                                                                                                                                               Disclosure; Fig 8; 122pp; English.
                                                                                                                                                                                                                                                                                                                                       sequences in non-human animals
                                                                    11-JAN-2000; 2000WO-US000559.
                                                                                    99US-00227881
99US-00306828
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                         Nguyen TD, Polansky JR,
                                                                                                          (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
                                                                                                                                        WPI; 2000-491060/43.
N-PSDB; AAA57509.
                                                                                                                                                                                                                                                                                                                                                                                                     260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                   144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                         Sequence 504 AA;
                                     WO200042220-A1
                       Homo sapiens.
                                                                                   11-JAN-1999;
07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1033405-A2.
         vision loss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-2000
                                                     20-JUL-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG51051;
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG51051
```

ð

```
99US-0125788P.
99US-0126264P.
99US-0126785P.
99US-0127462P.
99US-0128234P.
                                                                                                                                                                                                                                                 99US-0132485P
99US-0132486P
99US-0132863P
99US-013256P
99US-0134218P
99US-0134219P
99US-0134212P
99US-0134212P
                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0136021P
99US-0136392P
99US-0137222P
99US-0137528P
99US-0137562P
99US-0137724P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0138094P.
99US-0138540P.
99US-0138847P.
99US-0139119P.
                                                                                                                                                          99US-0130449P.
99US-0130510P.
99US-0131449P.
99US-0132448P.
99US-0132448P.
                                                                                                                                                                                                                                                                                                                                                                           99US-0134941P.
99US-0135124P.
99US-0135353P.
99US-0135629P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0139492P.
99US-0139454P.
99US-0139455P.
99US-0139456P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0139750P.
99US-0139763P.
99US-0139817P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0140353P.
99US-0140354P.
99US-0140695P.
25-FEB-2000; 2000EP-00301439
                                                                                                                          99US-0128714P.
99US-0129845P.
                                                                                                                                    99US-0129845P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0139458P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0139453P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0139457P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0139459P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0139460P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0139461P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0141842P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0139462P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0139463P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0139899P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1999;
```

99US-0155139P

```
9905-0142390P

9905-014230P

9905-0144262P

9905-0144362P

9905-0144332P

9905-0144333P

9905-0144333P

9905-0144333P

9905-0144333P

9905-0144333P

9905-0144333P

9905-0144333P

9905-0144332P

9905-0144332P

9905-0144332P

9905-0144332P

9905-0144332P

9905-0144332P

9905-0144332P

9905-0144332P

9905-0144332P

9905-0145268P

9905-0145268P

9905-0145268P

9905-0145268P

9905-0145268P

9905-014532P

9905-014532P

9905-014532P

9905-014532P

9905-014532P

9905-014532P

9905-014532P

9905-014532P

9905-0147332P

9905-0147332P

9905-0147332P

9905-0147332P

9905-0147332P

9905-0147332P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144334P

9905-0144342P

9905-0149368P

9905-0149368P

9905-0149368P

9905-0149323P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 990S-0151066P-
990S-0151060P-
990S-0151303P-
990S-0151438P-
990S-0151438P-
990S-0152363P-
990S-0153758P-
990S-0153758P-
990S-0154018P-
990S-0154018P-
  99US-0142055P
02-7UL-1999;
06-7UL-1999;
09-7UL-1999;
12-7UL-1999;
13-7UL-1999;
14-7UL-1999;
16-7UL-1999;
16-7UL-1999;
16-7UL-1999;
19-7UL-1999;
19-7UL-1999;
19-7UL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-AUG-1999)
31-AUG-1999)
01-SEP-1999)
10-SEP-1999;
11-SEP-1999;
11-SEP-1999;
11-SEP-1999;
20-SEP-1999;
                                                                                                                          20-JUL-1999;
20-JUL-1999;
20-JUL-1999;
                                                                                                                                                               21-JUL-1999;
22-JUL-1999;
22-JUL-1999;
                                                                                                                                                                                                                                                           28-JUL-1999;
02-AUG-1999;
02-AUG-1999;
02-AUG-1999;
04-AUG-1999;
04-AUG-1999;
                                                                                                                                                                                                                                                                                                               05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
06-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1999;
16-AUG-1999;
18-AUG-1999;
20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
25-AUG-1999;
25-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
                                                                                                                                                 21-JUL-1999
                                                                                                                                                                                                                                                                                                                                                       09-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                             12-AUG-1999;
```

```
Human; trabecular meshwork induced glucocorticoid response; TIGR, therapy; glucocorticoid; glaucoma; cardiovascular disorder; steroid; immunological disease; intraocular pressure; chromosome 1; chromosome 10; chromosome 11; chromosome 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human trabecular meshwork induced glucocorticoid response (TIGR) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .15 |
/label= Signal_peptide
16. .504
/note= "Mature human TIGR protein"
57. .60
/note= "Asn is N-Glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 2.1%; Score 7; DB 3; Ler
Local Similarity 100.0%; Pred. No. 7.4e+02;
Les 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE03744 standard; protein; 504 AA.
                990S-0155486F
990S-0155486F
990S-0156488P
990S-0157117P
990S-0157127P
990S-0158029P
990S-0158029P
990S-0158224F
990S-0159230P
990S-0159230P
990S-0159230P
990S-0159330P
990S-0159330P
990S-0159637P
990S-016976P
990S-016976P
990S-0160981P
990S-0160981P
990S-0160981P
990S-0160981P
990S-0160981P
990S-0160981P
990S-0160981P
990S-0160981P
990S-0160981P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0161361P.
99US-0161920P.
99US-0161992P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0162142P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0161993P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAFHVFK 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 EAFHVFK 278
                                                     28-SEP-1999

06-0CT-1999

06-0CT-1999

06-0CT-1999

06-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

14-0CT-1999

14-0CT-1999

14-0CT-1999

14-0CT-1999

14-0CT-1999

12-0CT-1999

12-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0CT-1999

13-0C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE03744;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE03744
ID AAEC
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

administration of steroids

```
/note= "Leucine zipper unit"
146. 150
/note= "Heparin sulphate binding residues"
                                  note= "Heparin sulphate binding residues"
                                                                                                                                     note= "O-glycosylation site"
                                                                                                                                                                                            note= "O-glycosylation site"
05. .306
                                                                                                                                                                                                           note= "O-glycosylation site"
                                                                                                                                                                                                                                                                   "O-glycosylation site"
                                                               note= "Leucine zipper unit"
                                                                                                                      'note= "Leucine zipper unit"
221. .222
                                                                                                                                                   "O-glycosylation site"
                                                                                                                                                                                                                                       note= "O-glycosylation site"
                                                                                                                                                                                                                                                      note= "O-glycosylation site"
        "Leucine zipper unit"
                     "Leucine zipper unit"
                                                 note= "Leucine zipper unit"
                                                                             "Leucine zipper unit"
                                                                                                                                                                               note= "Initiation domain"
                                                                                                                                                                 note= "Initiation domain"
                                                                                                                                                                                                                          note= "Initiation domain"
                                                                                                                                                                                                                                                                                                                                                                     Huang W;
                                                                                                                                                                                                                                                                                                              95US-00546568.
                                                                                                                                                                                                                                                                                                                           94US-00336235.
                                                                                    .149
                                                                                                                                                                                                                                                            457. .459
/note= "O-
                                                        .135
                                                                      .142
                                                                                                                .156
                                                                                                                                                                        .232
                            .113
                                                                                                                                            .223
                                                                                                                                                         .224
                                                                                                                                                                                                                 .325
                                                                                                                                                                                      .272
                                                                                                                                                                                                                                .401
                                                                                                                                                                                                                                              .457
                                                                                                                                                                                                                                                                                                                                                                                                                     binds to the TIGR protein,
              99
                                                                                                                                                                                                                                                                                                                                                                    Nguyen TD, Polansky JR,
               92. .99
/note=
                                                                             'note=
                                                                                                                                                   note=
        note=
                                                                                                                                                                                                                                                                                                                                        (NGUY/) NGUYEN T D.
(POLA/) POLANSKY J R.
                                                                                                                 49.
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-407325/43.
                                                                                                                                                                                                                                                                                                                                                      (HUAN/) HUANG W.
                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD08141
                                                                                                                             Modified-site
                                                                                                                                          Modified-site
                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                           Modified-site
                           Binding-site
                                                                                                Binding-site
                                                                                                                                                                                                                                                                                                            20-0CT-1995;
                                                                                                                                                                                                                                                                                                                          03-NOV-1994;
                                                                                                                                                                                                                                                                               US6248867-B1
                                                                                                                                                                                                                                                                                              19-JUN-2001.
Region
              Region
                                                       Region
                                                                      Region
                                                                                   Region
                                          Region
                                                                                                               Region
                                                                                                                                                         Domain
                                                                                                                                                                       Domain
                                                                                                                                                                                                                 Domain
```

```
The present sequence is human trabecular meshwork induced glucocorticoid response (TIGR) protein from clone II.2. TIGR gene is mapped to p36 of of hormosome 1 and to p13, q15 of chromosome 10, 11 or 12. The trabecular network has been proposed to play an important role in the normal flow of the aqueous and has been presumed to be the major site of outflow resistance in glaucomatous eyes. TIGR is highly induced by glucocorticoids in the endothelial lining of the human trabecular meshwork and so it is useful in diagnosing glaucomas, as well as disorders e.g. cardiovascular and immunological diseases related to expression of TIGR. IIGR is also useful in diagnosis or prediction of an individual's sensitivity to elevated intraocular pressure on
Novel fusion protein, useful in glaucoma diagnosis, comprises part of a
Trabecular Meshwork Induced Glucocorticoid Response (TIGR) protein and
                                                                                                                                                                                                                                          Claim 5; Fig 1; 22pp; English.
```

```
ö
                                                                                                                                                                                                                 Human; PRO9964; clone DNA96973; immune-related disorder; inflammatory disorder; infectious disorder; immunodeficiency disorder; autoimmune disorder; ranal disease; demyelinating disease; skin disease; neoplasia; transplantation associated immunosuppressive; anti-inflammatory; antiasthmatic; antidiabetic.
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Microbodies C-terminal targetting signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "cAMP- and cGMP-dependent protein kinase
                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Glycosaminoglycan attachment site"
                  2.1%; Score 7; DB 4; Length 504;
100.0%; Pred, No. 7.4e+02;
ive 0; Mismatches 0; Indele
                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Olfactomedin-like domain
                                                                                                                                                                                                                                                                                                                                            "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                /note= "N-glycosylation site"
143. .164
                                                                                                                                                                                                                                                                                                                        /label= Transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                     'note= "Leucine zipper"
                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "Leucine zipper"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Leucine zipper"
                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Leucine zipper"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Leucine zipper"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphorylation site"
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                AAU09184 standard; protein; 504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001; 2001WO-US006666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAR-2000; 2000US-0187202P.
                                                                                                                                                                          (first entry)
                                                                                                                                                                                             Human PRO9964 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                          .168
                                                                                                                                                                                                                                                                                                                                                                                                                                                             .185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .487
                                                                                                                                                                                                                                                                                                                                                                                                                      .178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .267
                                                                                                                                                                                                                                                                                                                                                                                                 .171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .531
                                         Conservative
                                                                                                                                                                                                                                                                                                                                   . 62
                                                                                                                                                                                                                                                                                                                                                       .86
                                                                                                                                                                                                                                                                                                                                                                                                                                                    note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                               'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note=
                                                            260 NLLRDKS 266
                                                                               144 NLLRDKS 150
                            Local Similarity
nes 7; Conserv
Sequence 504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200166740-A2
                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Binding-site
                                                                                                                                                                          16-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-2001
                                                                                                                                                     AAU09184;
                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                              RESULT 109
                                      Aatches
                                                                                                                         AAU0918
                                                                             g
                                                                                                                                          ð
```

```
The present invention relates to the isolation of 9 novel human PRO
20 polypeptides and the CDNA sequences (AAS15360-AAS15368) encoding them.
21 The novel PRO polypeptides include PRO1356, PRO1268, PRO1844,
22 PRO1351, PRO4322, PRO9964, PRO1008 and PRO19598. The CDNA sequences
23 Encoding these PRO polypeptides have been designated as clones DNA64886-
24 Encoding these PRO polypeptides and mestignated as clones DNA64886-
25 Encoding these PRO polypeptides and mestignated as clones DNA64886-
26 Encoding these PRO polypeptides and methods of using these
27 Encoding these PRO polypeptides and methods of using these
28 Encoding these PRO polypeptides and methods of inflammer leaded
29 Encoding are useful in the treatment and diagnosis of immune-related
20 Encoding are useful in the treatment and diagnosis of immune-related
21 Encoding are useful in the treatment and diagnosis of immune-related
22 Encoding these mellitus), infectious disorders (e.g. granulomatous hepatitis), immune-related renal diseases (e.g. cirrhosis),
22 Encoding arthitis), immune-related renal diseases (e.g. cirrhosis),
23 Encoding arthitis), immune-mediated stand diseases (e.g. contact
24 Encoding arthitis), immune-mediated stand diseases. The
25 Polymucleotide sequences of the invention may be used in gene therapy.
26 Encoding the present the novel human PRO polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; TIGR protein; trabecular meshwork induced glucocorticoid response; glaucoma; intraocular pressure; aqueous humour outflow; diagnosis; cardiovascular disorder; immunological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human TIGR (trabecular meshwork induced glucocorticoid response) protein.
                                                                                                                                                       Gurney AL;
                                                                                                                                                                                                                                                              Nucleic acids encoding PRO polypeptides, useful for detecting and treating immune related diseases and disorders in mammals including autoimmune diseases, inflammatory diseases and asthma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                       Grimaldi CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 4; Length 504;
100.0%; Pred. No. 7.4e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                   Godowski PJ,
                                                                                                                                                                          Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB48845 standard; protein; 504 AA.
                                                                                                                                                   Goddard A, Go
X, Wood WI,
                                                                                                                                                                                                                                                                                                                                         Claim 10; Fig 14; 122pp; English.
                 30-MAY-2000; 2000WO-US014941.
05-JUN-2000; 2000US-0209832P.
24-AUG-2000; 2000WO-US02328
01-DEC-2000; 2000WO-US03328
21-MAR-2000; 2000US-0191015P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-00220459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
                                                                                                                                               Fong S, Godo
Watanabe CK,
                                                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                                        2001-625876/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 NLLRDKS 266
                                                                                                                                                                                                                          N-PSDB; AAS15366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6150161-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-NOV-2000
                                                                                                                                                 Eaton DL,
                                                                                                                                                                      Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB48845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB48845
à
```

```
The invention relates to CDNA (AAC87528, AAC87529) encoding human TIGR (trabecular meshwork induced glucocorticoid response) protein (AAB48845). The invention also relates to a transgenic cell or progeny thereof comprising a human TIGR protein nucleic aid of the invention. TIGR comprising a plucocorticoids. It is thought that TIGR protein is deposited in the extracellular spaces of the trabecular meshwork and binds to the surface of endothelial cells of the trabecular meshwork. This interferes with the normal outfilw of aqueous humour from the eye, leading to an increase in intraccular pressure and resulting in glaucoma. Human TIGR protein cDNA is useful for diagnosing glaucoma and associated disorders and its use provides for an improved and more accurate diagnosis of this condition. TIGR protein cDNA may also be used in the diagnosis of this diseases and conditions which are associated with altered expression or allowance the new orders and encounter the new orders and encountered expression or allowanced the new orders and encountered expression or allowanced the new orders the new orders and encountered expression or allowanced the new orders the new orders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human trabecular meshwork-induced glucocorticoid response (TIGR) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; zsig58; gonadal development; pregnancy; pubertal change; menopause; ovarian cancer; fertility; ovarian function; pancreas; polycystic ovarian syndrome; diabetes; eye disease; pituitary function; osteoporosis; bone disease, wound healing; bacterial infection; viral infection; fungal infection; analgesic; antidiabetic; vulnerary; gynaecological; osteopathic; cytostatic; ophthalmological; trabecular meshwork-induced glucocorticoid response; TIGR.
                                                                                                                                                                                                                                                              Novel nucleic acid encoding trabecular meshwork induced glucocorticoid response protein, useful for diagnosing glaucoma, cardiovascular and immunological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders. The present sequence represents human TIGR protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 4; Length 504;
100.0%; Pred. No. 7.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                    Example 3; Fig 1A-D; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG75692 standard; protein; 504 AA.
                                                                                                                                                             Polansky JR, Nguyen TD;
                 94US-00336235.
95US-00546568.
96US-00649432.
                                                                               97US-00882238
                                                                                                                                                                                                                       N-PSDB; AAC87528, AAC87529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                    (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 NLLRDKS 150
                                                                                                                                                                                                        WPI; 2001-060016/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 504 AA;
                                                        17-MAY-1996;
25-JUN-1997;
                                      20-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JUN-2003
                                                                                                                                                               Huang W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG75692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 111
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

ö

26-FEB-2002; 2002US-00086135.

US2002182677-A1

Homo sapiens.

2003-210087/20.

N-PSDB; ABZ58478

(KONG/) KONG T H.

Kong TH;

```
diagnosing or treating disorders associated with gonadal development, programory, pubertal changes, menopause, ovarian cancer, fertility, ovarian function, polycystic ovarian syndrome, pancreas, diabetes, eye disease, pituitary function, osteoporosis and other bone disease. The zig58 polypeptide may also be used in promoting wound healing, in anti-microbial applications, as a cell culture reagent in in vitro studies of exogenous microorganism infections (e.g. bone pain), in identifying cells, infection), as an analgesic (e.g. bone pain), in identifying cells, tissues or cell lines that respond to a zsig58-stimulated pathway, in antibodies. The antibody may be used for tagging cells that express zig58, for isolating zsig58 and for other diagnostic and therapeutic applications. The polymucleotide is also usedful in identifying a region of the genome associated with human disease states. This sequence the genome associated with human disease states. This sequence represents the human trabecular meshwork-induced glucocorticoid response (TIGR) protein, which is related to the human zsig58 polypeptide
                                                                                                                                                                                                                    New pancreatic and ovarian zsig58 polypeptides useful for diagnosing or treating disorders associated with gonadal development, pregnancy, pubertal changes, menopause, ovarian cancer, fertility, and ovarian or
                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated pancreatic and ovarian zsig58 polypeptide and the polypucleotide encoding it. The polypeptide, polynucleotide and an antibody to the polypeptide are useful in
                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1; 49pp; English.
                                                                                                                        Sheppard PO, Chandrasekher YA;
                         99US-00366448
     98US-0095199P.
                                                                       (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                              pancreatic function.
                                                                                                                                                                      WPI; 2003-328618/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 504 AA;
  03-AUG-1998;
                            03-AUG-1999;
```

2.1%; Score 7; DB 6; Length 504; 100.0%; Pred. No. 7.4e+02; ive 0; Mismatches 0; Indels 7; Conservative 260 NLLRDKS 266 144 NLLRDKS 150 Query Match Best Local Similarity Matches à g

ABP72340 standard; protein; 504 AA. (first entry) Human myocilin. 08-MAY-2003 ABP72340; RESULT 112 ABP72340 ID ABP7

Trabecular meshwork inducible glucocorticoid responsive protein; TIGR; myocilin; MYOC; human; glaucoma; cardiovascular disease; retinal degenerative disease; diagnosis; genetic profiling; ophthalmological; cardiovascular-gen. WO2002102300-A2 Homo sapiens 27-DEC-2002. 

22-NOV-2000; 2000US-0252420P. 05-APR-2001; 2001US-0281422P. 23-JUL-2001; 2001US-0306889P. 01-NOV-2001; 2001WO-US045645.

The present sequence is the protein sequence of human trabecular meshwork inducible glucocorticoid responsive protein (TIGR), also known as inducible glucocorticoid responsive protein (TIGR), also known as myocilin (MYOC). The invention is based on the finding that in addition to full-length MYOC mRNA, shorter mRNAs of the TIGR gene are expressed in to full-length MYOC mRNA, shorter mRNAs are differentially expressed in normal and glaucoma subjects. A claimed method of determining whether a subject has, or is at risk of developing, glaucoma, retinal degenerative or cardiovascular disease comprises generating a transcriptional profile (i.e. a fingerprint) in the subject or in a sample obtained from the subject based on the comprises generating a transcriptional profile (i.e. a fingerprint) in the subject has or is at risk of developing these diseases. Claims are also included for methods of establishing a MYOC genetic population of that the subject has or is at risk of developing these diseases. Claims are also included for methods of establishing alucoma, retinal degenerative or cardiovascular disease, and for pharmacogenomically consecution of individual having glaucoma, retinal degenerative or cardiovascular disease. Fingerprinting techniques for the confluence or mathorator or is likely to develop, a glaucoma, retinal degenerative or cardiovascular disease comprises a probe comprising about 10 consecutive amino acid residues or more from the corpus present sequence or naturally occurring mutants of it Determining whether a subject has or is at risk of developing glaucoma, retinal degenerative or cardiovascular disease by generating a transcriptional profile in the subject, based on the expression of Claim 36; Fig 3; 52pp; English. myocilin. 

Sequence 504 AA;

ö

Gaps

.. 0

0; Indels

0; Gaps 2.1%; Score 7; DB 6; Length 504; 100.0%; Pred. No. 7.4e+02; Live 0; Mismatches 0; Indels Query Match Best Local Similarity 100.v. 7; Conservative

ö

260 NLLRDKS 266 144 NLLRDKS 150 g ð

25-SEP-2003 (first entry) ABO44238;

ABO44238 standard; protein; 504 AA.

RESULT 113 AB044238

Human TIGR/myocilin.

Human, latrophlin 3; LPH3; ophthalmological; hypotensive; gene therapy; eye disease; primary open-angle glaucoma; ocular hypertension; elevated intraocular pressure; TIGR; myocilin.

Homo sapiens,

US2003054347-A1. 

20-MAR-2003.

27-APR-2001; 2001US-00844653.

```
(first entry)
                                                                                                                                                                                                                                                                                                    Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                 260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                   144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                                                                                                                                          Sequence 504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-APR-1999;
21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                      AAG32190;
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                 115
                                                                                                                                                                                                                                                                                                                                                                                         AAG32190
    g
                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                               ö
                                                                                             diagnosing or treating subjects at risk for or having eye disease, e.g.
Primary Open-Angle Glaucoma, ocular hypertension, or elevated intraocular
                                                                                                                                                 The invention describes a new composition, which comprises an isolated Latrophilin (LPH) nucleic acid. The compositions are useful for diagnoshing or treating subjects at risk for or having eye disease, e.g. Primary Open-Angle Glaucoma (e.g. juvenile onset or adult onset), ocular hypertension, or elevated intraocular pressure. This is the amino acid sequence of human TIGR/myocilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                               Gaps
                                                                                  Latrophilin (LPH) polynucleotides and polypeptides, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                         Human, pain, neuronal tissue, gene therapy, spinal segmental nerve injury, chronic constriction injury, CCI, spared nerve injury, SNI, Chung.
                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                        2.1%; Score 7; DB 6; Length 504;
100.0%; Pred. No. 7.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Befort K, Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                         Human Protein Q99972, SEQ ID NO 320.
                                                                                                                                Disclosure, Fig 11; 153pp; English.
                                                                                                                                                                                                                                                                                                                                              ADE54517 standard; protein; 504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page; 1017pp; English
27-APR-2001; 2001US-00844653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2002; 2002WO-US025765
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                  (UNMI ) UNIV MICHIGAN.
                                                       WPI; 2003-521847/49.
N-PSDB; ACH03575.
                                                                                                                                                                                                                                                                                               144 NLLRDKS 150
                                                                                                                                                                                                                                                                             260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Woolf C, D'urso D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-268312/26.
                                                                                                                                                                                                                       Sequence 504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003016475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENBANK; Q99972.
                                      Richards JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                 ADE54517;
                                                                                                                                                                                                                                                                                                                           RESULT 114
                                                                                                                                                                                                                                                                                                                                      ADE54517
ð
```

```
The investion discloses or supposition comparison to comparison to the investion discloses or supposition comparison to comparison to comparison the comparison of disclose and comparison to comparison the comparison to comparison the comparison to comparison the comparison to comparison the comparison to comparison the comparison to comparison the comparison to comparison the comparison to comparison the comparison to comparison the comparison to comparison the comparison to comparison the comparison to comparison the comparison to comparison the comparison to comparison the comparison to comparison the comparison to comparison the comparison to comparison the comparison to comparison the comparison to compare the comparison to comparison the comparison to compare the comparison to compare the comparison to comparison to compare the comparison to compare the comparison to compare the comparison to compare the comparison to compare the comparison to compare the comparison to compare the comparison to compare the comparison to compare the comparison to compare the comparison to compare the comparison to compare the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that comparison the comparison that
```

20-70L-1999; 20-70L-1999; 21-40L-1999; 22-40L-1999; 22-40L-1999; 22-40L-1999; 22-40L-1999; 23-40L-1999; 23-40L-1999; 23-40L-1999; 23-40L-1999; 23-40L-1999; 23-40L-1999; 23-40L-1999; 23-40L-1999; 23-40L-1999; 23-40L-1999; 24-40L-1999; 27-40L-1999; 28-40L-1999; 28-40L-1999;	02-MG-1999; 04-MG-1999; 04-MG-1999; 05-MG-1999; 06-MG-1999; 06-MG-1999; 06-MG-1999; 09-MG-1999; 11-AUG-1999; 113-AUG-1999; 113-AUG-1999; 113-AUG-1999; 113-AUG-1999; 123-AUG-1999; 20-AUG-1999; 20-AUG-1999; 213-AUG-1999; 213-AUG-1999; 213-AUG-1999; 213-AUG-1999; 213-AUG-1999; 213-AUG-1999; 213-AUG-1999;	25-ANG-1999; 27-ANG-1999; 27-ANG-1999; 30-ANG-1999; 31-ANG-1999; 31-ANG-1999; 31-ANG-1999; 31-ANG-1999; 31-ANG-1999; 31-ANG-1999; 31-ANG-1999; 31-ANG-1999; 32-SEP-1999; 32-SEP-1999; 33-CCT-1999; 34-CCT-1999; 31-CCT-1999; 31-CCT-1999; 31-CCT-1999; 31-CCT-1999; 31-CCT-1999; 31-CCT-1999; 31-CCT-1999; 31-CCT-1999; 31-CCT-1999; 31-CCT-1999; 31-CCT-1999; 31-CCT-1999;
# # # # # # # # # # # # # # # # # # #	{	
990S-0130510P. 990S-0131891P. 990S-0131648P. 990S-0132048P. 990S-0132484P. 990S-0132484P. 990S-0132487P. 990S-0132487P. 990S-0132487P. 990S-0134218P. 990S-0134218P. 990S-013421P. 990S-013421P. 990S-0134370P. 990S-0134370P.	990S-0135629P 990S-013632P 990S-013722P 990S-013722P 990S-013752BP 990S-013752BP 990S-013752P 990S-0138640P 990S-0138640P 990S-0138640P 990S-0139652P 990S-0139652P 990S-0139652P 990S-0139652P 990S-0139652P 990S-0139652P 990S-0139652P 990S-0139652P 990S-0139652P	990S-0139462P. 990S-0139462P. 990S-0139763P. 990S-0139897P. 990S-0140353P. 990S-0140353P. 990S-014082P. 990S-014128P. 990S-014128P. 990S-014295P. 990S-014295P. 990S-014295P. 990S-014433P. 990S-014433P. 990S-014433P. 990S-014433P. 990S-014433P. 990S-014433P.
23 - APR - 1999; 28 - APR - 1999; 30 - APR - 1999; 30 - APR - 1999; 04 - MAY - 1999; 06 - MAY - 1999; 06 - MAY - 1999; 11 - MAY - 1999; 14 - MAY - 1999; 14 - MAY - 1999; 18 - MAY - 1999; 19 - MAY - 1999; 19 - MAY - 1999; 20 - MAY - 1999; 21 - MAY - 1999; 22 - MAY - 1999;	24-MAY-1999; 25-MAY-1999; 28-MAY-1999; 01-JUN-1999; 04-JUN-1999; 06-JUN-1999; 10-JUN-1999; 116-JUN-1999; 116-JUN-1999; 116-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999; 118-JUN-1999;	18 - UN 1999; 18 - UN 1999; 18 - UN 1999; 22 - UN 1999; 23 - UN 1999; 23 - UN 1999; 24 - UN 1999; 26 - UN 1999; 30 - UL 1999; 30 - UL 1999; 30 - UL 1999; 30 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999; 31 - UL 1999;
\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$	K K K K K K K K K K K K K K K K K K K	

9US-0144632P 9US-0144884P 9US-0144814P 9US-0145086P 9US-0145080P 9US-0145080P 9US-0145080P 9US-0145080P 9US-0145145P 9US-0145145P 9US-0145234P 9US-0145234P 9US-0145236P	900S-0145591 900S-0145595 900S-0146595 900S-0146595 900S-014703 900S-014703 900S-014726 900S-014726 900S-014741 900S-014741 900S-014741 900S-014741 900S-014741 900S-014741 900S-014741 900S-014741 900S-014741 900S-014741 900S-014741 90S-014741 90S-014741 90S-014741 90S-014741	44 44 44 44 44 44 44 44 44 44 44 44 44
0-JUL-1999 1-JUL-1999 1-JUL-1999 1-JUL-1999 1-JUL-1999 2-JUL-1999 2-JUL-1999 3-JUL-1999 3-JUL-1999 3-JUL-1999 3-JUL-1999	7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 - 7 -	20-Aug-1999 23-Aug-1999 23-Aug-1999 23-Aug-1999 23-Aug-1999 27-Aug-1999 27-Aug-1999 30-Aug-1999 30-Aug-1999 30-Aug-1999 30-Aug-1999 30-Aug-1999 30-Aug-1999 30-Aug-1999 30-Aug-1999 30-Aug-1999 30-Aug-1999 30-Aug-1999 30-Aug-1999 30-Aug-1999 30-Aug-1999 30-Aug-1999 30-Aug-1999 30-Aug-1999 30-Aug-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999 313-Oct-1999
# # # # # # # # # # # # # # # # # # #	***************************************	

```
multiple sclerosis, systemic lowes exthematosus and human immuno-
deficiency virus (HIV) infections), hyperproliferative disorders (e.g.
ancers and Gaucher's disease), cardiovascular diseases (e.g. Scimitar
syndrome, Chaga's cardiomyopathy and coronary arteriosclerosis),
angiogenic disorders (e.g. corneal graft neovascularisation and diabetic
retinopathy), neurological disorders (e.g. Huntington's chorea,
Alzheimer's disease and Parkinson's disease), infectious diseases and/or
for promoting wound healing, regeneration and/or chemotaxis. The nucleic
acid molecules may be used to produce the secreted polypeptides. They may
the presence of similar nucleic assays to detect and quantitate
the presence of similar nucleic acid sequences in samples. The
polypeptides may be used as antigens in the production of antibodies and
in assays to identify modulators of their expression and activity
                    present sequence is one of 32 novel human secreted polypeptides. The
                               nucleic acid molecules and polypeptides may be used in the prevention, diagnosis and treatment of diseases such as immune disorders (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to albumin fusion proteins comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; haqgestive disorder; immune disorder; endocrine disorder; haematopoletic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic; neuroporetective; antibarkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic.
                                                                                                                                                                                                                                                                                                    Query Match 2.1%; Score 7; DB 4; Length 514; Best Local Similarity 100.0%; Pred. No. 7.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 2040-2041; 2102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human albumin fusion protein #2147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG65472 standard; protein; 514 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-APR-2000; 2000US-0229358P.
25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-APR-2001; 2001WO-US011988,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA, Haseltine WA;
                                                                                                                                                                                                                                                                                                                                                                                              392 VAQLAQE 398
                                                                                                                                                                                                                                                                                                                                                                72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-010886/01.
                                                                                                                                                                                                                                                                                                                                                                66 VAQLAQE
                                                                                                                                                                                                                                                                         Sequence 514 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200177137-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG65472;
                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG6547;
   à
                                                                                                                                                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secreted protein; immunomodulatory; antisclerotic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding 32 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Komatsoulis GA;
SA, Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiinflammatory, anti-HIV, cytostatic; cardiant, vascular; anti-anglogenic; ophthalmological, neuroprotectent, noctropic; anticonvulsant; antialzheimers; antiparkinsonian; antimicrobial; vulnerary; vaccine; gene therapy; cancer; protein coordinate data;
                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                             2.1%; Score 7; DB 3; Length 508; 00.0%; Pred. No. 7.5e+02; ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        er KP, Birse CE, Ebner R, Fiscella M,
, Moore PA, Olsen HS, Rosen CA, Ruben
Wei P, Florence KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein, SEQ ID NO: 124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 805-807; 890pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB90586 standard; protein; 514 AA.
                                                                                                                               990S-0160980P.
99US-0160981P.
99US-0160989P.
99US-0161404P.
99US-0161405P.
                                                                     99US-0160768P.
99US-0160770P.
99US-0160814P.
99US-0160815P.
                                                                                                                                                                                                                                     99US-0161360P.
99US-0161361P.
99US-0161920P.
                                                                                                                                                                                                                                                                                 99US-0161992P.
99US-0161993P.
99US-0162142P.
                                       99US-0160741P.
                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0155709P
                            99US-0159584P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-SEP-2000; 2000WO-US026013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                         99US-0161359P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Lag 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                         301 LIEFLSS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-235311/24.
N-PSDB; AAF97926.
                                                                                                                                                                                                                                                                                                                                                                                                                                     126 LIEFLSS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baker KP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200121658-A1.
                                     21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
                                                                                                                                             22-OCT-1999;
22-OCT-1999;
25-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                         26-OCT-1999;
                                                                                                                                                                                                                                        26-OCT-1999
                                                                                                                                                                                                                                                      26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAR-2001
                                                                                                                                                                                                                                                                     28-OCT-1999
                                                                                                                                                                                                                                                                                                  28-OCT-1999
                                                                                                                                                                                                                                                                                                               29-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB90586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ni J, Ba
Lafleur
                                                                                                                                                                                                          25-OCT-1
                                                                                                                                                                                              25-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB90586
g
                                                                                                                                                                                                                                                                                                                                                                                                         à
```

Gaps

..

```
٠,
                                                                                                                                                                                                                                                                                                                  ö
         albumin, HSA). The process are useful for treating a disease or disorder that may be modulated by therapeutic procein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immunodisorders (e.g. acquired immunodeficiency syndrome, AlDS), endocrine disorders (e.g. diabetes), haemacopoietic disorders, neural disorders (e.g. Alzheimer's). Parkinson's, Creutzfeldt-Jacob disease, encephalomyellitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel enterchaemorragic Escherichia coli 0157:H7-specific nucleic acid molecule. A polymucleotide of the invention has anti-bacterial activity. The polypeptide can be used in detection and/or treatment of 0157:H7 infection. The nucleotide sequence of the genome of Exterchaemorragic B coli 0157:H7 was determined. The present sequence represents an E. coli 0157:H7-specific polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterohemorragic Escherichia coli 0157:H7-specific nucleic acid molecule and a polypeptide and its use, a polypeptide, a vector and a host cell.
therapeutic protein X and human albumin (HA, also known as human serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 1602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                  ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 7; DB 7; Length 523; 100.0%; Pred. No. 7.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                           Length 514;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                             DB 5; Len . 7.6e+02;
                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 5
100.0%; Pred. No. 7.6
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; SEQ ID NO 1602; 2067pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADC01554 standard; protein; 523 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enterohaemorragic; anti-bacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JAN-2001; 2001JP-00112010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JAN-2002; 2002JP-00015959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli; 0157:H7.
                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYTS-) UNIV TSUKUBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 PLAKIIL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          356 PLAKITL 362
                                                                                                                                                                                                                                                                                                                                                                                  392 VAQLAQE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-451640/43.
                                                                                                                                                                                                                                                                                                                                                   66 VAQLAQE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                        Sequence 514 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 523 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP2002355074-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-DEC-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC01554;
                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                              118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QC
ð
                                                                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

```
The invention relates to an isolated nucleic acid detection reagent expable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                                                     developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 1110; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 7; DB 4; Length 535; 100.0%; Pred. No. 7.9e+02; ive 0; Mismatches 0; Indels
                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 1110.
                                                                                                                                                                                                                                                                                                                                                                                                        EΧ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human diagnostic protein #16708.
                                                                                                                                                                                                                                                                                                                                                                                                        Myers
                             ABB58106 standard; protein; 535 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG16717 standard; protein; 550 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        PWD,
                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                         23-MAR-2000; 2000US-0191637P.
                                                                                                                                                                                                                                                                                                                                           11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                         26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                        ij
                                                                                                                                                                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                      Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 LIGELIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            515 LLGELIL 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABL02209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 535 AA;
                                                                                                                                                                                                                                  WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-2002
                                                                                                                                                       Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG16717;
                                                            ABB58106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 120
RESULT 119
ABB58106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG16717
                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          임
```

ó;

Gaps

```
Location/Qualifiers
                                                       note= "PPS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "PPS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-SEP-2001 (first entry)
                                        .551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lycopersicon esculentum.
                                                                                                                                                                                                             Rice J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 LLRDKSP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLRDKSP 489
                                                                                                                                                                                                                                     WPI; 2001-418081/44.
                                                                                                                                                                                                                                                   N-PSDB; AAH22901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 551 AA;
                                                                                WO200146446-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200146446-A1
                                                                                                                                                                                                           Crawford JM,
                                                                                                                                                          22-DEC-1999;
                                                                                                       28-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB85252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                 Protein
                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB85252
    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reaction (FCR) primers, oligomers, and for chromosome and gene mapping, reaction (FCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymciase chain reaction in the production of (II). The polymciase chain and in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polympeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymcleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thioredoxin, porphobilinogen synthase, T-PPS, PPS, enzyme, herbicide, delta-aminolevulinic acid, plant growth inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 4; Length 550;
100.0%; Pred. No. 8.1e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant thioredoxin-porpobilinogen synthase (T-PPS).
                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 47076; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB85251 standard; protein; 551 AA.
                                                                          30-MAR-2001; 2001WO-US008631
                                                                                                   31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                                                                                                                                                     Tang YT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon esculentum
                                                                                                                                                                                            2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 LYSSGLL 301
                                                                                                                                                                   Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 LYSSGLL 79
                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                           WPI; 2001-639362;
N-PSDB; AAS80904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 550 AA;
                        WO200175067-A2.
 Homo sapiens.
                                                                                                                                                                                                                                                                        biodiversity
                                                  11-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB85251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB85253
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
The invention provides novel DNA sequences encoding enzymes such as plant thioredoxin-porphobilinogen synthase (T-PPS) and plant porphobilinogen synthase (T-PPS) and plant porphobilinogen synthase (PPS). Methods of determining the enzymatic activity of T-PPS or PPS or its functional fragment are provided that involves contacting measuring the amount of porphobilinogen formed from it. Compounds which can modify the enzymatic activity T-PPS or PPS can also be identified similarly, which are useful for inhibiting plant growth by inhibiting enzymatic activity of T-PPS or PPS or pps can also be indentified enzymatic activity of T-PPS or pps or its functional fragment. The compounds thus identified are useful as herbicides. The present sequence represents the fusion protein T-PPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thioredoxin, porphobilinogen synthase, T-PPS, PPS, enzyme, herbicide, delta-aminolevulinic acid, plant growth inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel plant thioredoxin-porphobilinogen synthase or porphobilinogen synthase polypeptides, useful for identifying compounds for use as herbicides by inhibiting enzymatic activity of the polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 4; Length 551;
100.0%; Pred. No. 8.1e+02;
tive 0; Mismatches 0; Indels
...167
'note= "thioredoxin functional fragment"

    167
    /note= "thioredoxin functional fragment"
    168. .551

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant thioredoxin-porpobilinogen synthase (T-PPS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sevala V, Stewart S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 16-17; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB85252 standard; protein; 551 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PARA-) PARADIGM GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                      19-DEC-2000; 2000WO-US034584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0171785P.
```

Gaps

```
9905 - 0130047P

9905 - 0130449P

9905 - 0130449P

9905 - 013048P

9905 - 0132468P

9905 - 013248P

9905 - 013248P

9905 - 013248P

9905 - 013248P

9905 - 0134218P

9905 - 0134218P

9905 - 0134218P

9905 - 0134218P

9905 - 013421P

9905 - 013421P

9905 - 013421P

9905 - 013421P

9905 - 013421P

9905 - 013421P

9905 - 013421P

9905 - 013421P

9905 - 013421P

9905 - 013421P

9905 - 013421P

9905 - 013452P

9905 - 013452P

9905 - 013453P

9905 - 013453P

9905 - 013453P

9905 - 013453P

9905 - 013453P

9905 - 013453P

9905 - 013453P

9905 - 013453P

9905 - 013453P

9905 - 013453P

9905 - 013453P

9905 - 013453P

9905 - 013463P

9905 - 013463P

9905 - 014033P

9905 - 014033P

9905 - 014033P

9905 - 014033P

9905 - 014033P

9905 - 014039P

9905 - 014039P

9905 - 014039P

9905 - 014039P

9905 - 014039P

9905 - 014039P

9905 - 014039P

9905 - 014039P

9905 - 014039P

9905 - 014039P

9905 - 014039P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0144086P.
99US-0144325P.
99US-0144331P.
99US-0144332P.
       99US-0129845P
              19-APR-1999;
21-APR-1999;
23-APR-1999;
28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
                                                                                                                                                                                                                                                                                                                          1999;
                                                                                                                                           11-MAY-1999;
                                                                                                                                                                                                                                                                      28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                     1999;
                                                                                                  05-MAY-1999
                                                                                                            06-MAY-1999
                                                                                                                                                                           14-MAY-1999
                                                                                                                                                                                     14-MAY-1999;
                                                                                                                                                                                                         19-MAY-1999
                                                                                                                                                                                                                               21-MAY-1999
24-MAY-1999
                                                                                                                                                                                                                                                                                            03-JUN-1999
                                                                                                                                                                                                                                                                                                                 07-JUN-1999;
                                                                                                                                                                                                                                                                                                                                      1999;
                                                                                                                                                                                                                                                                                                                                              10-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                               8-JUN-1999;
                                                                                                                                                                                                                                                    25-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                             6-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                    8-JUN-8
                                                                                                                                                                                                                                                                                                                                                                                                     8-UUN-8
                                                                                                                                                                                                                                                                                                                                      -ND5-01
                                                                                                                                                                                                                                                                                                                           -NUL-80
     The invention provides novel DNA sequences encoding enzymes such as plant thioredoxin-porphobilinogen synthase (T-PPS) and plant porphobilinogen synthase (T-PPS) and plant porphobilinogen PPS or the factorial part of determining the enzymatic activity of T-PPS or PPS or its functional fragment are provided that involves contacting measuring the amount of porphobilinogen formed from it. Compounds which can modify the enzymatic activity T-PPS or PPS can also be identified enzymatic activity of T-PPS or PPS or PPS can also be identified enzymatic activity of T-PPS or IPS or PPS or plant growth by inhibiting compounds thus identified are useful as herbicides. The present sequence represents the fusion protein T-PPS
                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                  Novel plant thioredoxin-porphobilinogen synthase or porphobilinogen synthase polypeptides, useful for identifying compounds for use as herbicides by inhibiting enzymatic activity of the polypeptides.
                                                                                                                                                                                                                                                                                                                                                Query Match 2.1%; Score 7; DB 4; Length 551; Best Local Similarity 100.0%; Pred. No. 8.1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 38628.
                                                                                   Stewart S;
                                                                                                                                                                            Claim 4; Page 17-18; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG32076 standard; protein; 557 AA.
                                                                                   Sevala V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-012626P.
99US-0126785P.
99US-0126785P.
99US-0126785P.
                    19-DEC-2000; 2000WO-US034584.
                                                            (PARA-) PARADIGM GENETICS INC
                                         99US-0171785P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2000 (first entry)
                                                                                 Crawford JM, Rice J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
                                                                                                     WPI; 2001-418081/44.
                                                                                                                                                                                                                                                                                                                                                                                             261 LLRDKSP 267
                                                                                                                                                                                                                                                                                                                                                                                                          483 LLRDKSP 489
                                                                                                                N-PSDB; AAH22801.
                                                                                                                                                                                                                                                                                                                              Sequence 551 AA;
                                         22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
28-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-1999
25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG32076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 123
```

```
PR 19-7UL-1999; 99US-0144334P.
PR 20-7UL-1999; 99US-0144332P.
PR 20-7UL-1999; 99US-0144332P.
PR 20-7UL-1999; 99US-0144632P.
PR 21-7UL-1999; 99US-0144632P.
PR 22-7UL-1999; 99US-0144614P.
PR 22-7UL-1999; 99US-0144614P.
PR 22-7UL-1999; 99US-0145086P.
PR 22-7UL-1999; 99US-0145086P.
PR 22-7UL-1999; 99US-0145086P.
PR 23-7UL-1999; 99US-0145086P.
PR 23-7UL-1999; 99US-0145086P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0145132P.
PR 23-7UL-1999; 99US-0143132P.
PR 23-7UL-1999; 99US-0143132P.
PR 23-7UL-1999; 99US-0143132P.
PR 23-7UL-1999; 99US-0143132P.
PR 23-7UL-1999; 99US-0143132P.
PR 23-7UL-1999; 99US-0143132P.
PR 23-7UL-1999; 99US-0143132P.
PR 23-7UL-1999; 99US-0143132P.
PR 23-7UL-1999; 99US-0143132P.
PR 23-7UL-1999; 99US-0143132P.
PR 23-7UL-1999; 99US-0143132P.
PR 23-7UL-1999; 99US-0143132P.
PR 23-7UL-1999; 99US-015236P.
PR 23-7UL-1999; 99US-015236P.
PR 23-7UL-1999; 99US-015239P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015303P.
PR 23-7UL-1999; 99US-015
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                              DB 3; Length 557; . 8.2e+02;
                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 38627.
                                                                                                                                                                                                                           Query Match
2.1%; Score 7; DB 3
Best Local Similarity 100.0%; Pred. No. 8.2
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                        AAG32075 standard; protein; 567 AA
990S-0159330P
990S-0159330P
990S-0159637P
990S-0159634P
990S-0160741P
990S-0160741P
990S-0160768P
990S-0160814P
990S-0160814P
990S-0160814P
990S-0160814P
990S-0160981P
990S-0160981P
990S-0161406P
990S-0161406P
990S-0161360P
990S-0161360P
990S-0161360P
990S-0161360P
990S-0161360P
990S-0161360P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0121825P.
99US-0123548P.
99US-0125788P.
99US-0126264P.
99US-0126762P.
99US-0127462P.
99US-0127462P.
99US-0128714P.
99US-0138714P.
99US-013077P.
99US-0130810P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                                                                                                                                                                                         17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana.
                                                                                                                                                                                                                                                             EILLKNO 298
                                                                                                                                                                                                                                                                              EILLKNO 21
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
16-0CT-1999;
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
116-APR-1999;
21-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                         AAG32075;
                                                                                                                                                                                                                                                             292
                                                                                                                                                                                                                                                                              15
                                                                                                                                                                                                                                                                                                        RESULT 124
                                                                                                                                                                                                                                                                                                                 AAG32075
 ò
                                                                                                                                                                                                                                                                          g
```

21-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 23-JUL-1999; 23-JUL-1999; 23-JUL-1999; 24-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 28-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JUL-1999; 28-JU	04-AUG-1999; 04-AUG-1999; 05-AUG-1999; 06-AUG-1999; 06-AUG-1999; 06-AUG-1999; 10-AUG-1999; 11-AUG-1999; 11-AUG-1999; 13-AUG-1999; 13-AUG-1999; 13-AUG-1999; 13-AUG-1999; 14-AUG-1999; 16-AUG-1999; 17-AUG-1999; 17-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999; 18-AUG-1999;	23-AUG-1999; 25-AUG-1999; 26-AUG-1999; 26-AUG-1999; 27-AUG-1999; 27-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AUG-1999; 31-AU	29 - SEP - 1999   04 - 0cm - 1999   05 - 0cm - 1999   06 - 0cm - 1999   07 - 0cm - 1999   12 - 0cm - 1999   13 - 0cm - 1999   14 - 0cm - 1999   14 - 0cm - 1999   14 - 0cm - 1999   14 - 0cm - 1999   14 - 0cm - 1999   14 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1999   18 - 0cm - 1
	;		
வ வ வ வ வ வ வ வ வ வ வ வ வ வ வ வ			
0132480 0132486 0132486 0132486 0132486 0132486 013428 013421 013421 013421 013421 013421 013421 013421 0135529	990S-0136392P 990S-0136782P 990S-0137528P 990S-0137528P 990S-0137724P 990S-0137724P 990S-013847P 990S-013847P 990S-0139452P 990S-0139452P 990S-0139455P 990S-0139456P 990S-0139456P	0139461 0139462 0139462 0139750 0139763 0139817 0139817 0140823 0140823 0141842 0142823 0142823 0142823 0142823 0142823 0142823	99US - 0142977P 99US - 0143542P 99US - 0144086P 99US - 0144086P 99US - 0144086P 99US - 0144331P 99US - 0144331P 99US - 0144331P 99US - 0144334P 99US - 0144334P 99US - 01443484P 99US - 0144884P
-5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166 -5166	-50.66 -50.66 -50.66 -50.66 -50.66 -50.66 -50.66 -50.66 -50.66 -50.66 -50.66 -50.66 -50.66 -50.66 -50.66	900 100 100 100 100 100 100 100 100 100	S0666
	7 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	10000000000000000000000000000000000000	6666777666667766666776666677666667766666
30-APF 05-MAN 06-MAN 06-MAN 11-MAN 114-MAN 114-MAN 119-MAN 119-MAN 120-MAN 221-MAY 221-MAY	27 - MAY - 1999; 28 - MAY - 1999; 03 - UUN - 1999; 04 - UUN - 1999; 06 - UUN - 1999; 10 - UUN - 1999; 14 - UUN - 1999; 16 - UUN - 1999; 17 - UUN - 1999; 18 - UUN - 1999; 18 - UUN - 1999; 18 - UUN - 1999; 18 - UUN - 1999; 18 - UUN - 1999; 18 - UUN - 1999; 18 - UUN - 1999; 18 - UUN - 1999; 18 - UUN - 1999;	18-00N 18-00N 18-00N 18-00N 18-00N 18-00N 18-00N 23-00N 23-00N 23-00N 23-00N 23-00N 23-00N 23-00N 23-00N 23-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20-00N 20	13-40 14-40 14-40 15-40 16-40 16-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40 19-40
	<mark></mark>		

990S-0145088P 990S-0145088P 990S-0145087P 990S-0145192P 990S-0145214P 990S-0145214P 990S-0145218P 990S-0145218P 990S-0145218P 990S-0145318P 990S-0147204P 990S-0147302P 990S-0147302P 990S-0147302P 990S-0147302P 990S-0147302P 990S-0147302P 990S-0147302P 990S-0147302P 990S-0147302P 990S-0149302P 990S-0149302P 990S-0149302P 990S-0149302P 990S-0149302P 990S-0150884P 990S-0149302P 990S-0149302P 990S-015088P 990S-015088P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P 990S-01508P

```
9905-0134219

9905-0134219

9905-01343219

9905-0134941P

9905-0135124P

9905-0135124P

9905-0135124P

9905-0135124P

9905-0135262P

9905-0137520P

9905-0137520P

9905-0137520P

9905-0137520P

9905-0137520P

9905-0137520P

9905-0139452P

9905-0139452P

9905-0139452P

9905-0139452P

9905-0139452P

9905-0139452P

9905-0139452P

9905-0139452P

9905-0139452P

9905-0139452P

9905-0139452P

9905-0139452P

9905-0139452P

9905-0139452P

9905-0139452P

9905-0139452P

9905-0139452P

9905-0140633P

9905-0140633P

9905-0140635P

9905-0140635P

9905-0144332P

9905-0144332P

9905-0144333P

9905-0144332P

9905-0144333P

9905-0144333P

9905-0144333P

9905-0144332P

9905-0144333P

9905-0144333P

9905-0144333P

9905-0144331P

9905-0144331P

9905-0144331P

9905-0144331P

9905-0144331P

9905-0144331P

9905-0144331P
     99US-0134218P
           14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
25-MAY-1999;
27-MAY-1999;
27-MAY-1999;
30-JUN-1999;
01-JUN-1999;
03-JUN-1999;
04-JUN-1999;
07-JUN-1999;
                                                                                                                                                                                             18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                  18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                                                                                       1-JUN-1999;
                                                                                                                                 10-01-01-01;
                                                                                                                                                                                                                                                                                                            3-JUN-1999;
                                                                                                                                                                                                                                                        18-JUN-1999;
                                                                                                                                                                                                                                                                                                      1-000-1
                                                                                                                           08-JUN-1999
                                                                                                                                                                                      18-JUN-1999
                                                                                                                                                                                                                                                                                              23-JUN-1
                                                                                                                                                                                                                                         -NUL-8
                                                                                                                                                                                                                                                 8-JUN-8
    ;
0
                                                                                                                                                                                                                                                                                       Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter,
                                                                                                                                                               Gaps
                                                                                                                                                               ..
                                                                                                                                            2.1%; Score 7; DB 3; Length 567;
100.0%; Pred. No. 8.3e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 38626.
                                                                                                                                                                                                                             AAG32074 standard; protein; 576 AA
99US-0160767P
99US-0160814P
99US-0160814P
99US-0160818P
99US-0160880P
99US-0160980P
99US-0161980P
99US-0161404P
99US-0161406P
99US-0161360P
99US-0161360P
99US-0161360P
99US-0161360P
                                                                                                                                                                                                                                                                                                                                                                                 9905-0121825P.
9905-0123180P.
9905-0125788P.
9905-0126785P.
9905-0126785P.
9905-0126748P.
9905-0130047P.
9905-013048P.
9905-013048P.
9905-013048P.
9905-013048P.
9905-013246P.
9905-013248P.
9905-013248P.
9905-013248F.
                                                                                                                                                                                                                                                                                                                                                                  25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                                                                                          17-OCT-2000 (first entry)
                                                                                                                                          Query Match 2.1
Best Local Similarity 100.
Matches 7, Conservative
                                                                                                                                                                          EILLIGNO 298
                                                                                                                                                                                                                                                                                                       termination sequence.
                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                         EILLKNQ 31
21-0CT-1999;
21-0CT-1999;
21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                     EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                25-FEB-1999;
05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
12-APR-1999;
21-APR-1999;
21-APR-1999;
21-APR-1999;
21-APR-1999;
21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1999;
28-APR-1999;
30-APR-1999;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                    06-SEP-2000.
                                                                                                                                                                                                                                            AAG32074;
                                                                                                                                                                          292
                                                                                                                                                                                         25
                                                                                                                                                                                                               RESULT 125
                                                                                                                                                                                                                     à
                                                                                                                                                                                        임
```

```
PR 22-JUL-1999; 99US 0145224P.

PR 27-JUL-1999; 99US 0145224P.

PR 27-JUL-1999; 99US 0145234P.

PR 27-JUL-1999; 99US 0145234P.

PR 27-JUL-1999; 99US 014531B.

PR 27-JUL-1999; 99US 014531B.

PR 02-JUL-1999; 99US 014531B.

PR 02-JUL-1999; 99US 014531B.

PR 02-JUL-1999; 99US 014531B.

PR 03-JUL-1999; 99US 014531B.

PR 03-JUL-1999; 99US 014531B.

PR 04-JUL-1999; 99US 0141320.

PR 03-JUL-1999; 99US 0141321P.

PR 04-JUL-1999; 99US 0141321P.

PR 04-JUL-1999; 99US 0141321P.

PR 04-JUL-1999; 99US 0141321P.

PR 04-JUL-1999; 99US 014313P.

PR 13-JUL-1999; 99US 014313P.

PR 13-JUL-1999; 99US 014313P.

PR 13-JUL-1999; 99US 014313P.

PR 13-JUL-1999; 99US 014313P.

PR 13-JUL-1999; 99US 014313P.

PR 13-JUL-1999; 99US 014313P.

PR 20-JUL-1999; 99US 014313P.

PR 20-JUL-1999; 99US 014313P.

PR 20-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 014313P.

PR 21-JUL-1999; 99US 01
```

```
0
                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                             Gaps
                                                                                                                             ö
                                                                                                         2.1%; Score 7; DB 3; Length 576; llarity 100.0%; Pred. No. 8.4e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 49260.
                                                                                                                                                                                                          AAG39771 standard; protein; 614 AA.
990S-0160989P.
990S-0161406P.
990S-0161406P.
990S-0161359P.
990S-0161360P.
990S-0161361P.
990S-0161920P.
990S-0161922P.
                                                                                                                                                                                                                                                                                                                                                                                        990S-0121825P.
990S-0123180P.
990S-0125788P.
990S-012664P.
990S-01267462P.
990S-0128744P.
990S-0128744P.
990S-0128744P.
990S-0138449P.
990S-0138449P.
990S-0138449P.
990S-0131449P.
990S-0131449P.
990S-0132448P.
990S-0132488P.
990S-0132488P.
990S-0132488P.
990S-0132488P.
990S-0132488P.
990S-0132488P.
990S-0132488P.
990S-0132488P.
990S-0132488P.
990S-0132488P.
990S-0134219P.
990S-0134219P.
990S-0134219P.
                                                                                                                                                                                                                                                                                                                                                                       25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                                                                            18-OCT-2000 (first entry)
                                                                                                                                           292 EILLKNO 298
                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                             34 EILLKNO 40
                                                                                                                  Local Similarity
es 7; Conserv
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1999;
05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
26-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
19-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                    EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                      06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAY-1999
14-MAY-1999
                                                                                                                                                                                                                           AAG39771;
                                                                                                         Query Match
                                                                                                                                                                                         RESULT 126
                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                  AAG39771
q
                                                                                                                                                                                                          ð
```

02-AUG-1999; 02-AUG-1999; 03-AUG-1999; 04-AUG-1999; 05-AUG-1999; 05-AUG-1999; 06-AUG-1999; 09-AUG-1999; 10-AUG-1999; 11-AUG-1999;	PR 11-AUG-1999; 99US-0148565P. PR 16-AUG-1999; 99US-0149426P. PR 17-AUG-1999; 99US-0149426P. PR 20-AUG-1999; 99US-0149723P. PR 20-AUG-1999; 99US-0149723P. PR 20-AUG-1999; 99US-0149723P. PR 22-AUG-1999; 99US-0149929P. PR 22-AUG-1999; 99US-0149929P. PR 23-AUG-1999; 99US-0150566P. PR 23-AUG-1999; 99US-0150566P. PR 27-AUG-1999; 99US-015066P. PR 27-AUG-1999; 99US-015066P. PR 27-AUG-1999; 99US-015066P. PR 27-AUG-1999; 99US-015066P. PR 27-AUG-1999; 99US-015066P. PR 27-AUG-1999; 99US-015106F. PR 27-AUG-1999; 99US-015106P. PR 27-AUG-1999; 99US-015106P. PR 27-AUG-1999; 99US-015106P. PR 27-AUG-1999; 99US-015106P. PR 27-AUG-1999; 99US-015106P. PR 27-AUG-1999; 99US-015106P. PR 27-AUG-1999; 99US-0154018P. PR 28-SEP-1999; 99US-0154018P. PR 28-SEP-1999; 99US-015549P. PR 29-SEP-1999; 99US-015549P. PR 29-SEP-1999; 99US-015549P. PR 29-SEP-1999; 99US-015549P. PR 20-CT-1999; 99US-015753P. PR 13-OCT-1999; 99US-015923P. PR 13-OCT-1999; 99US-015923P. PR 13-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US-0159331P. PR 14-OCT-1999; 99US	21-OCT-1999; 21-OCT-1999; 21-OCT-1999; 21-OCT-1999; 22-OCT-1999; 22-OCT-1999; 22-OCT-1999; 25-OCT-1999; 25-OCT-1999; 25-OCT-1999; 26-OCT-1999; 26-OCT-1999; 26-OCT-1999;
	999 9905 0134453P. 999 9905 0134454P. 999 9905 0134454P. 999 9905 0134454P. 999 9905 0134454P. 999 9905 0134458P. 999 9905 0134458P. 999 9905 0134654P. 9905 0134654P. 9905 0134654P. 9905 0134654P. 9905 0134654P. 9905 0144285P. 9905 0142854P. 9905 0142854P. 9905 0142854P. 9905 0142854P. 9905 0142854P. 9905 0142854P. 9905 0142854P. 9905 0143854P. 9905 0143854P. 9905 0143854P. 9905 0144385P. 9905 0144382P. 9905 0144333P. 9905 0144333P. 9905 0144333P. 9905 0144333P. 9905 0144333P. 9905 0144333P. 9905 0144333P. 9905 0144333P. 9905 0144333P. 9905 0144333P. 9905 0144333P. 9905 0144333P. 9905 0144333P. 9905 0144333P. 9905 0144333P. 9905 0144333P. 9905 0144333P. 9905 014433P.	S066 S066 S066 S066 S066 S066 S066 S066
21 MAY-24-MAY-25-MAY-27-MAY-27-MAY-27-MAY-27-MAY-28-MAY-28-MAY-28-MAY-28-MAY-27-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28-MAY-28	PR 17-UW-1999; PR 18-UW-1999; PR 18-UW-1999; PR 18-UW-1999; PR 18-UW-1999; PR 18-UW-1999; PR 18-UW-1999; PR 18-UW-1999; PR 22-UW-1999; PR 22-UW-1999; PR 23-UW-1999; PR 23-UW-1999; PR 23-UW-1999; PR 23-UW-1999; PR 24-UW-1999; PR 24-UW-1999; PR 24-UW-1999; PR 24-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 19-UW-1999; PR 20-UW-1999; PR 20-UW-1999; PR 20-UW-1999; PR 20-UW-1999; PR 20-UW-1999; PR 20-UW-1999;	21-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22-741-22

```
990S-0113724P

990S-0113804P

990S-0113844P

990S-01139452P

990S-01139452P

990S-01139452P

990S-01139452P

990S-01139452P

990S-01139452P

990S-01139452P

990S-01139452P

990S-01139452P

990S-01139452P

990S-01139452P

990S-01139452P

990S-01139452P

990S-01139452P

990S-01139452P

990S-01139452P

990S-01139452P

990S-01139451P

990S-01139451P

990S-01139451P

990S-01139451P

990S-01139451P

990S-0144085P

990S-0144085P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0144334P

990S-0146338P

990S-014538P

990S-014538P

990S-014538P

990S-014538P

990S-014538P

990S-014738P

990S-014738P

990S-014738P
     04-JUN-1999;
07-JUN-1999;
08-JUN-1999;
10-JUN-1999;
14-JUN-1999;
16-JUN-1999;
16-JUN-1999;
17-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                        18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                   18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                                                                                                                         21-JUN-1999;
22-JUN-1999;
23-JUN-1999;
                                                                                                                                                                                                                                      23-JUN-1999;
24-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
       ó
                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                       Gaps
                                                                      ö
                                              Query Match 2.1%; Score 7; DB 3; Length 614; Best Local Similarity 100.0%; Pred. No. 8.9e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 38784.
                                                                                                                                                   AAG32189 standard; protein; 622 AA.
99US-0161920P.
99US-0161992P.
99US-0161993P.
99US-0162142P.
                                                                                                                                                                                                                                                                                                                                              990S-0121825P.
990S-0123180P.
990S-0125788P.
990S-012664P.
990S-012664P.
990S-0128234P.
990S-0128234P.
990S-0128234P.
990S-0130610P.
990S-0130649P.
990S-0130649P.
990S-0130649P.
990S-0130649P.
990S-0130649P.
990S-0130649P.
990S-0130649P.
990S-0131848P.
990S-0132488P.
990S-0132488P.
990S-0132488P.
990S-013448P.
990S-013448P.
990S-013448P.
990S-0134219P.
990S-0134219P.
990S-0134218P.
990S-0134219P.
990S-0134219P.
990S-0134219P.
990S-0134219P.
990S-0134219P.
990S-0134219P.
990S-0134219P.
                                                                                                                                                                                                                                                                                                                            25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                         17-OCT-2000 (first entry)
                                                                                                    261 LYSSGLL 267
                                                                                                                                                                                                                                                                      Arabidopsis thaliana.
                                                                                     73 LYSSGLL 79
 28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                        EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                             25-FEB-1999;
05-MAR-1999;
03-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                             19-APR-1999;
21-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 - APR - 1999

28 - APR - 1999

30 - APR - 1999

30 - APR - 1999

60 - MAX - 1999

60 - MAX - 1999

60 - MAX - 1999

61 - MAX - 1999

11 - MAX - 1999

14 - MAX - 1999

14 - MAX - 1999

18 - MAX - 1999

19 - MAX - 1999

19 - MAX - 1999

21 - MAX - 1999

21 - MAX - 1999

22 - MAX - 1999

24 - MAX - 1999

25 - MAX - 1999

26 - MAX - 1999

27 - MAX - 1999

28 - MAX - 1999

29 - MAX - 1999

20 - MAX - 1999

21 - MAX - 1999

22 - MAX - 1999

24 - MAX - 1999

25 - MAX - 1999

26 - MAX - 1999

27 - MAX - 1999

28 - MAX - 1999

28 - MAX - 1999

29 - MAX - 1999

20 - MAX - 1999

21 - MAX - 1999

21 - MAX - 1999

22 - MAX - 1999

23 - MAX - 1999

24 - MAX - 1999
                                                                                                                                                                                                                                                                                                           06-SEP-2000
                                                                                                                                                                        AAG32189;
                                                                                                                                   RESULT 127
                                                                                                                                          g
  PR
PR
PR
                                                                                     ઠે
```

```
990S-0147303P.
990S-0147416P.
990S-0147935P.
990S-0148131P.
990S-01481319P.
990S-0148341P.
990S-0148565P.
990S-0149328P.
990S-0149328P.
990S-0149728P.
990S-0149728P.
990S-0149929P.
990S-0149929P.
990S-015066P.
990S-015108P.
990S-015108P.
990S-015108P.
990S-015108P.
990S-015108P.
990S-015108P.
990S-015108P.
990S-015108P.
990S-015108P.
990S-015108P.
                                                                                                                                                                                                                                                                                                    990S-0160767P
990S-0160768P
990S-0160710P
990S-0160814P
990S-0160980P
                                                                                                                                                                                                    990S-01565969
990S-0157117P-
990S-01578659-
990S-0158029P-
990S-0158232P-
990S-0159294P-
990S-0159294P-
990S-0159294P-
990S-0159294P-
                                                                                                                                                                                                                                                                   99US-0159330P.
99US-0159331P.
99US-0159637P.
99US-0159584P.
99US-0160741P.
                                                                                                                                                                                                                                                                                                                                                                   99US-0161359P.
                                                                                                                                                                                                                                                                                                                                            99US-0160989P.
                                                                                                                                                                                                                                                                                                                                                        99US-0161405P
                                                                                                                                                                                                                                                                                                                                                                               99US-0161361P.
                     10-AUG-1999;
11-AUG-1999;
12-AUG-1999;
13-AUG-1999;
                                                 16-AUG-1999;
17-AUG-1999;
18-AUG-1999;
20-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                     06-0CT-1999;
                                                                                                                                                                                                                                                                              14-OCT-1999
                                                                                                                                                                                                                                                                                                                21-OCT-1999
                                                                                                                                                                                                                                                                                                                      21-OCT-1999
                                                                                                                                                                                                                                                                                                                                       22-OCT-1999
                                                                                                                                                                                                                                                                                                                                                              25-0CT-1999
```

```
Query Match 2.1%; Score 7; DB 3; Length 622; Best Local Similarity 100.0%; Pred. No. 9e+02;
99US-0161992P.
99US-0161993P.
99US-0162142P.
```

Sequence 647 AA;

```
The present invention describes new human secreted proteins which were isolated from adult placenta, adult retina, foetal brain, foetal kidney, adult blood, adult brain, adult thyroid, adult bladder, adult neural tissue, adult testes, and adult lymph node cDNA libraries. The human secreted proteins, and the polymucleotides encoding them, are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include mutritional activity, cotokine and correctives or suppressing activity, hemmatopoiesis regulating (e.g. as vaccines) or suppressing activity, hemmatopoiesis regulating activity, tissue growth activity, activin/inhibin activity, cadherin/tumour consequence of receptor/ligand activity, and tumour inhibition activity. The polymucleotides are also stated to be useful for gene therapy. AA23316 to AA23373 encode human secreted proteins, and AAY52998 to AAY53060 represent human secreted proteins, given in the present invention
     ö
                                                                                                                                                                                                                                                                                       Human; secreted protein, nutritional; cytokine; cell proliferation; differentiation; immune stimulating; vaccine; suppression; haematopoiseis regulation; tissue growth; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; cadherin; tumour invasion suppressor; tumour inhibition; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides encoding secreted human proteins, derived from adult placenta, adult retina, fetal brain, fetal.
     Gaps
                                                                                                                                                                                                                                                        Human secreted protein clone dn721_8 protein sequence SEQ ID NO:6.
   .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collins-Racie LA, Evans C;
Steininger RJ, Bowman MR;
     Indels
   ;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; Page 365-367; 492pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lavallie ER,
Agostino MJ,
                                                                                                                                                      AAY53000 standard; protein; 647 AA.
   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0087645P.
98US-0087645P.
98US-0093712P.
98US-0094935P.
98US-0096068P.
99US-00306111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US009970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Merberg D, Treacy M, Agos
Diblasio-Smith E, Widom A;
                                                                                                                                                                                                                     29-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEMY ) GENETICS INST INC.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jacobs K, Mccoy JM,
Merberg D, Treacy M,
                                  301 LIBFLSS 307
                                                                  240 LIEFLSS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-052937/04.
N-PSDB; AAZ33318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9957132-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-AUG-1998;
11-AUG-1998;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JUL-1998
                                                                                                                                                                                      AAY53000;
                                                                                                                      RESULT 128
Matches
                                                                                                                                      AAY53000
                                  à
                                                            qq
```

```
The invention relates to a novel pharmaceutical composition comprising a nucleic acid molecule or polypeptide which is a human homologue of a brosophila melangaster polypeptide or polymuclectide. The composition of the invention may be utilised during the diagnosis, study, prevention and treatment of diseases related to body-weight regulation and thermogenesis including metabolic disorders such as obeatty, Syndrome x and insulineresistance syndrome and eating disorders e.g. cachexia, diabetes mellitus, hypertension, pancreatic dysfunctions, arteriosclerosis, coronary heart disease, hypercholesterolaemia, dyslipidaemia, osteonary heart disease, Phypercholesterolaemia, dyslipidaemia, osteoarthritis and gallstones. Furthermore, disorders related to reactive oxygen species (ROS) defence may be addressed by the invention including neurodegenerative disorders or mitochondrial disorders. Finally, the
                                                                                                                                                                                                                                                                                                                                                                    Anorectic; antiinflammatory; cardiant; hypotensive; antidiabetic; OPA1; neuroprotective; pharmaceutical composition; body-weight regulation; thermogenesis; metabolic; obesity; Syndrome X; insulin-resistance; eating disorder; cachexia; diabetes mellitus; hypertension; gallstone; hypercholesterolaemia; dyslipidaemia; ocronary heart disease; hypercholesterolaemia; dyslipidaemia; osteoarthritis; ROS defence; reactive oxygen species; neurodegenerative; mitochondrial; gene therapy; human; optic atrophy 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New pharmaceutical composition, useful for the manufacture of an agent for diagnosing, treating or preventing disorders related to body-weight regulation and thermogenesis, e.g., metabolic diseases such as obesity.
                                                            Gaps
                                                            ;
                   2.1%; Score 7; DB 3; Length 647;
100.0%; Pred. No. 9.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eulenberg K, Broenner G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Encoded by TCCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                      AAO23969 standard; protein; 658 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Fig 2C; 144pp; English.
                                                                                                                                                                                                                                                                                                                                    Human optic atrophy 1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002EP-00003473.
2002EP-00004687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-2002; 2002EP-0009475.
18-JUN-2002; 2002EP-00013329.
30-DEC-2002; 2002EP-00029081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JAN-2003; 2003WO-EP000738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002EP-00001806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molitor A,
Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 633. .634
                                                                                                                              585 EEVSKSL 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2003-627418/59.
                                                                                           40 EEVSKSL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-627418/
N-PSDB; AAL57523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO2003061681-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Steuernagel A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-FEB-2002;
28-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUL-2003
                                                                                                                                                                                                                                                            AA023969;
                                                                                                                                                                                    RESULT 129
                                                                                                                          d
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences (ABL101840-ABL10117) expressed DNA sequences (ABL101840-ABL10175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
composition of the invention may be useful in gene therapy. The current sequence is that of the human optic atrophy 1 (OPA1) protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                             developmental biology; cell signalling; insecticide;
                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 40554; 21pp + Sequence Listing; English.
                                                                                               Length 658;
                                                                                                                            0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 4; Length 685; 100.0%; Pred. No. 9.9e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 40554.
                                                                                             2.1%; Score 7; DB 6; Let
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myers EW;
                                                                                                                                                                                                                                                                   ABB71254 standard; protein; 685 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                          231 LIGELIL 237
                                                                                                                                                                                         210 ilGÉLÍL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 ISKPENL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISKPENL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                Sequence 658 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABL15357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 685 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                 pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interactions.
                                                                                                                                                                                                                                                                                                                                                                                             Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
                                  invention
                                                                                                                                                                                                                                                                                                 ABB71254;
                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                    RESULT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                  ន្តដូន្ត
                                                                                                                                                          ò
                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                            .
0
```

```
WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                04-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2001.
                                                                                                                                                                                                                                                                                                         activity.
                                                                                                                                       (SILV/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 133
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to proline-rich extensin-like receptor kinase (PBRK). The PERK nucleic acids and polypeptides are useful for increasing the resistance of plants to wounding and pathogens. These are also useful for producing transgenic plants with increased wounding and pathogen resistance compared with a wild type plant, as well as in assays for identifying and developing compounds to inhibit and/or enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New proline-rich, extensin-like receptor kinase nucleic acids and polypeptides useful for increasing plant wounding or pathogen resistance, or for producing transgenic plants with increased wounding or pathogen
                                                                                                                                                     Proline-rich extensin-like receptor kinase; PRRK; resistance; plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERKI; transgenic; plant; proline-rich extensin-like receptor kinase; wound; pathogen resistance; plant growth; seed production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; Score 7; DB 4; Length 731;
100.0%; Pred. No. 1.1e+03;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis PERK1 receptor related protein.
                                                                                                                          Protein encoded by Arabidopsis gene #1.
                                 AAB74206 standard; protein; 731 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABR82939 standard; protein; 731 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Fig 11; 91pp; English.
                                                                                                                                                                                                                                                                              18-AUG-2000; 2000WO-CA000966.
                                                                                                                                                                                                                                                                                                              99US-0149466P
                                                                                                                                                                                                                                                                                                                              99US-0159122P
                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                     Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 KVLVADF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           519 KVLVADF 525
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-244305/25
                                                                                                                                                                                                                                                                                                                                                                                                        Goring D, Silva N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity es 7; Conserv
                                                                                                                                                                                                                                                                                                                                                        (GORI/) GORING D. (SILVA) SILVA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 731 AA;
                                                                                                                                                                                                                  WO200114563-A1.
                                                                                                                                                                                                                                                                                                              19-AUG-1999;
                                                                                                                                                                                                                                                                                                                             13-OCT-1999;
                                                                                           17-MAY-2001
                                                                                                                                                                                                                                                 01-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resistance,
                                                              AAB74206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR82939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
```

WO2003072763-A1.

```
The invention relates to producing a transgenic plant having increased plant height, number of branches, number of seed pods and/or seed production compared to a non-transgenic plant, and/or guitcker flowering or later sensecence compared to a non-transgenic plant. The method Extensin-like Receptor Kinase (PEKF) nucleic acid molecule or a mucleic acid molecule having PEKR activity. The method, as well as the PEKR nucleic acid molecule and polypeptide, are useful in increasing plant resistance to wounding and pathogens and in increasing plant growth and seed production. The mucleic acid molecule and polypeptide may also be used in producing transgenic plants or transgenic host cells. The present sequence represents a PERKI polypeptide related protein from A. thaliana
                                                                                                                                                                                                                                                                                                                                                        Producing a transgenic plant having an increased plant resistance, plant growth or seed production comprises transforming a plant with a nucleic acid molecule having a Proline-rich Extensin-like Receptor Kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7; Length 731;
5. 1.1e+03;
ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
2.1%; Score 7; DB 7
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #25920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fig 11, 123pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG25929 standard; protein; 760 AA.
                                                                                                                                                                                                                                  Soring D, Silva N, Haffani YZ;
28-FEB-2003; 2003WO-CA000274,
                                                28-FEB-2002; 2002CA-02373903.
28-FEB-2002; 2002US-00086464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Accession NO. AAC98010)
                                                                                                                                                                                                                                                                                WPI; 2003-712727/67.
N-PSDB; ACF36550.
                                                                                                                                                                            (HAFF/) HAFFANI Y Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 KVLVADF 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     519 KVLVADF 525
                                                                                                                              (GORI/) GORING D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 731 AA;
```

ö

```
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed correct corrections. (II) is useful in gene therapy techniques to restore normal cutvity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a supplement. (II) and its binding partners are useful in medical imaging copypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging (II). (I) and (II) are useful in medical imaging copypaptide and polynucleotide sequences have applications in the prince of the sequence of muscations conditions in the produce other types of data and products dependent on DNA and and and to produce other types of data and products dependent on DNA and mino acid sequences. Abgonolo-Abgo3037 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the printed patences.
                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purine/pyrimidine triphosphate type nucleotidyltransferase #156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotidylyltransferase, enzyme, active site engineering, alpha-D-glucopyranosyl phosphate thymidylyltransferase, Ep, substrate specificity, nucleotide sugar, glycosylated bioactive natural product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 7; DB 4
100.0%; Pred. No. 1.1.
live 0; Mismatches
                                                                                                                                                                                                                  Claim 20; SEQ ID NO 56288; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SLOK ) SLOAN KETTERING INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG91571 standard; protein; 831 AA.
                                        Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-DEC-2001; 2001WO-US047953.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-DEC-2000; 2000US-0254927P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 7; Conservative
                                                                        2001-639362/73.
                                   Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 IGTRSPT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 İĞİRSPİ 242
(HYSE-) HYSEQ INC.
                                                                                         N-PSDB; AAS90116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 760 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200248331-A2.
                                                                                                                                                                                     biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG91571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG9157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
```

```
The invention relates to a Nucleotidylyltransferase mutated at one or more amino acids selected from V173, G147, W224, N112, G175, D111, E162, T201, 1200, E199, E195, E897, L109, Y146 or Y177 (with reference to the Salmonella enterica rmlA-encoded alpha-D-glucopyranosyl phosphate the Salmonella enterica rmlA-encoded alpha-D-glucopyranosyl phosphate the Salmonella enterica rmlA-encoded alpha-D-glucopyranosyl phosphate altering nucleotidylyltransferase substrate specificity of the enzymes. The mutants and methods altering nucleotidylyltransferase substrate specificity. The nucleotidylyltransferase exhibits different substrate specificity for GTP, CTP, TTP, UTP and ATP than a non-mutated mucleotidylyltransferase. The mutant may also exhibit a high degree of sequence identity to Salmonella enterica LT2 alpha-D-glucopyranosyl phosphate thymidylyltransferase (Ep) and can convert a wide variety of phosphates. The mutants can be exploited in the biosynthesis of glycosylated bloactive natural products of pharmacological use. The present sequence identity to Salmonella enterica LT2 alpha-D-glucopyranosyl phosphate of sequence identity to Salmonella enterica LT2 alpha-D-glucopyranosyl phosphate the specification but was obtained from Genbank
                                                                                                                         Nucleotidylyltransferase mutated at one or more amino acids, useful in the synthesis of nucleotide sugars.
                                                                                                                                                                                                    Claim 3; Page; 182pp; English.
                          Thorson JS, Nikilov DB;
                                                                           WPI; 2002-608282/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 831 AA;
```

0; Gaps Query Match 2.1%; Score 7; DB 5; Length 831; Best Local Similarity 100.0%; Pred. No. 1.2e+03; Matches 7; Conservative 0; Mismatches 0; Indels AAE17313 standard; protein; 855 AA. 18-APR-2002 (first entry) 219 SENYVTK 225 533 SENYVIK 539 AAE17313; RESULT 135 d ò 

·,

Gaps

.; 0

Human protocadherin protein, abg419582PROTOCADHERIN #2.

ö

Human; therapy; wound healing disorder; vaccine; cancer; infection; particis, autoimmune disorder; haematopoietic disorder; inflammation; arthritis; Parkinson; a disease; huntington's chizophrenia; antiarrhythmic; multiple sclarosis; Alzheimer's disease; analgesic; cardiant; asthma; ischaemia; stroke; AlDS; bone disease; atherosclerosis; brain disorder; depression; cardiovascular disease; atherosclerosis; brain disorder; respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder; type II diabetes mellitus; skeletal muscle disorder; immunosuppressive; type II diabetes mellitus; disease; hypoglycaemia; gastrointestinal disease; nootropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory; haemostatic; vulnerary; anticonvulsant; antirheumatic; neuroprotective; allergy; protocadherin.

WO200198342-A1. Homo sapiens.

27-DEC-2001.

22-JUN-2001; 2001WO-US019929.

```
The invention relates to secreted and membrane-associated polypeptides and polymucleotides. The sequences of the invention are useful in cliagoratic assays for detecting diseases associated with inappropriate activity or levels of these polymucleotides, and in identifying their sequences of the invention are useful in therapy. The sequences of the invention are useful in therapy. The immunological response. The sequences of the invention are useful for cliamunological response. The sequences of the invention are useful for inflammation, congenital muscrolar disorders, haematopoietic clisorders, wound healing disorders, cholesteryl ester storage disease, inflammation, congenital muscrolar dystrophy, junctional epidermolysis bullosa, parkinson's disease, Huntington's chorea, multiple sclerobis, bullosa, parkinson's disease, Huntington's chorea, multiple sclerobis, alteraphrenia, sbg42445pRoa-associated disorders, collection, cliftammatory bowel disease, asthma, arthritis, cliftamia, psoriasis, inflammatory bowel disease, asthma, arthritis, cliftamia, psoriasis, inflammatory bowel disease, atherosclerosis, spridcome, restenosis, brain injury, AIDS, bone diseases, atherosclerosis, diseases including paraeupranuclear palsy, myotonic dystrophy, depression, anxiety disorders and aleep disorders, cardiovascular crespiratory disease, including congestive heart failure and myocardial infarction, crespiratory diseases including congestive heart failure and myocardial infarction, crespiratory diseases including characterial constructive pulmonary disease, including paraeupranicle obstructive pulmonary disease, including dypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral cliftuding acute and chronic renal failure, glomentulonaphritis, proper including disease including acute and chronic renal failure, including acute and chronic renal failure, including acute and chronic renal failure including acute and chronic renal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       syndrome, cystinuria, skeletal muscle disorders including hypoglycaemia and tendinitis, gastrointestinal diseases including intestinal obstruction and tropical sprue, spleen disorders including hypersplenism, Hodgkin's disease and malignant lymphoma, testicular cancer, male reproductive diseases including low testosterone and male infertility.
                                                                                                                                                                                                                                                                                          Novel secreted and membrane-associated polypeptides and polynucleotides useful for preventing, ameliorating or correcting dysfunction or disease including diabetes, cancer, hypertension and growth abnormalities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                Martensen SA;
Xie Q, Rizni SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 5; Length 855;
100.0%; Pred. No. 1.2e+03;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                               Kabnic KS, Lai x, .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is human protocadherin protein
                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 125-127; 138pp; English.
                                                                                                                                                                                Strum JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE24242 standard; protein; 873 AA.
                                                               (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. (GLAX ) GLAXO GROUP LTD.
22-JUN-2000; 2000US-0213156P. 22-JUN-2000; 2000US-0213161P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                         Cogswell JP,
                                                                                                            GLAXO GROUP LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
                                                                                                                                                                                Smith RF,
                                                                                                                                                                                                                           2002-139783/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSGLLVT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                N-PSDB; AAD27808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSGLLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 855 AA;
                                                                                                                                                         Agarwal P,
Murdock PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE24242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
à
```

```
cardiovascular disorder; atherosclerosis; arrhythmia; ischaemia; anaemia; myocardial infarction; blood clotting disorder; dermatological; virucide; endothelial cell disorder; immunosuppressive; transgenic animal; cancer; hypertension; drug screening; vasotropic; blood vessel related disorder;
neurological disorder; systemic lupus erythematosus; Parkinson's disease;
                                                                                                                                                                                                                                                                                                   'note= "Cadherin extracellular domain signature motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cadherin extracellular domain signature motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cadherin extracellular domain signature motif"
                                                                                                                                                            'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                            /note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                               'note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                   'note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                      note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                           "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                           "RGD cell attachment sequence"
                                                                                                                                                      "Human mature 57779 protein"
                                                                                                                                                                                                                                       "N-myristylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "N-myristylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "N-glycosylation site"
                                                                                                                                   "Cadherin domain"
                                                                                                                                                                                                                                                                                                                    /note= "Cadherin domain"
147. .154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cadherin domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cadherin domain"
                                                                                                              label= Signal_peptide
                                                                                            location/Qualifiers
                                                                                                                                                                                                                                                                     .111
                                                                                                                                                                                                                                                                                                             .229
                                                                                                                                                                                                                                                                                                                                                      .155
                                                                                                                                                                                                                                                                                                                                                                          .172
                                                                                                                                                                                                                                                                                                                                                                                                                                    .189
                                                                                                                                                                                                                                                                                         .127
                                                                                                                                                                                                                                                                                                                                                                                              .183
                                                                                                                                                                                                                                                                                                                                                                                                                  .183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 249
                                                                                                                          .120
                                                                                                                                              .873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .376
                                                                                                                                                                                                                                                                                                                                                                                                                                                           .207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435. .437
                                                                                                                                                                                                                                                 .98
                                                                                                                                                                                                                             . 84
                                                                                                                                                                                                                                                                                                                                            'note=
                                                                                                                                                                                                                                        note=
                                                                                                                                    'note=
                                                                                                                                                        note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note=
                                                                                                                                                                                                                                                                                                                                                                                                                            'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                  psoriasis; nootropic.
                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                    Peptide
                                                                                                                                             Protein
                                                                                                                         Domain
                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
```

Human; carboxypeptidase; scramblase; protocadherin protein; gene therapy; inflammatory disorder; diabetes mellitus; arthritis; Alzheimer's disease;

Human 57779 (protocadherin) protein.

Meyers RA, Curtis RAJ, Kapeller-Libermann R;

(MILL-) MILLENNIUM PHARM INC.

```
"Cadherin extracellular domain signature motif"
                                                                                                                                                                                                 "Cadherin extracellular domain signature motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49. .751
'note= "Protein kinase C phosphorylation site"
'note= "Protein kinase C phosphorylation site"
                                                76. .479
'note= "Casein kinase II phosphorylation site"
                                                                   76. .478
note= "Protein Kinase C phosphorylation site"
                                                                                                                                                                              'note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                               "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                   note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                      note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                           note= "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                              "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                           /note= "Glycosaminoglycan attachment site"
508. .611
                                                                                                'note= "N-myristylation site"
                                                                                                                     "N-glycosylation site"
                                                                                                                                                                                                                      "N-glycosylation site"
                                                                                                                                                           "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                  note= "N-glycosylation site"
                                                                                                                                         "N-myristylation site"
                                                                                                                                                                                                                                                                                                                                                                                                     note= "Transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                          note= "N-myristylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                            "Intracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "N-myristylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Extracellular domain"
                                       "Cadherin domain"
                                                                                                                                                                                                                                         "Cadherin domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-OCT-2000; 2000US-0241989P.
20-OCT-2000; 2000US-0242324P.
23-OCT-2000; 2000US-0242518P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-2001; 2001WO-US046717.
                                                                                                     /note= "w
                                                                                                                                                                                                                                                                                                                                                                                                                              835
/note= "T-"
                                                                                                                                                                                    . .561
/note= "C~
                                                                                                                                                  .549
                                                                                                                                                                   .550
                                                                                         .488
                                                                                                                                                                                                                                                   .584
                                                                                                                                                                                                                                                                                          .628
                                                                                                                                                                                                                                                                                                              .632
                                                                                                                                                                                                                                                                                                                                                     .639
                                                                                                                                                                                                                                                                                                                                                                        .679
                              . 554
                                                                                                                                                                                                                                .663
                                                                                                                                                                                                                                                                                                                                 .635
                                                                                                                                                                                                                                                                                                                                                                                           .701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35. .738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .859
            .451
                                                                                                                                                                                                                                                                                                                                                                                                               686. .691
                                                                                                                                         note=
                                                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                                                               note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note=
                                        note=
                                                                                                                                                                                                                       note=
                                                                                                                                                                                                                                           'note=
                   note=
                                                                                                                                                                                                                                                                                 note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200233088-A2
                                               Modified-site
                                                                                       Modified-site
                                                                                                                                                Modified-site
                                                                                                                                                                   Modified-site
                                                                   Modified-site
                                                                                                           Modified-site
                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                  Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-APR-2002
                                                                                                                                                                                        Domain
           Domain
                              Domain
                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
```

```
The invention relates to isolated human carboxypeptidase, scramblase and protocadherin protein. The nucleic acids encoding the polypeptides are designated as 23566, 33489 and 57779 respectively. Examples of the conditions related to aberrant activity or expression of the invention include, inflammatory disorders such as diabetes mellitus, arthritis, conditions erythematosus; neurological disorders acid as athariance, gisedematic lupus erythematosus; neurological disorders (e.g. disease, Parkinson's disease; cardiovascular disorders (e.g. the heart and/or blood vessels) such as atherosclerosis, arthythmia, conditionation blood vessels include endothelial cell disorders e.g. thrombocytopaenia; or cellular proliferation or differentiation disorders controlling assays in competition blood clotting disorders e.g. thrombocytopaenias, blood vessel related disorders e.g. hypertension and disorders involving red blood cells e.g. anammia; and viral diseases e.g. hepatitis but invention is useful for producing antibodies, in drug correening assays, in competition binding assays to discover compounds that interact with the protein, in pharmacogenomic analysis and for monitoring therapeutic effects during clinical trials and treatment. The antibody is useful to assess abnormal tissue distribution or abnormal expression during development, to identify protein turnover, to assess correnal and aberrant subcellular localisation of cells in various tissues of that macogenomic analysis, for tissue typing, forensic identification, in pharmacogenomic analysis, for tissue typing, forensic identification, in the chromosomal positions of the polymucleotides, for expressing antigenic paptides, for expressing antigenic paptides, for designing ribozymes, constructing host cells, transgenic animals. The
                                                                                                                                                                                                                           polynucleotides for identifying modulators for use in diagnosing,
treating diabetes mellitus, atherosclerosis, cancer, Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               depression; cardiovascular disease; myocardial infarction; renal failure; respiratory disease; liver disorder; Fanconi's syndrome; spleen disorder; type II diabetes mellitus; skeletal muscle disorder; immunosupressive; hypersplenism; renal disease; hypoglycaemia; gastrointestinal disease; nootropic; cirrhosis; Hodgkin's disease; neuroleptic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, therapy; wound healing disorder; vaccine; cancer; infection; autoimmune disorder; haematopoietic disorder; inflammation; arthritis; Parkinson's disease; Huntingfon's chorea; schizophrenia; antiarrhythmic; multiple sclerosis; Alzheimer's disease; analgesic; cardiant; asthma; ischaemia; stroke; AlDS; bone disease; atherosclerosis; brain disorder;
                                                                                                                                                                                              New human carboxypeptidase, scramblase, and protocadherin protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protocadherin protein, sbg419582PROTOCADHERIN #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 5; Ler
100.0%; Pred. No. 1.2e+03;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE17312 standard; protein; 888 AA.
                                                                                                                                                                                                                                                                                                   Claim 5; Page 144; 170pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
7; Conserva
                                                                                                                       WPI; 2002-471400/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 SSGLLVT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSGLLVT 81
                                                                                                                                                 N-PSDB; AAD39055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 873 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE17312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 137
%X4X4X4X4444X4X6CCCCCCCCCCX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

ó

```
and polymucheotides. The sequenced and membrane associated with inappropriate diagnostic assays for detecting diseases associated with inappropriate activity or levels of these polymucheotides, and in identifying their activity or levels of these polymucheotides, and in identifying their agonists and antagonists that are potentially useful in therapy. The sequences of the invention are useful in therapy. The immunological response. The sequences of the invention are useful for treating cancers, infections, autoimmune disorders, haematopoietic disorders, wound healing disorders, cholesteryl ester storage disease, inflammation, congenical muscular dystrophy, junctional epidermolysis bullosa, Parkinson's disease, Holican's chorea, multiple sclerosis, viral and bacterial infections, Alzheimer's disease, asthma, arthritis, septicaemia, psoriasis, inflammation, bowel disease, transplant rejection, graft verse host disease, isohaemia, stroke, acute respiratory disease septicaemia, psoriasis, inflammation, bowel diseases, tatasplant rejection, depression, anxiety disorders and sleep disorders, cardiovascular respiratory diseases including parasupranuclear pallsy, myotonic dystrophy, diseases including parasupranuclear pallsy, myotonic dystrophy, diseases including parasupranuclear pallsy, myotonic dystrophy, diseases including congestive heart failure and myocadial infarction, respiratory disease including congestive heart failure and myocadial infarction,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         respiratory diseases including chronic obstructive pulmonary disease, acute bronchits and adult respiratory distress syndrome, liver disorders including hypercholesterolaemia, hypertriglyceridaemia, cirrhosis, viral and non-viral hepatitis, type II diables mellitus, renal disease including acute and chronic renal failure, glomerulonephritis, Fanconi's syndrome, cystimuria, skeletal muscle disorders including hypoglycaemia and tendinitis, gastronitestinal diseases including intestinal obstruction and tropical sprue, spleen disorders including hypersplenism, Hodgkin's disease and malignant lymphoma, testicular cancer, male reproductive diseases including low testosterone and male infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel secreted and membrane-associated polypeptides and polymucleotides useful for preventing, ameliorating or correcting dysfunction or disease including diabetes, cancer, hypertension and growth abnormalities.
haemostatic, vulnerary, anticonvulsant, antirheumatic, neuroprotective, nephrotropic, hypotensive, vasotropic, cytostatic, cerebroprotective, allergy, protocadherin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to secreted and membrane-associated polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kabnic KS, Lai Y,
Strum JC, Xiang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 123-125; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                        BEECHAM CORP.
BEECHAM PLC.
                                                                                                                                                                                                                                               22-JUN-2001; 2001WO-US019929.
                                                                                                                                                                                                                                                                                              2000US-0213156P.
2000US-0213161P.
                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECH!
(SMIK ) SMITHKLINE BEECH!
(GLAX ) GLAXO GROUP LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cogswell JP,
Smith RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-139783/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAD27807
                                                                                                                                             WO200198342-A1.
                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                              22-JUN-2000;
22-JUN-2000;
                                                                                                                                                                                              27-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agarwal P,
Murdock PR,
```

The present sequence is human protocadherin protein Sequence 888 AA; Query Match

2.1%; Score 7; DB 5; Length 888; 100.0%; Pred. No. 1.3e+03; ive 0; Mismatches 0; Indels Local Similarity 100. es 7; Conservative 75 SSGLLVT 81 Best Loca Matches

77 SSGLLVT 83

g

ó

Gaps

.,

```
New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                      Zyskind JW;
Xu HH;
                                                                                                                                                                                                                     Ohlsen KL,
Forsyth RA,
                                                  Protein encoded by Prokaryotic essential gene #27589.
                                                                                                                                                                                                                     Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                    Claim 25; SEQ ID NO 69986; 1766pp; English.
ABU42062 standard; protein; 891 AA.
                                                                                                                                                                                                                     Malone C,
Carr GJ,
                                                                                                                                                  21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
                                                                                                                                                                            08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                  21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                     Malone
                                19-JUN-2003 (first entry)
                                                                                                                                                                                                    (ELIT-) ELITRA PHARM INC.
                                                                                  Pseudomonas syringae.
                                                                                                                                                                                                                    Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                             2003-029926/02
                                                                                                                                                                                                                                                     N-PSDB; ACA45932.
                                                                                                 WO200277183-A2.
                                                                                                                                                                           08-FEB-2002;
                                                                                                                  03-OCT-2002
                ABU42062;
                                                                                                                                                                                                                    Wang L,
Wall D,
                                                                                                                                                                                                                                            WPI;
```

Martensen SA; Xie Q, Rizni SK;

the foll antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense of nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that inhibits estimate a biological pathway required for proliferation, or that inhibits proliferation of an identifying a gene required for cellular proliferation of an identifying a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound specific compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound specific compound that inhibits proliferation of an organism; or (13) identifying the target of a compound that inhibits the compound that inhibits the proliferation of an organism. The antisense nucleic acids required to relinkar proliferation of an organism. The antisense nucleic acids required to confidence or cellular proliferation of an organism. The antisense nucleic acids required for cellular proliferation of an organism. The antisense nucleic acids required for cellular proliferation of an organism. The antisense nucleic acids are useful for for discretions or screening for homologous molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present eqquence is encoded by the target prokaryotic essential genes. Note: The sequence data for this patent din ont form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences The invention relates to an isolated nucleic acid comprising any

Sequence 891 AA;

Gaps

; 0

0; Indels

Pred. No. 1.3e+03;

100.0%;

Best Local Similarity 100. Matches 7; Conservative

ð

·.

Gaps

..

0; Mismatches

```
The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain caection (PCR) primers, Oilgomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed construction of (II). The polymucleotides are also used in activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a colypoptide in tissue, as molecular weight markers and as a food supplement. (III) and its binding partners are useful in medical imaging of supplement. (III) and its binding partners are useful for treating disorders cupulypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations of diagnostics, for genefic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from WHDD at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
   Length 891;
                                       0; Indels
 2.1%; Score 7; DB 6; Ler
100.0%; Pred. No. 1.3e+03;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID NO 52997; 103pp; English.
                                                                                                                                                                                                                                                                                                                       Novel human diagnostic protein #22629.
                                                                                                                                                                                                           ABG22638 standard; protein; 896 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US008631,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                    (first entry)
                                       7; Conservative
                                                                                                                639 AQLAQEL 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-639362/73.
                                                                            67 AQLAQEL 73
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS86825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 896 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biodiversity.
                                                                                                                                                                                                                                                                                    18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-2001.
                                                                                                                                                                                                                                              ABG22638;
                                       Matches
                                                                              à
                                                                                                            g
```

2.1%; Score 7; DB 4; Length 896;

Query Match

```
The invention relates to an isolated nucleic acid molecule (a promoter of rice chemically induced cDNA (RCI-1), which encodes a lipoxygenase) capable of driving demaically-inducible but not wound- or pathogen-inducible expression of an associated nucleotide sequence. Also included are the RCI-1 cDNA, its encoded protein, a 4.5kb genomic clone for the lipoxygenase gene, promoter fragments, the lipoxygenase transit peptide which directs expressed proteins to the plastid, a vector comprising the promoter or fragments are useful for expressing an uncleotide sequence of interest. The transit peptide is useful for targeting an associated protein of interest to plastids. A nucleic acid which expresses protein of interest to plastids. A nucleic acid which expresses protein of interest to plastids. A nucleic acid which expresses contoxins when transformed into a plant. The lipoxygenase is useful for inhibiting fungal mycotoxins. The promoter is useful for regulating transcription of a chemically inducible but not wound or pathogen transcription of a chemically inducible but not wound or pathogen inducible gene, which involves applying a chemical pregulating a resolution or seed containing a chemically regulatable nucleotide sequence.

Transgenic plants as described above are useful for breeding improved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter of
                                                                                                                                                                                                                                                                                                                                                                             /note= "This sequence is specifically claimed in claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid encoding a promoter which is capable of driving chemically inducible but not wound- or pathogen-inducible expression of an associated nucleotide sequence.
                                                                                                                                                                                               Rice, lipoxygenase, RCI-1; transgenic; plant; plant antifungal; rice chemically induced cDNA; promoter; transit peptide; plastid; fungal mycotoxin inhibitor; plant breeding; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Mature_lipoxygenase
                                                                                                                                                                                                                                                                                                                                        1. .37
/label= Transit_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lawton KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 33; Page 62-65; 88pp; English.
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SYGN ) SYNGENTA PARTICIPATIONS AG. (UYZU-) UNIV ZUERICH.
                                     AAU76150 standard; protein; 922 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-JUL-2001; 2001WO-EP008085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUL-2000; 2000GB-00017275.
15-SEP-2000; 2000GB-00022739.
                                                                                                                    (first entry)
                                                                                                                                                         Rice lipoxygenase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dudler R, Schaffrath U,
                                                                                                                                                                                                                                                                                                                                                                                                                     . 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-188550/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABK15653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200206490-A1.
                                                                                                                                                                                                                                                                                Oryza sativa.
                                                                                                                    21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JAN-2002.
                                                                          AAU76150;
                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
RESULT 140
                    AAU76150
```

```
ö
plant lines that for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with the methods due to their modified genetic properties. New crops with improved stress tolerance can be obtained that, due to their optimised genetic equipment yield harvested product of better quality than products that were not able to tolerate comparable adverse developmental conditions. The present sequence represents rice liboxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents an isoform of a human mitochondrial polypeptide designated MSP1. MSP1 belongs to the dynamin family, and is a Grase which is implicated in mitochondrial function and cell division. MSP1 mutants are associated with dominant optical atrophy 1 (OPA1). Seven isoforms of human MSP1 also exist. MSP1, and its isoforms, are used to screen for specific modulators, potentially useful for treating disorders of mitochondrial function and cell division, especially neurodegenerative diseases, particularly optical neuropathy and specifically OPA1. MSP1 and its isoforms may also be used for development of antiproliferative treatments, e.g. for cancer. Vectors that contain the nucleic acid encoding MSP1 are useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human mitochondrial polypeptide MSP1 and its isoforms, useful for identifying agents for treating neurodegeneration, also related nucleic
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mitochondrial function; cell division; dominant optical atrophy 1; 7 MSP1-X; neurodegenerative disease; optical neuropathy; antiproliferative; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of mitochondrial protein MSP1 isoform MSP1-F.
                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delettre C, Belenguer P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; mitochondrial protein; MSP1; dynamin; GTPase; OPA1;
                                                                                                                                                                                    Length 922;
                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                    DB 5; Len . 1.3e+03;
                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                  2.1%; Score 7; D
100.0%; Pred. No.
ative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYTO-) UNIV TOULOUSE SABATIER PAUL.
(INRM ) INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                      ABB09658 standard; protein; 961 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hamel C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 56-60; 76pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUN-2001; 2001WO-FR001999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-2000; 2000FR-00008140.
                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ducommun B,
                                                                                                                                                                                                                                                        189 DLLTRHK 195
                                                                                                                                                                                                                                                                                             64 DLLTRHK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002-139920/18.
                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABL41815
                                                                                                                                                Sequence 922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200200878-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lenaers G,
                                                                                                                                                                                                                                                                                                                                                                                                                        ABB09658;
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                     ABB09658
   888888888888
                                                                                                                                                                                                                                                                                         Db
                                                                                                                                                                                                                                                                                                                                                                                      ò
```

2.1%; Score 7; DB 5; Length 961;

Sequence 961 AA;

Query Match

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences given in AAR44192-94 represent the rat N-methyl D-aspartic acid (NMDA) receptor subunits, NR2A, NR2B and NR2C, respectively. The CDNA encoding these proteins were isolated using the primers given in AAQ50993-94 which were derived from a strongly conserved peptide region within the glutamate receptor subunit transmembrane domain III. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA coding for N-methyl-D-aspartic acid receptor subunits - useful for
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; mitochondrial protein; MSP1; dynamin; GTPase; OPA1; mitochondrial function; cell division; dominant optical atrophy 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of mitochondrial protein MSP1 isoform MSP1-G.
              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                               Polymerase chain reaction; NMDA; N-methyl D-aspartic acid.
              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           identifying N-methyl-D-aspartic acid receptor ligands.
100.0%; Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 2;
100.0%; Pred. No. 1.4e+C
iive 0; Mismatches
             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 PH;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Seeburg
                                                                                                                            AAR44194 standard; protein; 962 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB09659 standard; protein; 979 AA.
                                                                                                                                                                                                                      Rat NMDA receptor subunit, NR2C.
              .
0
                                                                                                                                                                                                                                                                                                                                                    92DE-04216321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 3; 25pp; German.
                                                                                                                                                                                                                                                                                                                                                                              92DE-04216321.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Monyer H,
                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                 (revised)
                                    231 LLGELIL 237
                                                              174 LLGELIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-369850/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 TEAVAQL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 TEAVAQL 69
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 Herb A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ50997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 962 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     (BADI ) BASF AG.
                                                                                                                                                                                                                                                                          Rattus rattus.
                                                                                                                                                                                                                                                                                             DE4216321-A1,
                                                                                                                                                                                                                                                                                                                                                    16-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                              16-MAY-1992;
                                                                                                                                                                                                                                                                                                                           18-NOV-1993.
                                                                                                                                                                                25-MAR-2003
                                                                                                                                                                                           11-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAY-2002
                                                                                                                                                      AAR44194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB09659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                               Bach A,
         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                  AAR44194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB09659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                      à
                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAXHXHXAXA
MAXHXHXAXA
```

```
The present sequence represents an isoform of a human mitochondrial polypeptide designated MNSP1. MSP1 belongs to the dynamin family, and is a GTPase which is implicated in mitochondrial function and cell division. MSP1 mutants are associated with dominant optical atrophy 1 (OPA1). Seven isoforms of human MSP1 also exist. MSP1, and its isoforms, are used to screen for specific modulators, potentially useful for treating disorders of mitochondrial function and cell division, especially neurodegenerative diseases, particularly optical neuropathy and specifically OPA1. MSP1 and its isoforms may also be used for development of antiproliferative treatments, e.g. for cancer. Vectors that contain the nucleic acid encoding MSP1 are useful for gene therapy
                                                                                                                                                                     New human mitochondrial polypeptide MSP1 and its isoforms, useful for identifying agents for treating neurodegeneration, also related nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human mitochondrial polypeptide MSP1 and its isoforms, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; mitochondrial protein; MSP1; dynamin; GTPase; OPA1;
micochondrial function; cell division; dominant optical atrophy 1;
7 MSP1-X; neurodegenerative disease; optical neuropathy;
antiproliferative; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of mitochondrial protein MSP1 isoform MSP1-H.
                                                                                      Belenguer P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hamel C, Delettre C, Belenguer P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; Score 7; DB 5; Length 997;
100.0%; Pred. No. 1.4e+03;
live 0; Mismatches 0; Indels
                                                                                      Ducommun B, Hamel C, Delettre C,
                                    (UYTO-) UNIV TOULOUSE SABATIER PAUL.
(INRM ) INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYTO-) UNIV TOULOUSE SABATIER PAUL.
(INRM ) INST NAI SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB09660 standard; protein; 1015 AA.
                                                                                                                                                                                                                                       Claim 2; Page 52-56; 76pp; French.
     26-JUN-2000; 2000FR-00008140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUN-2001; 2001WO-FR001999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUN-2000; 2000FR-00008140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ducommun B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 LLGELIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 LUGELIL 216
                                                                                                                      WPI; 2002-139920/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-139920/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                         N-PSDB; ABL41814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 997 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABL41817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200200878-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JAN-2002.
                                                                                      Lenaers G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lenaers G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB09660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB09660
      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents an isoform of a human mitochondrial polypeptide designated WSPL MSPL belongs to the dynamin family, and is a GTPase which is implicated in mitochondrial function and cell division. MSPL mutants are associated with dominant optical atrophy 1 (OPAL) seven isoforms of human MSPL also exist. MSPL, and its isoforms, are used to screen for specific modulators, potentially useful for treating disorders of mitochondrial function and cell division, especially neurodegenerative diseases, particularly optical neuropathy and specifically OPAL MSPL and its isoforms may also be used for development of antiproliferative treatments, e.g. for cancer. Vectors that contain the nucleic acid encoding MSPL are useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                               New human mitochondrial polypeptide MSP1 and its isoforms, useful for identifying agents for treating neurodegeneration, also related nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; mitochondrial protein; MSP1; dynamin; GTPase; OPA1;
mitochondrial function; cell division; dominant optical atrophy 1;
7 MSP1-X; neurodegenerative disease; optical neuropathy;
antiproliferative; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of mitochondrial protein MSP1 isoform MSP1-E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                               Ducommun B, Hamel C, Delettre C, Belenguer P;
7 MSP1-X; neurodegenerative disease; optical neuropathy; antiproliferative; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 5; Ler
100.0%; Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. No. -
                                                                                                                                                                                                                (UYTO-) UNIV TOULOUSE SABATIER PAUL.
(INRM ) INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB09657 standard; protein; 997 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 60-64; 76pp; French.
                                                                                                                                              25-JUN-2001; 2001WO-FR001999.
                                                                                                                                                                                 26-JUN-2000; 2000FR-00008140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUN-2001; 2001WO-FR001999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                            WPI; 2002-139920/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 LLGELIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLGELIL 198
                                                                                                                                                                                                                                                                                                                   N-PSDB; ABL41816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 979 AA;
                                                                                 WO200200878-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200200878-A2
                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JAN-2002
                                                                                                                                                                                                                                                                 Lenaers G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB09657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB09657
 à
```

ô

Gaps

;

```
The present sequence represents an isoform of a human mitochondrial polypeptide designated MSP1. MSP1 belongs to the dynamin family, and is a GTPsse which is implicated in mitochondrial function and cell division. MSP1 mutants are associated with dominant optical atrophy 1 (OPA1). Seven screen for specific modulators, potentially useful for treating disorders of mitochondrial function and cell division, especially neurodegenerative diseases, particularly optical neuropathy and specifically OPA1. MSP1 and tris isoforms may also be used for development of antiproliferative treatments, e.g. for cancer. Vectors that contain the mucleic acid encoding MSP1 are useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense
 identifying agents for treating neurodegeneration, also related nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 5; Length 1015; 100.0%; Pred. No. 1.4e+03; Ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by Prokaryotic essential gene #27151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; SEQ ID NO 69548; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU41624 standard; protein; 1053 AA.
                                                    Claim 2; Page 64-68; 76pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2001, 2001US-00815242.
06-SEP-2001, 2001US-00948933.
25-OCT-2001, 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002, 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas syringae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                             231 LLGELIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                             228 LLGELIL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-029926/02.
                                                                                                                                                                                                                                                                                                      Sequence 1015 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ACA45494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200277183-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU41624;
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 146
                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU41624
g
```

Gaps . 0 Zyskind JW; Xu HH;

```
uniferration or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide, (5) inhibiting callular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway required for proliferation-required gene or the biological pathway in which a proliferation-required gene or the biological cora gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for dentifying proteins or screening for homologous nucleic acids are useful for for cellular proliferation to isolate encledic acide required for for cellular proliferation to a candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                       drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. preumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp, wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast and fungal nucleic acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative disorders, yeast and fungal infections, or for preventing apoptosis in certain diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast, fungus; apoptosis; infection; proliferative disease; vaccine; autoimmune disease; ischaemia; neurodegeneration.
nucleic acid; (2) a host cell containing the vector; (3) an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 6; Length 1053; 100.0%; Pred. No. 1.5e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Luyten WHML, Malcorps IKL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C albicans apoptosis associated protein #51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG70871 standard; protein; 1072 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33-JUL-2000; 2000WO-BE000077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99EP-00870141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Backer MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               De Backer MD
Reekmans RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         647 TLIADIQ 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-367042/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 TLIADLO 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1053 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Candida albicans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAH29907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200102550-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nelissen BJM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contreras RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG70871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG7087
8888888888888888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó:
```

ö

```
number of apoptosis associated proteins from the years Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identify treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaemia and neurodegeneration. The present sequence is one of the C. albicans proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yan BM, Thangavelu K, Honchell CD, Ding L;
R, Kallick DA, Lee S, Warren BA, Xu Y, Tran UK,
Hafalia AJA, Yao MG, Nguyen DB, Gandhi AR;
Griffin JA, Chinn MA, Elliott VS, Rankumar J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell adhesion and extracellular matrix protein 5; CADECM-5; human; anti-HIV; virucide; antiallergic; antianflammatory; antianaemic; antiparkinsonian; nootropic; anticonvulsant; antianfertility; antiatretiosclerotic; antiathmatic; lumunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological; antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective; osteopathic; antiarthritic; antiparastiti; anthelminic; antiporiatic; uropathic; ophthalmological; antirheumatic; haemostatic; antipacterial; protozoacide; fungicide; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human cell adhesion and extracellular matrix proteins, useful for diagnosing, treating or preventing autoimmune or inflammatory disorder (e.g. AlDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis.
                                               The present invention provides the protein and coding sequences of a
                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                    2.1%; Score 7; DB 4; Length 1072; 100.0%; Pred. No. 1.5e+03; Ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cell adhesion and extracellular matrix protein 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gynaecological; cadherin; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 150-153; 178pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        ABP58228 standard; protein; 1148 AA.
                 Claim 24; Fig 2; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-0292468P.
2001US-0298616P.
2001US-0301672P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2002; 2002WO-US013874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAY-2001; 2001US-0288290P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JAN-2002; 2002US-0345008P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jee EA, Duggan BM,
JL, Baughn MR, Kal
Thornton M, Hafali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Forsythe
                                                                                                                                                                                                  WPI; 2003-167112/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Walhia NK
                                                                                                                                                                                                                                                                                     40 EEVSKSL 46
                                                                                                                                                                                                                                                                                                                       EEVSKSL 19
                                                                                                                                                                                    Sequence 1072 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABZ24582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200288322-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L5-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Khan FA, Wa
Arvizu CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yue H, Lee
Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP58228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lal PG,
                                                                                                                                                                                                                                                                                                                                                                        RESULT 148
                                                                                                                                                                                                                                                                                                                                                                                          ABP58228
                                                                                                                                                                                                                                                                                                                                                                                                          X & X D D D D D D D D X &
                                                                                                                                                                                                                                                                                     ò
```

```
The present sequence is the protein sequence of Incyte polypeptide

(CADREWA-5). The protein is encoded by a clone isolated from a temporal

(CADREWA-5). The protein is encoded by a clone isolated from a temporal

(CADREWA library. Homology searches indicate it to be a cadherin. The

cortex cDNA library. Homology searches indicate it to be a cadherin. The

invention provides CADECM-1 to -11 polypeptides (see ABPS8224-34) and

contex cDNA library. Homology searches indicate it to be a cadherin. The

contex cDNA library. Homology searches indicate it to be a cadherin. The

cortex cDNA library. Homology searches indicate it to be a cadherin. The

cortex cDNA library expension of antagonists. These are useful for diagnosing,

treating or preventing disorders associated with aberrant expression of

catherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal

catherosclerosis, cirrhosis, hepatitis, paroxysmal nocturnal

charmolocytopaenia or cancer), developmental disorders (e.g. renal

cubular acidosis, anaemia or mental retardation), neurological disorders

(e.g. Alzheimer's disease, Parkinson's disease or epilepsy), reproductive

disorders (e.g. infertility or a disruption in the menstrual cycle), or

cutoimmune/inflammatory disorders (e.g. AIDS, allergy, asthma, autoimmune

chyproiditis, contact dermatitis, forn's disease, disease, disease,

chyproiditis, contact dermatitis, forn's disease, disease,

coteoarthritis, singeoprosis, pancreatitis, Reiter's syndrome, untolic,

arthritis, Siggren's syndrome, uveitis), or viral, bacterial, fungal,

coteoarthritis, syndrome, uveitis), or viral, bacterial, fungal,

coteoarthritis, syndrome, uveitis), or viral, bacterial, fungal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalian lysosomal trafficking regulators LYST1, Lyst1, LYST2 and Lyst2 - useful to diagnose Chediak-Higashi syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYST1; human; lysosomal trafficking regulator; Chediak-Higashi syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CH syndrome; autoimmune disease; tumour; asthma; urticaria; inflammatory bowel disease; psoriasis; systemic lupus erythematosus; rheumatoid arthritis; systemic vasculitis; glomerulonephritis; multiple sclerosis; post-angioplasty restenosis; vaccine; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.1%; Score 7; DB 6; Length 1148; Best Local Similarity 100.0%; Pred. No. 1.6e+03; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW23593 standard; protein; 1185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kingsmore SF, Barbosa-Alleyne MDFS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0011146P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0033599P.
96US-0034346P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-402616/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human LYST1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 SSGLLVT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 SSGLLVT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9728262-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW23593
ò
```

```
polypeptide that is encoded by a gene that is mutated in several Chediak-
Higashi syndrome (CHS) patients. LYST1 can be expressed in host cells
Higashi syndrome (CHS) patients. LYST1 can be expressed in host cells
using an isolated LYST1 gene for use in various pharmacological and
immunological applicatins. LYST1 products (see AAW33596-97) of long and
short isoforms of human LYST1 are also claimed. LYST1 regulates
degranulation of lysosomes, late endosomes and acidic secretory granules,
containing truncated LYST1 peptides may be used to treat
inflammatory and autoimmune diseases e.g. asthma, urticaria, inflammatory
contains systemic lugus erythematosus, rheumatorid arthritis,
psoriasis, systemic vasculitis, glomerulonephritis, multiple sclerosis
and post-angioplasty restenosis, while LYST1 peptides that minic or
augment LYST1 function may be used to treat neoplasia. (NB. the amino
correspond in the C-terminal region to the translated sequence of the
LYST1 gene provided (see AAT74198))
                                                                                                                                                                                                                                                                                                                                                                                            0;
                                This protein sequence comprises a lysosomal trafficking regulator (LYST1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glutamic acid receptor; synaptic signal translation; diagnosis; brain disease; nerve signal; gene therapy; NWDA; cerebellum; ICR; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New glutamic acid receptor and gene - for use in analysis of synaptic signal translation, and diagnosis of brain disease.
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361. .369
/note= "This line is ommited in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               883. .891
/note= "This line is ommited in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "This line is ommited in the specification"
                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 2; Length 1185; 100.0%; Pred. No. 1.7e+03; ive 0; Mismatches 0; Indels
 Claim 3; Page 129-133; 237pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR45945 standard; protein; 1239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 25-31; 35pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MITU ) MITSUBISHI KASEI CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92JP-00173155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92JP-00173155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glutamic acid receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                       228 SLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                     844 SLKLIGE 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nerve cell necrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1994-061478/08.
                                                                                                                                                                                                                                                                                                                          Sequence 1185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ56916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP06014783-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR45945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR45945
```

```
preference for non-homologous recombination. The method comprises

cretering an integration pathway towards homologous recombination. The
method is useful for directing integration of a nucleic acid of interest

to a subtelomeric and/or telomeric region in an eukaryote with a

preference for non-homologous recombination. The nucleic acid of interest

comprises an inactive gene to replace an active gene, or vice versa, is a

comprises an inactive gene to replace an active gene, or vice versa,

comprises an inactive gene to replace an active gene, or vice versa,

comprises an inactive gene to replace an activities substance or a

substance conferring resistance for an antibiotic substance or a

cukaryotic cell, or encodes a therapeutic proteinaceous substance or a

substance conferring resistance for an antibiotic substance or a cell.

The method is useful for improving gene targeting efficiency. The method

is useful in the replacement of an active gene by an inactive gene, for

is useful in the replacement of an active gene by an inactive gene, for

c. g. for the inactivation of genes controlling undesired side branches of

metabolic pathways, to increase the production of specific secondary metabolites

c. to inhibit formation of unwanted metabolites, and also to inactive

genes controlling senescence in fruits and flowers or that determine

t. Hower pigments. The method is also useful for replacing an inactive gene

by an active gene. For e.g. the replacement of a defective p53 by an
                                                                                                                                                                                                                         ö
The sequence shows a glutamic acid receptor. The receptor is useful for the analysis of nerve signal translation; within the synapse, expresssion of synapse platicity, nerve cell necrosis, brain structure and brain disease. It can also be used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The specification describes a method for directing integration of a nucleic acid of interest to a pre-determined site, where the nucleic acid has homology at or around the pre-determined site, in a eukaryote with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Directing integration of nucleic acid of interest to a sub-telomeric region in an eukaryote with preference for non-homologous recombination, by steering an integration pathway towards homologous recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid integration; homologous recombination; telomeric region;
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                         .
                                                                                                                                                                      DB 2; Length 1239; 1.7e+03;
                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of an Arabidopsis RAD50 homologue.
                                                                                                                                                                 Query Match
2.1%; Score 7; DB 2
Best Local Similarity 100.0%; Pred. No. 1.7
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hooykaas PJJ, Van Attikum H, Bundock P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYLE-) RIJKSUNIV LEIDEN.
(BINA-) STICHTING BINAIR VECTOR SYSTEEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB77986 standard; protein; 1292 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 5; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-DEC-2000; 2000EP-00204693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-DEC-2000; 2000EP-00204693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                            101 TEAVAOL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
                                                                                                                                                                                                                                                                 63 TEAVAQL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-550409/59.
                                                                                                                         Sequence 1239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1217074-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB77986;
                                                                                                                                                                                                                                                                                                                                                                                     RESULT 151
                                                                                                                                                                                                                                                                                                                                                                                                               ABB77986
  ð
```

```
intact p53. Many tumours acquire a mutation in p53 during their development which renders it inactive and often correlates with a poor response to cancer therapy. By replacing the defect p53 by an intact p53, e.g. through gene therapy, conventional anti cancer therapy have better changes of succeeding. The method is also useful for therapeutic proteinaceous substance integration. A tumoricidal gene can be delivered to a pre-determined site present only in e.g. proliferating cells, or present only in tumour cells, e.g. to the site where a tumour antigen is expressed form. ABB77984-86 represent RAD50 homologues. RAD50 is involved
                                                                                                                                                                                                                                                                                n non-homologous recombination
                                                                                                                                                                                                                                                                                                                                            Sequence 1292 AA;
   888888888888888
```

```
DB 5; Length 1292;
5. 1.8e+03;
                                0; Indels
 2.1%; Score 7; DB 5
100.0%; Pred. No. 1.8
tive 0; Mismatches
Query Match 2.1
Best Local Similarity 100.
Matches 7; Conservative
                                                                 15 AEIVKIL 21
                                                                 à
```

0

Gaps .

1058 AEIVKIL 1064

ABG76501 standard; protein; 1537 AA. 05-NOV-2002 (first entry) ABG76501; 

DNA encoding protein modification and maintenance molecule #5.

Protein modification and maintenance molecule; gastrointestinal disorder; dysphagia; esophageal spaem; gastritis; ancrexia; nausea; hypertension; cardiovascular disorder; atherosclerosis; vasculitis; aneryem; allergy; ischaemic heart disease; attoinmune disorder; inflammatory disorder; acquired immunodeficiency syndrome; AIDS; ankylosing spondylitis; cancer; anaemia; anylolosis; cell proliferative; arteriosclerotic bursitis; cirrhosis; developmental disorder; renal tubular acidosis; anaemia; bone resorption; epilepsy; epithelial disorder; keratosis pilaris; allergic contact dermatitis; insect bite; keloid; dermatcfibroma; eczema; neurological disorder; stroke; cerebral neoplasm; Alzheimer's disease; Huntington's disease; dementia; reproductive disorder; infertility; endometriosis; gynecomastia; ectopic pregnancy; gene therapy.

WO200260942-A2.

08-AUG-2002

30-JAN-2002; 2002WO-US002813.

31-JAN-2001; 05-FEB-2001;

2001US-0265705P. 2001US-026572P. 2001US-026581P. 2001US-0272813P. 2001US-0275868P. 2001US-0275586P. 16-FEB-2001; 23-FEB-2001; 01-MAR-2001; 13-MAR-2001; 23-MAR-2001; 30-MAR-2001;

(INCY-) INCYTE GENOMICS INC.

Yue H, Lee S; Honchell CD, Lu Y, Walia NK, Burford N, Delegeane AM; Baughn MR, Griffin JA, Gietzen KJ, Lu DAM, Ison CH; Tang TY, Lal PG, Borowski ML, Duggan BM, Hafalia AJA; Thangavelu K, Yao MG, Elliott VS, Ding L, Yue H, Lee S Xu Y; Gandur J, Tang ...,
Ramkumar J, Tang ...,
Thangavelu K, Warren BA, Gandhi AR,

WPI; 2002-608499/65. N-PSDB; ABS58372.

The invention describes an isolated human polypeptide (I), a naturally occurring amino acid sequence at least 90 % identical to the protein, or a biologically active fragment or an immunogenic fragment of the protein.

The protein modification and maintenance molecules are useful in the diagnosis, treatment, and prevention of gastrointestinal (e.g. dysphagia, esophagal spasm, gastritis, anorexia or nausea), cardiovascular (e.g. atheroselerosis, hypertension, vaculitis, aneutysms, or ischaemic heart disease), autoimmune/inflammatory (e.g. acquired immunodeficiency carborisis, altergies, ankylosing spondylitis, ansemia or amyloidosis), altergies, ankylosing spondylitis, ansemia or amyloidosis), cell proliferative (e.g. renal tubular acidosis, bursitis, or cirrhosis), developmental (e.g. renal tubular acidosis, canemia, bone resorption, or epilepsy), epithelial (e.g. altergic contact dermatitis, keratosis pilaris, insect bites, keloid, dermatofibroma or eczema), neurological (e.g. stroke, cerebral neoplasms, Alzheimer's disease, Huntington's disease or dementia), and reproductive disorders (e.g. infertility, endometriosis, gynecomastia or ectopic pregnancy).

These may also be used in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of protein modification and maintenance molecules polynucleotides are useful in somatic and germline gene therapy. This is the amino acid sequence of a protein modification and maintenance molecules described in the invention ö New protein modification and maintenance molecules useful for treating or preventing gastrointestinal, cardiovascular, autoimmune/inflammatory, cell proliferative, developmental, neurological and reproductive Gaps ö Length 1537; 0; Indels Query Match 2.1%; Score 7; DB 5; Ler Best Local Similarity 100.0%; Pred. No. 2.1e+03; Matches 7; Conservative 0; Mismatches 0; Claim 1; Page 137-140; 172pp; English. 876 VAQLAQE 882 66 VAQLAQE 72 Sequence 1537 AA; disorders. q

AAW23595 standard; protein; 1545 AA. AAW23595; RESULT 153 AAW23595

Murine Lystl short isoform. 10-FEB-1998 (first entry)

Lystl; mouse; lysosomal trafficking regulator; Chediak-Higashi syndrome; CH syndrome; autoimmune disease; tumour; vaccine; therapy; diagnosis.

Mus musculus

WO9728262-A1

97WO-US001748. 31-JAN-1997; 07-AUG-1997.

96US-0011146P. 96US-0033599P. 96US-0034346P 01-FEB-1996; 23-DEC-1996; 

(UYFL ) UNIV FLORIDA.

Kingsmore SF, Barbosa-Alleyne MDFS;

WPI; 1997-402616/37. N-PSDB; AAT74200 Mammalian lysosomal trafficking regulators LYST1, Lyst1, LYST2 and Lyst2

```
0;
                                                          This protein comprises the shorter isoform of murine lysosomal trafficking regulator Lystl, a protein that regulates degranulation of lysosomes, late endosomes and acidic secretory granules primarily in leukocytes. Its sequence was deduced from a Lystl cDNA clone (AAT74200) artificial chromsome. Alternative splicing also yields a longer isoform artificial chromsome. Alternative splicing also yields a longer isoform (see AAW23594) of Lystl. Homologous human sequences (see AAW35595 AAW23597) have been identified that are associated with Chediak-Higashi syndrome (CHS). Murine Lystl and human Lystl polypeptides (see AAW355939) and be expressed in recombinant host cells for use in raising antibodies, in vaccines and in the development of therapeutic approaches to treatment of autoimmune diseases and certain types of tumours. The existence of an animal model of CHS with a similar genetic lesion will assist efforts to develop novel therapies for this disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secreted protein; immunomodulatory; antisclerotic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birse CE, Ebner R, Fiscella M, Komatsoulis GA, e PA, Olsen HS, Rosen CA, Ruben SA, Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory; anti-HIV; cytostatic; cardiant; vascular;
anti-angiogenic; ophthalmological; neuroprotectant; nootropic;
anticonvulsant; antialzheimers; antiparkinsonian; antimicrobial;
vulnerary; vaccine; gene therapy; cancer; protein coordinate data;
                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 2; Length 1545; 100.0%; Pred. No. 2.1e+03; tive 0; Mismatches 0; Indels

    useful to diagnose Chediak-Higashi syndrome.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein, SEQ ID NO: 89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB90551 standard; protein; 1745 AA.
                                Claim 3; Page 103; 237pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baker KP, Birse CE, Lun
r DW, Moore PA, Olsen HS
PE, Wei P, Florence KA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-SEP-2000; 2000WO-US026013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0155709P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1204 SLKLLGE 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                      228 SLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-235311/24.
                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                  Sequence 1545 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAF97891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200121658-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lafleur DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB90551;
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ni J,
```

Nucleic acids encoding 32 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease

The present sequence is one of 32 novel human secreted polypeptides. The

Claim 11; Fig 4; 890pp; English.

and diabetic retinopathy.

```
nucleic acid molecules and polypeptides may be used in the prevention, diagnosis and treatment of diseases such as immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immuno-deficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases (e.g. Scimitar Syndrome, Chagas s cardiomyopathy and coronary arteriosclerosis), angiogenic disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promoting wound healing, regeneration and/or chemotaxis. The nucleic acid molecules may be used to produce the secreted polypeptides. They may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples. The collypeptides may be used as antigens in the production of antibodies and in assays to identify modulators of their expression and activity
                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New fusion protein for treating disease e.g. diabetes comprises an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Albumin fusion protein; therapeutic protein X; human albumin; HA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human serum albūmin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                        Length 1745;
                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 4; Ler
Local Similarity 100.0%; Pred. No. 2.4e+03;
les 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 2042-2047; 2102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       albumin fused to a therapeutic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG65473 standard; protein; 1745 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human albumin fusion protein #2148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-APR-2001; 2001WO-US011988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-APR-2000; 2000US-0229358P.
25-APR-2000; 2000US-0199384P.
21-DEC-2000; 2000US-0256931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haseltine WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1084 VÁQĽÁQÉ 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-010886/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 VAQLAQE 72
                                                                                                                                                                                                                                                                                                                                Sequence 1745 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200177137-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG65473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 155
                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG6547
      g
```

Sequence 1762 AA;

S

```
that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention
                                                                                                                                                                                                                                                                                                                                                  Sequence 1745 AA;
```

```
;
0
2.1%; Score 7; DB 5; Length 1745; 100.0%; Pred. No. 2.4e+03; tive 0; Mismatches 0; Indels
            Local Similarity 100.
Les 7; Conservative
                                                                                              1084 VAQLAQE 1090
                                                                66 VAQLAQE 72
 Query Match
                               Matches
                                                                  ઠે
```

ö

Gaps

RESULT 156 AAU99587

AAU99587 standard; protein; 1762 AA. AAU99587;

(first entry) 21-OCT-2002

Novel human protease.

Novel human protein; NHP; protease; drug screening; cosmetic; clinical trial monitoring; nutriceutical; forensic biology; gene expression; enzyme.

Homo sapiens.

WO200255714-A2.

18-JUL-2002

11-JAN-2002; 2002WO-US000790.

12-JAN-2001; 2001US-0261684P.

(LEXI-) LEXICON GENETICS INC

Turner CA;

WPI; 2002-599670/64. N-PSDB; ABK89926.

New human protease - like proteins and polynucleotides encoding the proteins, useful e.g., in mapping a unique gene to a particular chromosome, in identifying mutations associated with a particular 

Claim 2; Page 38-42; 42pp; English.

The present invention relates to the isolation of a novel human protein (MHP), and the polymucleotide sequence encoding it. The NHP shares equence homology to proteases. The gene encoding the protease of the invention maps to chromosome 9. The polypeptide and polymucleotide sequences of the invention can be used for diagnosis, drug screening, clinical trial monitoring, treatment of biological or medical disorders, and cosmetic or nutriceutical applications. The polymucleotide sequence is useful in forensic biology, in identifying mutations associated with a particular disease, in assessing gene expression patterns, and in gene therapy. The polypeptide sequence can be used to generate antibodies which can be used as reagents in disapnostic or screening assays. The present sequence represents the human protease of the invention

. 0

Gaps

.. 0

0; Indels

2.1%; Score 7; DB 7; Length 1762;

100.0%; Pred. No. 2.4e+03; ative 0; Mismatches 0;

7; Conservative

Best Local Similarity

Matches

Query Match

Sequence 1762 AA;

CADECM

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human cell adhesion and extracellular matrix proteins (CADECM) and nucleic acid molecules encoding such proteins. CADECM proteins are useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overexpression of functional CADECM e.g., immune disorders or cancer. The invention is also useful in gene therapy. The present sequence is human
                                                                                                                                                                                                                                                                                                                Human; cell adhesion and extracellular matrix protein; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baughn MR, Becha SD, Bhatia U, Blake JJ, Borowsky ML, Burrill JD, Delegeane AM, Blliott VS, Gandhi AR, Gietzen KJ, Gorvad AE; Griffin JA, Ho A, Jin P, Kable AE, Lal PG, Lee EA, Lee SI, Gracquis JP, Lehr-ason PM, Ramkumar J, Richardson TW, Sprague WW; Swarnakar A, Tang TY, Tran B, Tran UK, Chawla NK, Warren BA, Xu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human cell adhesion and extracellular matrix proteins (CADECM) polypeptide, useful for preparing a composition for treating a disease associated with decreased expression or overexpression of CADECM e.g.,
                                Gaps
                                                                                                                                                                                                                                                                               Human cell adhesion and extracellular matrix protein (CADECM)-24.
                                ö
2.1%; Score 7; DB 5; Length 1762;
100.0%; Pred. No. 2.4e+03;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 305-309; 374pp; English.
                                                                                                                                                                                AAO30834 standard; protein; 1762 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-NOV-2002; 2002WO-US038437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-2001; 2001US-0340278P-
04-JAN-2002; 2002US-0345069P-
25-JAN-2002; 2002US-035132P-
14-FFB-2002; 2002US-0357168P-
29-MAR-2002; 2002US-0369128P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-NOV-2001; 2001US-0334343P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-2002; 2002US-0370802P
                                                                                                                                                                                                                                                                                                                                   CADECM; cancer; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                22-SEP-2003 (first entry)
                                Conservative
                                                                                                1101 VAQLAQE 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-513695/48.
                                                                72
          Local Similarity
wes 7; Conserv
                                                                66 VAQLAQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAL62036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zheng W;
                                                                                                                                                                                                                                                                                                                                                                                                  WO2003047526-A2
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUN-2003.
                                                                                                                                                                                                                 AAO30834;
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yue H,
                                                                                                                                                 RESULT 157
                                Matches
                                                                                                                                                                  AA03083
                                                                                                                                                                                  g
```

```
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231444P.
08-SEP-2000; 2000US-0231444P.
08-SEP-2000; 2000US-0231444P.
08-SEP-2000; 2000US-0231444P.
08-SEP-2000; 2000US-0231444P.
08-SEP-2000; 2000US-0231444P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
14-SEP-2000; 2000US-0231308P.
15-SEP-2000; 2000US-0231308P.
15-SEP-2000; 2000US-0231308P.
15-SEP-2000; 2000US-0231308P.
13-OCT-2000; 2000US-0231308P.
13-OCT-2000; 2000US-0231308P.
13-OCT-2000; 2000US-0246178P.
13-OCT-2000; 2000US-0246178P.
13-OCT-2000; 2000US-0246178P.
13-OCT-2000; 2000US-0246178P.
13-OCT-2000; 2000US-024613P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-024921P.
17-NOV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000; 2000US-0249218P
17-NOV-2000; 2000US-0249244P
17-NOV-2000; 2000US-0249245P
         Human; gene therapy, neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; inflammation.
                                                                                                                                                             ABB10246 standard; protein; 1766 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0186350P.
2000US-0189874P.
2000US-01998123P.
2000US-01998135P.
2000US-015135P.
2000US-015135P.
2000US-0215135P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-022526F.
2000US-022526F.
2000US-022526F.
2000US-022526F.
2000US-022526F.
2000US-022526F.
2000US-022526F.
2000US-022526F.
2000US-022526F.
2000US-022526F.
2000US-022526F.
2000US-022526F.
2000US-022526F.
2000US-022526F.
2000US-022528F.
2000US-0225287P.
2000US-0225387P.
2000US-0225387P.
2000US-0225387P.
2000US-0225387P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0179065P.
2000US-0180628P.
2000US-0184664P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0230437P.
2000US-0230438P.
2000US-0231242P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-2001; 2001WO-US001349
                                                                                                                                                                                                                                                        10-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                      Human cDNA SEQ ID NO: 554
                                         1101 VAÇLAÇE 1107
66 VAQLAQE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200154474-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-2000; 2
16-MAR-2000; 2
18-APR-2000; 2
18-APR-2000; 2
19-MAY-2000; 2
28-JUN-2000; 2
30-JUN-2000; 2
30-JUN-2000; 2
11-JUL-2000; 2
11-JUL-2000; 2
11-JUL-2000; 2
11-JUL-2000; 2
11-JUL-2000; 2
11-JUL-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG-2000; 2
16-AUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-AUG-2001
                                                                                                                                                                                                         ABB10246;
                                                                                                         RESULT 158
ABB102-X
XX
AC ABB102-X
XX
DT 10-JAM
XX
DY 10-JAM
XX
DY Human;
XW Human;
XW Human;
XW Human;
XW Hollicit
XX
OS Homo Si
PR 24-FEB
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-JAM
PR 31-
                                         임
à
```

```
14-AUG-2000), 2000US-0225270P.
14-AUG-2000), 2000US-0225570P.
14-AUG-2000), 2000US-0225570P.
14-AUG-2000), 2000US-0225575P.
14-AUG-2000), 2000US-0225575P.
22-AUG-2000), 2000US-0228924P.
01-SEP-2000), 2000US-0229349P.
01-SEP-2000), 2000US-0229349P.
01-SEP-2000), 2000US-0229349P.
05-SEP-2000), 2000US-0229509P.
05-SEP-2000), 2000US-0229513P.
06-SEP-2000), 2000US-0239513P.
21-SEP-2000), 2000US-0239534P.
27-SEP-2000), 2000US-023934P.
27-SEP-2000), 2000US-0236363P.
29-SEP-2000), 2000US-0236363P.
                                                                                                                                                                                                                                                                    14-UUL-2000; 2000US-0218290P.
26-UUL-2000; 2000US-0218959P.
26-UUL-2000; 2000US-0228953P.
14-AUG-2000; 2000US-0224518P.
14-AUG-2000; 2000US-0224518P.
14-AUG-2000; 2000US-0225567P.
                                                                                             04-FEB-2000; 2000US-0180628P
28-JUN-2000; 2000US-021488EP
07-JUL-2000; 2000US-0216647P
07-JUL-2000; 2000US-0216880P
                                                                                                                                                                                                            11-JUL-2000; 2000US-0217487P
11-JUL-2000; 2000US-0217496P
               17-JAN-2001; 2001US-00764853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OC
               \mathcal{C}_{\mathcal{C}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; SEQ ID NO 554; 859pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 4; Length 1766; 100.0%; Pred. No. 2.4e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA, Barash SC, Ruben SM;
                                                                          17-NOV-2000; 2000US-0249299P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-0251988P.
05-DEC-2000; 2000US-025199P.
                                                                                                                                                                                                                                                                                       2000US-0251479P.
2000US-0251856P.
2000US-0251868P.
2000US-0251869P.
                           2000US-0249265P.
2000US-0249297P.
2000US-0249299P.
                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0251989P.
2000US-0251990P.
2000US-0254097P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JAN-2001; 2001US-0259678P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1105 VAQLAQE 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-476161/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 VAQLAQE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1766 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABA06468
                                                                                                                                                                                                                                                                                       06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                              08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                         08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
PRANTAL STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STANFORM STAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
```

2000US-0236369P. 2000US-0236370P. 2000US-0236802P.

2000US-0237037P. 2000US-0237038P.

2000US-0237040P

2000US-0241809P

```
The invention relates to novel genes (ABV83682-ABV84101) and proteins (ABV86710-ABR67129) useful for preventing, treating or ameliorating medical conditions e.g. by protein egene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptide useful for diagnosis, prognosis, prevention, and treatment of immune, hyperproliferative, renal, respiratory, cardiovascular, reproductive, endocrine, gastrointestinal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; SEQ ID NO 554; 369pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                            Barash SC;
08-DEC-2000; 2000US-0251868P
08-DEC-2000; 2000US-0251869P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurological disorders.
                                                                                                                                                                                                                                                                            Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-681727/73.
                                                                                                             (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABV83805
```

Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antiirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.

US2002090672-A1.

11-JUL-2002.

Homo sapiens.

ABP66833 standard; protein; 1766 AA

ABP66833

Human polypeptide SEQ ID NO 554.

(first entry)

09-DEC-2002

ABP66833;

```
The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, autoimmune bytoiditis, diabetes mellitus, Crohn's disease, cardiovascular disorders such as myocardial ischaemis; (d) wound healing if e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), in expressed DNA ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 19467; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                         2.1%; Score 7; DB 5; Length 1766;
100.0%; Pred. No. 2.4e+03;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 19467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB64225 standard; protein; 1838 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                     1105 VAQLAQE 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams M,
                                                                                                                                                                                                                                                                                                                                                                                  66 VAQLAQE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                  Sequence 1766 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABL08328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB64225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB64225
     à
```

Gaps

.; 0

```
The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II). (I) and (2) comprising (I) or (II). (I) and (II) and polyclonal antisers or a monoclonal antibody raised to imfection. (I) and polyclonal antisers or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Purthermore, (I) (especially when they care rifins or secreted or membrane proteins) can aid the identification of drugs to treat or prevent P. falciparum infection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the conformed by the complexity of the parasitic lifecycle, and concoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquitor essistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18152 invention, but which are not specifically mentioned within the
                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide.
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum chromosome 2 related protein SEQ ID NO:122.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the
                                                                          ;
0
                                        Length 1838;
                                                                        0; Indels
                                     2.1%; Score 7; DB 4; Ler 100.0%; Pred. No. 2.5e+03; live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 285-291; 577pp; English.
                                                                                                                                                                                                                                 AAB18265 standard; protein; 2013 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum, useful as ant
diagnosis of P.falciparum infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gardner M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US026796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0107131P.
                                                                                                                                                                                                                                                                                                      (first entry)
                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carucci D,
                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum.
                                                                                                                                        1258 KNPAEIV 1264
                                                                                                      12 KNPAEIV 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-365347/31.
                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HOFFMAN S.
CARUCCI D.
GARDNER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VENTER J C.
   Sequence 1838 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200025728-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-1998;
                                                                                                                                                                                                                                                                                                      07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hoffman S,
                                                                                                                                                                                                                                                                   AAB18265;
                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HOFF/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (VENT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CARU/)
                                                                                                                                                                                              RESULT 161
                                                                    Matches
                                                                                                                                                                                                                AAB18265
g
                                                                                                                                                                                                                                                엄
                                                                                                        ठ
```

Sequence 2013 AA;

```
Zhong M;
                                                                                                                                                                                                                                                     Human; NOV; gene therapy; endocrine related disease; diabetes; metabolism-related disease; obesity; central nervous system disorder; Alzheimer's disease; Derkinson's disease; peilepsy; multiple sclerosis; schizophrenia; depression; autoimmune disorder; inflammatory disorder; psoriasis; allergy; lupus erythematosus; asthma; cancer; tilammatory bowel disease; rheumatoid arthritis; osteoarthritis; colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer; prostate cancer; brain cancer; melanoma; liver disease; inver cirrhosis; lung disease; emphysema; obstructive pulmonary disease; haemophilia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GORMAN L, Li L, Anderson DW, Zhong M;
Ellerman K, Berghs C, Rothenberg ME, Guo X
Catterton E, Kekuda R, Ji W, Miller CE;
Shenoy SG, Liu X, Padigaru M, Alsobrook JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX) and polynucleotides, useful in gene therapy, e.g. for treating or preventing obseity, multiple sclerosis, allergy, cancers, hemophilia, stroke or infections.
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes a new isolated polypeptide (NOVX). The NOVX
                             ..
2.1%; Score 7; DB 3; Length 2013; 100.0%; Pred. No. 2.7e+03; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shenoy SG, ]
Burgess CE;
                                                                                                                                             ABO14706 standard; protein; 3064 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 256; 586pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20010S-0318130P

20010S-0318430P

20010S-0322636P

20010S-0322816P

20010S-0322816P

20010S-0323819P

20010S-0323631P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-0323636P.
2001US-0324969P.
2001US-0325091P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-0324990P.
2002US-0373212P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-2002; 2002WO-US028539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002US-00236177
                                                                                                                                                                                               25-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patturajan M,
                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAM,
                                                                                                                                                                                                                            Novel human protein #79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spytek KA, Pac.
Spilach VL, Vernet C.
Shimkets RA, Leach MD,
'ager DK, Taupier RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                  100 IFNNILR 106
                                                                             539 IFNNILR 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-313242/30.
N-PSDB; ACD19399.
           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           stroke; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003023002-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-2001; 2
17-SEP-2001; 2
17-SEP-2001; 2
17-SEP-2001; 3
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAR-2003
                                                                                                                                                                         ABO14706;
Query Match
                                                                                                                   RESULT 162
              Best Loc
Matches
```

```
particularly in the manufacture of a medicament for treating a syndrome associated with a human disease, which includes a pathology associated with a human disease, which includes a pathology associated with NoVX polypeptide. The DNA encoding the protein is useful in gene therapy for treating the disease or condition. In particular, the NoVX polypeptide or polymucleotide is useful for treating endocrine/

C metabolism-related diseases (e.g. obesity or disbetes), central nervous system disorders (e.g. plantiment or dispets), autoimmune system disorders (e.g. psoriasis, allergy, upus erythematosus, callengy, multiple sclerosis, schizophrenia or depression), autoimmune athma, inflammatory disorders (e.g. psoriasis, allergy, upus erythematosus, athma, inflammatory disease, rheumatoid arthritis or obserthitis), cancers (e.g. colon, lung, liver, breast, ovarian, prostate or brain cancers, or melanoma, liver diseases (e.g. liver cirrhosis), lung diseases (emphysema or obstructive pulmonary disease), haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic).

C These are also useful in developing powerful assay system for functional analysis of various human disorders, as well as in diagnostic analysis of various human disorders, a novel human NOV protein
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "residues 238-250 (all encoded by codon NNN) may comprise the sequence DKKSIIMYLTSL, absolutely conserved in human, mouse and rat utrophins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding utrophin, truncated forms and related vectors also transformed mammalian cells, used for alleviating symptoms of
polypeptide, nucleic acid and antibody are useful as therapeutics,
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Utrophin; minigene; Duchenne muscular dystrophy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                           Length 3064;
                                                                                                                                                                                                                                                                                                                                                                                2.1%; Score 7; DB 6;
100.0%; Pred. No. 4e+03.
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW22017 standard; protein; 3433 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95GB-00025962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96GB-00015797.
96GB-00022174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-GB003156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Finsley JM, Davies KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1182 VKILKDN 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-341687/31.
N-PSDB; AAT74666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 VKILKDN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                muscular dystrophy.
                                                                                                                                                                                                                                                                                                                                                 Sequence 3064 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9722696-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW22017;
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Utrophin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW22017
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
```

Claim 5; Fig 9; 78pp; English.

existence of an animal model of CHS with a similar genetic lesion will assist efforts to develop novel therapies for this disease

ö

Gaps ö

Length 3788; 0; Indels

Score 7; DB 2; Le: Pred. No. 4.9e+03;

2.1%;

Query Match
Best Local Similarity 100.u

Sequence 3788 AA;

SSXS

1204 SLKLIGE 1210

228 SLKLLGE 234

ò d

100.0%; Pred. Mv. ...

ABP96902 standard; peptide; 9 AA.

RESULT 165 ABP96902 (first entry)

16-JUN-2003

ABP96902;

ö

Gaps .,

Length 3433;

```
Human utrophin (AAW22017) is 395 kDa protein which shows strong sequence similarity to dystrophin and which may protect muscle from the consequences of dystrophin loss. It comprises an actin binding domain, rod domain and dystrophin potent complex (DPC) binding domain. A includes only the actin binding and DPC binding domains, but which retains utrophin polypeptide (AAW22016) has been produced which retains utrophin function. Its expression in an animal model significantly decreased the severity of the dystrophic muscle phenotype, indicating usefulness in the treatment of muscular dystrophy. Utrophin polypeptides can also be used to screen for substances that modulate utrophin binding to actin and/or the DPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse; lysosomal trafficking regulator; Chediak-Higashi syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CH syndrome; autoimmune disease; tumour; vaccine; therapy; diagnosis.
                                                                                                                                                                                    Score 7; DB 2; Length 3*32., Pred. No. 4.5e+03;
                                                                                                                                                                                               Query Match
2.1%; Score 7; DB 2
Best Local Similarity 100.0%; Pred. No. 4.5
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kingsmore SF, Barbosa-Alleyne MDFS;
                                                                                                                                                                                                                                                                                                                                            AAW23594 standard; protein; 3788 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US001748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0011146P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96US-0033599P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0034346P
                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       Murine Lyst1 long isoform.
                                                                                                                                                                                                                                                                           1182 VKILKDN 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-402616/37.
                                                                                                                                                                                                                                                  18 VKILKDN 24
                                                                                                                                                                         Sequence 3433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT74199
                                                                                                                                                                                                                                                                                                                                                                                               10-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9728262-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-1996;
23-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-AUG-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lystl;
                                                                                                                                                                                                                                                                                                                RESULT 164
X8888888888888888
                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                          g
```

```
The present invention describes an immunogenic composition (I) comprising a CASB933 polymuclectide, polypeptide or its immunogenic fragment, or an antigen presenting cell modified to express the polypeptide, and a pharmaceutical carrier. (I) has cytostatic and immunosuppressive activities, and can be used in gene therapy and vaccines. The immunogenic composition is useful in medicine. The CASB933 polypeptides or its immunogenic fragments, or CASB933 polymuclectides encoding the polypeptides are useful for manufacturing an immunogenic composition for
                                                                                                                                                                                  Human; CASB933; immunogenic; cytostatic; immunosuppressive; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          properting or treating a patient suffering from or susceptible to preventing or treating a patient suffering from or susceptible to preneoplastic lesions of lung cancer or lung cancer, such as small cell lung carcinoma, e.g. squamous (epidermoid) carcinoma, non-small cell lung carcinoma, e.g. squamous (epidermoid) carcinoma, adenocarcinoma including bronchoalveolar or large cell (undifferentiated) carcinoma, carcinoids, bronchial gland tumours, or mesotheliomas. The CASB933 polymorlectides and polymeptides are also useful for diagnosing the presence of, or a susceptibility to, preneoplastic lesions of lung cancer or lung cancer in a subject, or for treating autoimmune diseases. The present sequence represents an immunogenic peptide fragment of human CASB933, which is given in the exemplification of the present invention
                                                                                                                                                                                                     vaccine; cytostatic; immunosuppressive; gene therapy; vaccine; medicine; preneoplastic lesion; lung cancer; small cell lung carcinoma; carcinoma; carcinoma; carcinoma; epidermoid; adenocarcinoma; bronchoalveclar carcinoma; large cell carcinoma; bronchial gland tumour; mesothelioma; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An immunogenic composition comprising a CASB933 polynucleotide, polypeptide or its immunogenic fragment, for preventing or treating a patient suffering from or susceptible to preneoplastic lesions of lung
                                                                                                                                        Human CASB933 immunogenic peptide fragment SEQ ID NO:17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLAX ) GLAXOSMITHKLINE BIOLOGICALS SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaulis SRJ, Vinals Y De BassolsC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 66; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-AUG-2002; 2002WO-EP009006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-2001; 2001GB-00019823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer or lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-342415/32.
                                                                                                                                                                                                                                                                                                                                                                                                 WO2003016344-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-2003.
```

This protein comprises the longer isoform of murine lysosomal trafficking regulator Lystl, a protein that regulates degranulation of lysosomes, late endosomes and acidic secretory granules primarily in leukocytes. Its sequence was deduced from a Lystl cDNA clone (AAT74199) that had been identified from a beige (bg) mutation critical region yeast artificial chromosome. Alternative splicing also yields a shorter isoform (see AAW23595) of Lystl. Homologous human sequences (see AAW23596 and AAW23597) have been identified that are associated with Chediak-Higashi syndrome (CHS). Murine Lystl and human LYSTl polypeptides (see AAW23593-98) can be expressed in recombinant host cells for use in raising autibodies, in vaccines and in the development of therapeutic approaches to treatment of autoimmune diseases and certain types of tumours. The

Mammalian lysosomal trafficking regulators LYST1, Lyst1, LYST2 and Lyst2

- useful to diagnose Chediak-Higashi syndrome.

Claim 3; Page 101-103; 237pp; English.

```
Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                   AAW71167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG70315;
                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                            RESULT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 168
                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG7031
X 8
                                                                                                                                                                                                                                                                                                                                                                 ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SXXXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, is useful for treating cancer. The polypeptide is also polypeptide, is useful for treating cancer. The polypeptide is also class II MHC-binding polypeptide. The polypeptides and polymedides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, myeloma or leukaemia. These are also useful for streating an expressed protein tag (EPT) isolated from human tissue for translational expresses protein tag (EPT) isolated from human tissue for translational specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Translational profiling, expressed protein tag, BPT; kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor, transcription factor, cancer, MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
                                                                                                            Gaps
                                                                                                               ..
0
                                                                                                          0; Indels
                                                                 Length 9;
                                                              DB 6; Len
                                                1.8%; Scor.
100.0%; Pred. No. 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; SEQ ID NO 139; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human expressed protein tag (EPT) #139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicz RM, Tomlinson AJ, Urban RG;
                                                                                                                                                                                                                                                                                                                ABU03359 standard; protein; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-0292544P.
2001US-0310801P.
2001US-0326370P.
2001US-0336780P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-2002; 2002WO-US009671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002US-0358985P
                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2003 (first entry)
                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-040607/03
                                                            Query Match
Best Local Similarity
                                                                                                                                                      64 EAVAQL 69
                                                                                                                                                                                                    4 EAVAOL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ZYCO-) ZYCOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200278524-A2.
                   Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-AUG-2001;
01-OCT-2001;
04-DEC-2001;
20-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAY-2001;
                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-2002
                                                                                                                                                                                                                                                                                                                                                            ABU03359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leukemia.
                                                                                                          Matches
                                                                                                                                                                                                                                                                                      ABD03359

XX
ABU0
XXX
ABU0
XXX
ABU0
XXX
ABU0
XXX
BE Huma
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
XXX
BE HUMA
BE HUMA
XXX
BE HUMA
BE HUMA
XXX
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HUMA
BE HU
                                                                                                                                                        ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, Cdc25C; Chk1; Chk2; G2 checkpoint; cell cycle regulation; cancer;
cell proliferation; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW71164-67 represent peptides of electric charge used in an absorption material for hyperlipidemia therapy. The material enables the safe removal of LDL from blood
                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Absorption material for hyperlipidaemia therapy - comprises peptide containing amino acid satisfying predetermined formulae.
                                                                                                                                                                                                                                                                                                                                                                                                          Peptide used in an absorption material for hyperlipidemia therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Absorption material; hyperlipidemia therapy; removal; LDL; blood.
                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 2; Length 10;
100.0%; Pred. No. 1.8e+02;
Live 0; Mismatches 0; Indels
  DB 6; Length 9;
                           1.4e+06;
1.8%; Score 6; DB 6
100.0%; Pred. No. 1.4
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Chk2 kinase inhibitory peptide #1936.
                                                                                                                                                                                                                                                              AAW71167 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 9; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG70315 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96JP-00354650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96JP-00354650.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ASAH ) ASAHI KASEI KOGYO KK.
(ASAH ) ASAHI MEDICAL CO LTD.
                                                                                                                                                                                                                                                                                                                                                           26-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                      Local Similarity 100.
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-440253/38.
                                                                                               230 KLLGEL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165 FRDFFK 170
                                                                                                                                            1 KLLGEL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 FRDFFK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP10179733-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUL-2001
```

```
0
                                                                                                                                                                                                                                                                                        The present invention describes a number of peptides which disrupt the G2 cell cycle checkpoint when administered to a cell. They act by inhibiting Chk1 and Chk2 kinases, and may be derived from Cdc25C. The peptides, an example of which is shown here, are useful in the treatment of cell proliferation diseases, such as cancer, as the inhibition of the Chks allows DNA damage and induces apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosis of hemochromatosis, by detecting a specific deletion in the transferrin receptor-2 gene, or corresponding deletion from the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; TFR2-alpha; diagnosis; haemochromatosis; transferrin receptor-2.
                                                                                                                                                                                                                               or
                                                                                                                                                                                                                            treating cell proliferative disorders, e.g. to stop the growth of, or kill cancer cells, by disrupting the G2 cell cycle arrest checkpoint.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                              Isolated or recombinant polypeptide of 7-11 amino acids, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                             ·,
                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 4; Length 11;
100.0%; Pred. No. 2e+02;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (VIEN-) VIENNALAB LABORDIAGNOSTIKA GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oberkanins C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human TFR2-alpha peptide fragment #2
                                                                                                                                                                                                                                                                  Example 2; Page 97; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG74903 standard; peptide; 11 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 3; 23pp; German.
                                                                                         99JP-00269398.
                                                                21-SEP-2000; 2000WO-IB001438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-AUG-2002; 2002WO-AT000250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-2001; 2001AT-00001295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-JUL-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Camaschella C, Kury F,
                                                                                                                                                          Suganuma M, Kawabe T;
                                                                                                                                (CANB-) CANBAS CO LID.
                                                                                                                                                                                    WPI; 2001-343125/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-268341/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 SKPENL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 SKPENL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003016557-A1.
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11 AA;
           WO200121771-A2
                                                                                      22-SEP-1999;
                                                                                                    30-NOV-1999;
                                     29-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG74903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 169
```

```
ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, epitope, autoimmune disease, myasthenia gravis,
Human leukocyte antigen, acetylcholine receptor, HLA DR3; HLA DR2; AChR;
antigen; immunosuppressive; major histocompatibility complex; MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a composition comprising an isolated acetylcholine receptor (AChR) oligopeptide of about 12 to 20 amino acids. The peptides form a set of 69 overlapping antigenic peptide epitopes which show various affinities for human leukocyte antigens (HLA) HLA-DR2 and DR3. Also included is a composition comprising an antigenic peptide and a Major histocompatibility complex (MHC) component having an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide epitopes of the acetylcholine receptor target helper T cells recognize an antigen in association with an MHC component and are useful to treat autoimmune disease particularly myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigenic binding sife, where binding of the peptide to the binding site induces non-responsiveness in a target T cell in a mammal, where the MHC component is an MHC class II component. Peptides with affinity for HIA-DR2 and DR-3 from proteins other than ACMR are also included. The composition is used to treat myasthenia gravis and other autoimmune
                 This invention describes a novel method for diagnosing haemochromatosis
                               by testing a biological sample for a sequence that represents a 12 musleocide deletion from exon 16 of the cDNA for TFR2 (transferrin receptor-2). The method can detect haemochromatosis before clinical symptoms are manifest (by which time irreversible damage to organs has occurred). This sequence represents a fragment of the human TFR2-alpha (see Genbank NM 003227) which is used in the method described in the disclosure of the invention
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Acetylcholine receptor alpha subunit peptide AChR 330-343.
                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases. The present sequence is an antigenic peptide epitope
                                                                                                                                                                                                                                  2e+02;
.~~ 0; Indels
                                                                                                                                                                                                                          Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wehner N, Arimilli S;
                                                                                                                                                                                                                          DB 6;
                                                                                                                                                                                                                      1.8%; Score 6; DB 6
100.0%; Pred. No. 2e+
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              AAU69193 standard; peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 2; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US010450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-0193745P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                        Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spack E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-648547/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                 65 AVAQLA 70
                                                                                                                                                                                                                                                                                                                                  2 AVAOLA 7
                                                                                                                                                                                    Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200174848-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deshpande S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU69193;
                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 170
                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 AAU69193
$$888888888$8
                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
```

DB 4; Length 14;

1.8%; Score 6;

Query Match

```
16-JUL-1999 (first entry)
                                                                                                          Synthetic.
                                                                                                                                                                                                                                    Black ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW97143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Негрев
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW97143
   ö
             ö
                                                                                                                                                                                      HSV-1; thymidine kinase; mutation; DRH nucleoside binding site; enzyme; pathogen; tumour; hyperkeratosis; psoriasis; prostate hypertrophy; hyperthyroidism; endocrinopathy; autoimmune disease; allergy; restenosis; viral disease; AIDS; hepatitis; parasite; bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                        New Herpesviridae thymidine kinase mutants - useful for treating prostate hypertrophy, allergies, cystic fibrosis and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a mutant form of amino acids 159-173 of the herpes simplex virus type 1 (HSV-1) thymidine kinase (TK) protein which was used to generate mutant TK proteins. The invention relates to the generation of novel HSV-1 TK or guanylate kinase (GK) genes with a mutation upstream, within or downstream from a DRH nucleoside binding site. The TK enzymes can be used for inhibiting pathogenic agents, e.g. tumours, hyperkardosis, psoriasis, prostate hypertrophy, hyperthyroidism, endocrinopathies, autoimmune diseases, allergies, restenosis, viral diseases such as ADS, hepatitis, intracellular parasitic diseases or bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
             Gaps
             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 2; Length 15; 100.0%; Pred. No. 2.7e+02; ative 0; Mismatches 0; Indels
Pred. No. 2.5e+02; Mismatches 0;
                                                                                                                                                                  HSV-1 TK amino acids 159-173 mutant #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 15; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY07418 standard; peptide; 15 AA.
                                                                                                     AAY07411 standard; peptide; 15 AA.
                                                                                                                                                                                                                                           Herpes simplex virus unknown type.
           .
                                                                                                                                                                                                                                                                                                                                                           (DARW-) DARWIN MOLECULAR CORP
 100.08;
                                                                                                                                                                                                                                                                                                                   98WO-US021672.
                                                                                                                                                                                                                                                                                                                                       97US-0061812P.
                                                                                                                                              16-JUL-1999 (first entry)
            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-277631/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 LILDRH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
 Best Local Similarity
                              29 EKQDKK 34
                                                  EKODKK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LILDRH 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                  14-OCT-1998;
                                                                                                                                                                                                                                                                          W09919466-A2
                                                                                                                                                                                                                                                                                                                                       14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                               22-APR-1999
           9
                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                          AAY07411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY07418;
                                                                                                                                                                                                                                                                                                                                                                              Black ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 172
                                                                                 RESULT 171
         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY07418
ID AAY0
XX
AC AAY0
XX
                                                                                                               셤
                                ਨੇ
```

```
ô
                                                                                                         pathogen; tumour; hyperkeratosis; psoriasis; prostate hypertrophy;
hyperthyroidism; endocrinopathy; autoimmune disease; allergy; restenosis;
viral disease; AIDS; hepatitis; parasite; bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Herpesviridae thymidine kinase mutants - useful for treating prostate hypertrophy, allergies, cystic fibrosis and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSV-1; thymidine kinase; mutation; DRH nucleoside binding site; enzyme; pathogen; tumour; hyperkeratosis; psoriasis; prostate hypertrophy; hyperthyroidism; endocrinopathy; autoimmune disease; allergy; restenosis; viral disease; AIDS; hepatitis; parasite; bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a mutant form of amino acids 159-173 of the herpes simplex virus type 1 (HSV-1) thymidine kinase (TK) protein which was used to generate mutant TK proteins. The invention relates to the generation of novel HSV-1 TK or guanylate kinase (GK) genes with a mutation upstream, within or downstream from a DRH nucleoside binding site. The TK enzymes can be used for inhibiting pathogenic agents, e.g. tumours, hyperkeatosis, profitsis, profitsis, profitse, hyperthyroidism, endocrinopathies, autoimmune diseases, allergies, restenosis, viral diseases such as AIDS, hepatitis, intracellular parasitic diseases or bacterial infection
                                                                      HSV-1; thymidine kinase; mutation; DRH nucleoside binding site; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 6; DB 2; Length 15; 100.0%; Pred. No. 2.7e+02; Live 0; Mismatches 0; Indels
HSV-1 TK amino acids 159-173 mutant #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSV-1 TK amino acids 159-173 mutant #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Fig 15; 126pp; English.
                                                                                                                                                                                                                                                             Herpes simplex virus unknown type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW97143 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           simplex virus unknown type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DARW-) DARWIN MOLECULAR CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0061812P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US021672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-277631/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 LILDRH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 іліржя 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                           WO9919466-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5877010-A
```

```
1.8%; Score 6;
                                                                                                                                                                                                                             235 LILDRH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-268341/26.
                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                 1 LILDRH 6
                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003016557-A1.
                                                                                                                                                                  Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                           04-JUL-2003
                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                               27-FEB-2003.
                                                                                                                                                                                                                                                                                                                        ABG74902;
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                              RESULT 175
                                                                                                                                                                                                         Matches
   ₽
                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pathogen; tumour; hyperkeratosis; psoriasis; prostate hypertrophy; hyperthyroidism; endocrinopathy; autoimmune disease; allergy; restenosis; viral disease; AIDS; hepatitis; parasite; bacterial infection.
                                                                                                                                                                               This sequence represents a mutant form of amino acids 159-173 of the herpes simplex virus type 1 (HSV-1) thymidine kinase (TK) protein which was used to generate mutant TK proteins. The invention relates to the generation of novel HSV-1 TK or guanylate kinase (GK) genes with a mutation upstream, within or downstream from a DRH nucleoside binding site. The TK enzymes can be used for inhibiting pathogenic agents, tumours, hyperkardosis, psoriasis, prostate hypertrophy, hypertratosis, ondocrinopathies, autoimmune diseases, allergies, restenosis, viral diseases such as AIDS, hepatitis, intracellular parasitic diseases or bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSV-1; thymidine kinase; mutation; DRH nucleoside binding site; enzyme;
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                      New Herpesviridiae thymidine kinase mutant nucleic acids - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Herpesviridiae thymidine kinase mutant nucleic acids - used to
                                                                                                                                develop products for treating e.g. tumours, autoimmune diseases, allergies, restenosis or viral, bacterial or parasitic diseases.
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                      Length 15;
                                                                                                                                                                                                                                                                                                                   DB 2; Len
                                                                                                                                                                                                                                                                                                           1.8%; Scc...
v 100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSV-1 TK amino acids 159-173 mutant #11.
                                                                                                                                                            Disclosure; Fig 15; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                AAW97150 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herpes simplex virus unknown type.
                   95US-00432871.
                                       94US-00237592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-00432871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-00237592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                         (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNIW ) UNIV WASHINGTON.
                                                                                                  WPI; 1999-189650/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-189650/16.
                                                                              Black ME, Loeb LA;
                                                                                                                                                                                                                                                                                                                                                          235 LILDRH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Loeb LA;
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                               LILDRH
                                                                                                                                                                                                                                                                                                 Sequence 15 AA;
                   02-MAY-1995;
                                       02-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-1994;
 02-MAR-1999
                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Black ME,
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 174
                                                                                                                                                                                                                                                                                                                                      Matches
à
```

```
This sequence represents a mutant form of amino acids 159-173 of the herpes simplex virus type 1 (HSV-1) thymidine kinase (TK) protein which was used to generate mutant TK proteins. The invention relates to the generation of novel HSV-1 TK or quanylate kinase (GK) genes with a mutation uperceam, within or downstream from a DRH nucleoside binding site. The TK enzymes can be used for inhibiting pathogenic agents, e.g. tumours, hyperkeratosis, psoriasis, prostate hypertrophy, e.g. restenosis, viral diseases such as AIDS, hepatitis, intracellular parasitic diseases or bacterial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel method for diagnosing haemochromatosis by testing a biological sample for a sequence that represents a 12 nuclectide deletion from exon 16 of the CDNA for TFR2 (transferrin receptor-2). The method can detect haemochromatosis before clinical symptoms are manifest (by which time irreversible damage to organs has occurred). This sequence represents a fragment of the human TFR2-alpha (see Genbank NM_003227) which is used in the method described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosis of hemochromatosis, by detecting a specific deletion in the transferrin receptor-2 gene, or corresponding deletion from the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; TFR2-alpha; diagnosis; haemochromatosis; transferrin receptor-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
develop products for treating e.g. tumours, autoimmune diseases, allergies, restenosis or viral, bacterial or parasitic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 2
100.0%; Pred. No. 2.7
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (VIEN-) VIENNALAB LABORDIAGNOSTIKA GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oberkanins C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human TFR2-alpha peptide fragment #1.
                                                                                                                               Disclosure; Fig 15; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG74902 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 3; 23pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-AUG-2002; 2002WO-AT000250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-AUG-2001; 2001AT-00001295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Camaschella C, Kury F,
```

Length 15;

DB 6;

ö

Sequence 15 AA;

SXS

```
ö
            Gaps
           ;
0
          Indels
          0;
Pred. No. 2.7e+02;
0; Mismatches 0;
 100.08;
          Conservative
 Best Local Similarity
         9
         Matches
```

ð

ABG99202 standard; peptide; 15 AA.

ABG99202;

15-JAN-2003 (first entry)

Thymidine kinase (TK) residues 159-173 mutant #5.

Herpesviridae; thymidine kinase; TK; DRH nucleoside binding region; viral inhibitor; bacterial inhibitor; parasite inihibitor; tumour; autoreactive immune cell; cancer; hyperkeratosis; psoriasis; prostate hypertrophy; hyperthyroidism; endocrinopathy; allergy; autoimmune disease; restenosis; viral disease; AIDS; hepatitis; HCV; HBV; acquired immunodeficiency syndrome; intracellular parasitic disease; gene therapy; adenosine deaminase deficiency; Alzheimer's disease; mutant; mutein.

Herpesviridae. Synthetic.

US6451571-B1

99US-00270956. 17-MAR-1999;

94US-00237592. 02-MAY-1994;

95US-00552304. 95US-00432871. 02-MAY-1995; 02-NOV-1995;

(UNIW ) UNIV WASHINGTON.

Loeb LA, Black ME;

WPI; 2003-045581/04.

Novel Herpesviridae thymidine kinase mutant useful for inhibiting pathogens e.g. viruses, bacteria, tumor in animals, has one or more mutations encoding amino acid substitutions upstream from the DRH nucleoside binding site.

Disclosure, Col 83-84; 78pp; English.

The invention describes an isolated Herpesviridae thymidine kinase (TK) comprising a 12 amino acid (aa) nucleoside binding region having a site 3 made up of a DRH nucleoside binding site and a site 4 and mutation(s), at least one of the mutations being an as substitution 2 or 3 as upstream or 5 or more as downstream from the DRH motif that increases a biological activity, preferably ability of TK to phosphorylate a nucleoside analogue, as compared to unmutated TK. TK mutants are useful for inhibiting a pathogenic agent such as viruses, bacteria, parasites, tumour cells or autoreactive immune cells in a warm-blooded animal. TK proper expression using gene therapy, e.g. including adenosine deaminase deficiency, and Alzheimer's disease. The mutants are utilised as a conditionally lethal marker for homologous recombination. This is the amino acid sequence of a herpesviridae thymidine kinase (TK) mutant mutant is useful for inhibiting a tumour or cancer in a warm-blooded animal, for treating a variety of disease e.g., hyperkeratosis (psoriasis), prostate hypertrophy, hyperthyroidism, endocrinopathies, autoimmune diseases, allergies, restenosis, viral diseases such as acquired immunodeficiency syndrome (AIDS) hepatitis (HCV or HBV), intracellular parasitic diseases, and to correct aberrant expression of gene within a cell, or to replace a specific gene which is defective in

comprising a 12 amino acid (aa) nucleoside binding region having a site 3 made up of a DRH nucleoside binding site and a site 4 and mutation(s), at least one of the mutations being an aa substitution 2 or 3 aa upstream or 5 or more aa downstream from the DRH motif that increases a biological

activity, preferably ability of TK to phosphorylate a nucleoside analogue, as compared to unmutated TK. TK mutants are useful for inhibiting a pathogenic agent such as viruses, bacteria, parasites, tumour cells or autoreactive immune cells in a warm-blooded animal.

The invention describes an isolated Herpesviridae thymidine kinase (TK)

Disclosure; Col 85-86; 78pp; English.

nucleoside binding site.

pathogens e.g. viruses, bacteria, tumor in animals, has one or more mutations encoding amino acid substitutions upstream from the DRH

Novel Herpesviridae thymidine kinase mutant useful for inhibiting

WPI; 2003-045581/04.

Loeb LA, Black ME;

mutant is useful for inhibiting a tumour or cancer in a warm-blooded animal, for treating a variety of disease e.g., hyperkeratosis (postiasis), prostate hypertrophy, hyperthyroidism, endocrinopathies, autoimmune diseases, allergies, restenosis, viral diseases such as acquired immunodeficiency syndrome (AIDS) hepatitis (HCV or HBV), intracellular parasitic diseases, and to correct aberrant expression of a

```
.;
0
                                                                                                                                                                                                    Herpesviridae, thymidine kinase, TK; DRH nucleoside binding region; viral inhibitor; bacterial inhibitor; prassite inhibitor; tumour; autoreactive immune cell; cancer; hyperkeratosis; psoriasis; prostate hypertrophy; hyperthyroidism; endocrinopathy; allergy; prostate hypertrophy; hyperthyroidism; endocrinopathy; allergy; actoimmune disease; restenosis; viral disease; AIDS; hepatitis; HCV; HBV; acquired immunodeficiency syndrome; intracellular parasitic disease; gene therapy; adenosine deaminase deficiency; Alzheimer's disease;
                     Gaps
                     .
0
                     0; Indels
1.8%; Score 6; DB 6; Length 15;
100.0%; Pred. No. 2.7e+02;
                                                                                                                                                                                Thymidine kinase (TK) residues 159-173 mutant #12.
     100.0%; Prec. ...
                                                                                                                 ABG99209 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                              99US-00270956.
                                                                                                                                                                                                                                                                                                                                                                                                             95US-00432871.
                                                                                                                                                                                                                                                                                                                                                                                                  94US-00237592
                                                                                                                                                                                                                                                                                                                                                                                                                      95US-00552304
                                                                                                                                                            (first entry)
                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            (UNIW ) UNIV WASHINGTON
                                         235 LILDRH 240
          Local Similarity
                                                            1 LilbkH 6
                                                                                                                                                                                                                                                                                mutant; mutein.
                                                                                                                                                                                                                                                                                                     Herpesviridae,
                                                                                                                                                                                                                                                                                                                                    US6451571-B1.
                                                                                                                                                                                                                                                                                                                                                                             17-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                  02-MAY-1994;
                                                                                                                                                            15-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                             02-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                       02-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                        7-SEP-2002
                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                       ABG99209;
Query Match
                     Matches
                                                                                                                                      δ
```

Matches

ö

```
(SENP: see ANII0068-AA128459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                proper expression using gene therapy, e.g. including adenosine deaminase deficiency, and Alzhahimer's diseases. The mutants are utilised as a conditionally lethal marker for homologous recombination. This is the amino acid sequence of a herpesviridae thymidine kinase (TK) mutant
   or to replace a specific gene which is defective in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to human single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide #8548 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                            0; Indels
                                                                                                                                                         1.8%; Score 6; DB 6; Length 15;
100.0%; Pred. No. 2.7e+02;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 4; Length 18; 100.0%; Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 26940; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                    AAM22114 standard; protein; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US000670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0236359P
                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK,
gene within a cell,
                                                                                                                                                                                                                               235 LILDRH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-488901/53
                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                              1 LILDRH
                                                                                                                          Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2000;
                                                                                                                                                                                          ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                     AAM22114;
                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                 RESULT 178
                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                   AAM22114
 8888888888
```

Best Local Similarity

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
   Gaps
                                                                                                                                                                                                                                              Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                 Peptide #12026 encoded by human foetal liver single exon probe.
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 37155; 639pp + Sequence Listing; English.
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 18;
   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 4; Ler
100.0%; Pred. No. 3.2e+02;
tive 0; Mismatches 0;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W, Rank DR;
                                                                                                                               ABB44520 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM38567 standard; protein; 18 AA.
 ö
                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-0508408.
03-AUG-2000; 2000US-053466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0235959P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000669.
                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000; 2000US-0180312P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2001 (first entry)
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483447/52
                            250 SKPENL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 SKPENL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                        11 SKPENL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 SKPENL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18 AA;
                                                                                                                                                                                                                                                                                                          WO200157277-A2.
                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                        04-FEB-2002
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM38567;
                                                                                                                                                            ABB44520;
                                                                                                  RESULT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM38567
                                                                                                                                                           셤
                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HXXXH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

```
brains.
                                                                                                                                                                                                                                                                                                                                     AAM6570
 ò
                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
        Peptide #12604 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human bone marrow expressed probe encoded protein SEQ ID NO: 38627.
                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 4; Length 18;
100.0%; Pred. No. 3.2e+02;
tive 0; Mismatches 0; Indels
                      Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
                                                                                                                                                                                                                                                                            Claim 27; SEQ ID NO 38836; 654pp; English.
                                                                                                                                                                                                                Chen W, Rank DR;
                                                                                                                                                                                                                                                            gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM78321 standard; protein; 18 AA.
                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                               26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608408
03-AUG-2000; 2000US-0063336
21-SEP-2000; 2000US-02368PP.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000; 2000US-0180312P.
                                                                                                      30-JAN-2001; 2001WO-US000663
                                                                                                                        2000US-0180312P
                                                                                                                                                                             04-OCT-2000; 2000GB-00024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US000668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                 from human placenta. The
                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                 WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                 250 SKPENL 255
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 6: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                11 SKPENL 16
                                                                                                                                                                                                                                                                                                                                                             Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157276-A2.
                                                                   WO200157272-A2
                                                   Homo sapiens.
                                                                                                                        04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-2001
                                                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM78321;
                                                                                                                                                                                                              Penn SG,
                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 181
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human brain expressed single exon probe encoded protein SEQ ID NO: 37810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; SEQ ID NO 38627; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.8%; Score 6; DB 4; Length 18; Best Local Similarity 100.0%; Pred. No. 3.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                 Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                            gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM65705 standard; protein; 18 AA.
26-MAY-2000, 2000US-0207456P.
30-JUN-2000; 2000US-0060B408.
03-AUG-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023458P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0207456P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US000667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000; 2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-00632366
2000US-0234687P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000GB-00024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                 Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                       WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 SKPENL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 SKPENL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM65705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 182
```

ô

```
The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhobesis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesteroleamia which is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence
                                                             probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                     Gaps
                                                    invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
                                                                                                                                                                                                                                                                   ;
              Example 4; SEQ ID NO 37810; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                1.8%; Score 6; DB 4; Length 18;
100.0%; Pred. No. 3.2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ ID NO 38577; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human liver peptide, SEQ ID No 38577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                             ABG59929 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-003356.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US000664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
انام 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                     250 SKPENL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488898/53
                                                                                                                                                                                                                                                                                                                                       11 SKPENL 16
                                                                                                                                                                                              Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-2000;
21-SEP-2000;
                                                  The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG59929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 183
                                                                                                                                                                                                                                                                                                                                                                                                              ABG59929
à
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 1287 open reading frames derived from the 1261 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the
information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human peptide encoded by genome-derived single exon probe SEQ ID 37011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary haemosiderosis; pulmonary histiccytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; single exon probe; asthma; lung cancer; COPD; ILD;
                                                                                                                                                      0; Indels
                                                                                                                Length 18;
                                                                                                              DB 4; Len
                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27; SEQ ID NO 37011; 634pp; English.
                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                      ABG47346 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0201456P.
30-UJN-2000; 2000US-00608408
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023468PP.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US000665.
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spatially-addressable set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-114183/15.
                                                                                                                                                                                       250 SKPENL 255
                                                                                                                                                                                                                             11 SKPENL 16
                                                                           Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200186003-A2
                                                                                                                                                                                                                                                                                                                                                                                                 19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-NOV-2001,
                                                                                                                                                                                                                                                                                                                                                             ABG47346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG,
                                                                                                                                                                                                                                                                                    RESULT 184
88888
                                                                                                                                                                                                                                                                                                                                                           셤
```

us-10-025-730-1.oligo.rag

Page 122

```
array, identifying exons in a eukaryotic genome, comprising of the eukaryote; and (b) detecting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably above muclaic acids from enkaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridiation to a single exon microarrays having a probe with the exon, where a common pattern of microarrays having a probe with the exon, where a common pattern of microarrays having a probe with the exon, where a common pattern of the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the correct of and for identifying exons in a gene; particularly using human ung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary diseases (CDP), interstitial lung diseases (LDD), familial idiopathic pulmonary fibrosis, pulmonary are an expedience is a peptide/protein encoded by a single exon probe of the study. Implantagioleionyomicosis, pulmonary haemosiderosis, pulmonary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ionophore; antimicrobial; antiviral; antibacterial; antiparasitic;
spermicide; wound healing; burns; anticancer; preservative; sterilant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
array; identifying exons in a eukaryotic genome, comprising (a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New ion channel forming amphiphilic - useful as antimicrobial, antitumour, antiparasitic and spermicidal agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 6; DB 5; Length 18;
100.0%; Pred. No. 3.2e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ion channel forming amphiphilic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR54884 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disinfectant; plant protection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93WO-US010337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-00965663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MAGA-) MAGAININ PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1994-167120/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 SKPENL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 SKPENL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9409810-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2003
03-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maloy WL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AARS4884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR54884
```

```
.
0
                      The peptide sequence is that of an ion forming peptide used to inhibit the growth of target cells, viruses and virally infected cells in a host, i.e. they are antimicrobial, antiviral, antibacterial, anticiancer and antiparasitic agents or spermicides. They can also be used to stimulate wound healing and can be used to treat burns. The peptides can be used in human or veterinary medicine as preservatives, sterilants or disinfectants and in plant protection. See also AAKS4880-906. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to analogues of a magainin I or II, D-form analogues, deletion analogues or related peptides. It also relates to basic polypeptides having at least 16 amino acids, including at least 8 hydrophobic amino acids and at least 8 hydrophilic amino acids. The peptides may be used as antimicrobial agents, antiviral agents, antibiotics, antitumour agents, antiparasitic agents, spermicides, preservatives or sterilants, or agents for promoting wound healing. The present sequence represents a specific example of a peptide disclosed in the specification
                                                                                                                                                                                                                                                Gaps

    .22
/note= "All residues except Gly are D-form residues"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 magainin; analogue; antimicrobial; antitumour; wound healing; CPF; amphiphilic; XPF peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Magainin peptide analogues - useful as antimicrobial or antitumour
                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                               Query Match 1.8%; Score 6; DB 2; Length 22; Best Local Similarity 100.0%; Pred. No. 3.8e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   AAW66527 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Col 21; 25pp; English.
Claim 6; Page 37; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-00343882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90US-00522688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-00133740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90US-00476629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92US-00874685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MAGA-) MAGAININ PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amphiphilic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-456190/39
                                                                                                                                                                                                                                                                                  17 IVKILK 22
                                                                                                                                                                                                                                                                                                                   16 IVKILK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 1.
                                                                                                                                                                                  Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5792831-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agents, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maloy WL;
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW66527;
                                                                                                                                                                                                                                                                                                                                                                    RESULT 186
                                                                                                                                                                                                                                                                                                                                                                                  AAW66527
à
```

```
The invention relates to a composite binding polypeptide comprising a first natural binding domain derived from a first natural binding to polypeptide and a second natural binding domain derived from a second natural binding polypeptide, where the first and second natural binding polypeptide, where the first and second natural binding polypeptide. The invention also relates to a chimeric comprising a binding polypeptide cited above and a biological second binding polypeptide. The invention also relates to a chimeric polypeptide comprising a binding polypeptide cited above and a biological category of natural zinc finger nucleic acid binding domains, a library of natural zinc finger nucleic acid binding domains, a library of natural zinc finger nucleic acid binding domains composition of binding to a target site and a method for designing a composite binding colypeptide. The methods and compositions of the present invention are useful for designing sequence-specific binding proteins for regulation of gene expression in the fields of molecular biology. They can also be used for the diagnosis and treatment of autoimmune disorders, and as research
                                                                                                                                                                                                                                                                                                                                                                                                         Composite binding polypeptide, zinc finger nucleic acid binding domain, autoimmune disorder, immunosuppressive, zinc finger DNA binding domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tools and in transgenic animals. This sequence represents a human zinc finger DNA binding domain used in the scope of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composite binding zinc finger polypeptide, useful for designing sequence-specific binding proteins regulating gene expression in the fields of molecular biology, and for the diagnosis and treatment of
                                                                           ;
                                                                         0; Indels
                                    Length 22;
                          1.8%; Score 6; DB 2; Len
                                                     100.0%; Pred. No. 3.8
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Human zinc finger DNA binding domain #535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choo Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 82; 157pp; English.
                                                                                                                                                                                                                                                  ABO12236 standard; peptide; 23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-APR-2002; 2002WO-US022272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-2001; 2001GB-00008491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sepp A, Isalan M,
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-278214/27.
                              Query Match
Best Local Similarity
                                                                                                              IVKILK 22
                                                                                                                                                  16 İVKİLK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23 AA;
Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200299084-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                              25-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-DEC-2002.
                                                                         9
                                                                                                                                                                                                                                                                                       AB012236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moore M,
                                                                     Matches
                                                                                                                                                a
```

```
The invention relates to a composite binding polypeptide comprising a first natural binding domain derived from a first natural binding polypeptide and a second natural binding domain derived from a second natural binding polypeptide, where the first and second natural binding polypeptide, where the first and second natural binding polypeptides, where the first and second natural binding polypeptides. The invention also relates to a chimeric second binding polypeptide in a library of natural since a binding polypeptide comprising a binding polypeptide cited above and a biological natural zinc finger nucleic acid binding domains, a library of natural zinc finger nucleic acid binding domains comprising a linker attached to it, a method for selecting a binding polypeptide capable of binding to a target site and a method for designing a composite binding polypeptide. The methods and compositions of the present invention are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for designing sequence specific binding proteins for regulation of gene expression in the fields of molecular biology. They can also be used for the diagnosis and treatment of autoimmune disorders, and as research
                                                                                                                                                                                                                                                                                                       Composite binding polypeptide; zinc finger nucleic acid binding domain; autoimmune disorder; immunosuppressive; zinc finger DNA binding domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tools and in transgenic animals. This sequence represents a human zinc finger DNA binding domain used in the scope of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New composite binding zinc finger polypeptide, useful for designing sequence-specific binding proteins regulating gene expression in the fields of molecular biology, and for the diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 6; Length 23;
100.0%; Pred. No. 4e+02;
ive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                  Human zinc finger DNA binding domain #224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moore M, Sepp A, Isalan M, Choo Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 75; 157pp; English.
                                                                                                                                         ABO11924 standard; peptide; 23 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SANG-) SANGAMO BIOSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-2001; 2001GB-00008491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-APR-2002; 2002WO-US022272.
                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.0
--- 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-278214/27.
191 LTRHKV 196
                                  16 LTRHKV 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200299084-A2.
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                           25-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-DEC-2002
                                                                                                                                                                                  ABO11924;
                                                                                                 RESULT 188
```

RESULT 189

ó

Gaps .;

Query Match 1.8%; Score 6; DB 6; Length 23; Best Local Similarity 100.0%; Pred. No. 4e+02; Matches 6; Conservative 0; Mismatches 0; Indels

```
neovascularisation disorder; wound healing; estimated in cell proliferation; neurological disease; Alzheimer's disease; Parkinson's disease; mania; dementia; infectious disease.
                                                                              superoxidase, SOD, catalase; DNA repair protein, oncogene; tumour suppressor; tumour necrosis factor; TNF; inflammation; tumour suppressor; tumour necrosis factor; TNF; inflammation; hyperproliferative disorder; neoplasm; cardiovascular disorder; peripheral artery disease; limb ischaemia; arterio-arterial fistula; arteriovenous fistula; congenital heart defect;
                                                                       human; secreted protein; insulin; haemoglobin S; haemoglobin B;
                                                     Novel human secreted protein associated polypeptide #35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ebner R, Olsen HS, Young PE,
ADB47956 standard; protein; 24 AA.
                                                                                                                                                                                                                                                                                  9705-0054806P
9705-0054809P
9705-0054809P
9705-0055310P
9705-0055312P
9705-0055312P
9705-005536P
9705-005596EP
9705-005596EP
9705-005596EP
9705-005596EP
9705-005596EP
                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0056557P.
97US-0056563P.
97US-0056731P.
97US-0056732P.
98WO-US016235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001US-00774639.
                                                                                                                                                                                                                                       04-OCT-2001; 2001US-00969730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0238291P
                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soppet DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROSEN CA.
BREWER LA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RUBEN S M.
SOPPET D R.
EBNER R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GREENE J M. FERRIE A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OLSEN H S.
YOUNG P E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JANAT F.
BIRSE C E.
                                                                                                                                                                                                   US2003054443-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ϋ́З G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-2001;
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000;
                                    04-DEC-2003
                                                                                                                                                                                                                      20-MAR-2003
                                                                                                                                                                                                                                                                                                                         997
                                                                                                                                                                                                                                                                                                                                                            997
                                                                                                                                                                                                                                                                                                                                                                                        266
                                                                                                                                                                                                                                                                                                      997
                                                                                                                                                                                                                                                                                                                                                   05-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                      997
                                                                                                                                                                                                                                                                                                                                                                              997
                                                                                                                                                                                                                                                                                                                                                                                                                                   997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM,
                   ADB47956;
                                                                                                                                                                                                                                                                                                     05-AUG-1
                                                                                                                                                                                                                                                                                                                                                           05-AUG-1
                                                                                                                                                                                                                                                                                                                                                                              18-AUG-1
                                                                                                                                                                                                                                                                                                                                                                                                                          19-AUG-1
                                                                                                                                                                                                                                                                                                                                                                                                                                 19-AUG-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JANA/)
(BIRS/)
                                                                                                                                                                                                                                                                                                                                                                                                        9-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-
                                                                                                                                                                                                                                                                                                                                                                                       19-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SOPP/)
(EBNE/)
                                                                                                                                                                                                                                                                                                                                                                      8-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RUBE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FERR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROSE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BREW/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OLSE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YUGG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GREE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIJJ,
```

```
The invention relates to novel human secreted proteins. The protein is useful for diagnosing a pathological condition. The protein is useful for diagnosing a pathological condition or protein is useful for diagnosing a pathological condition or a susceptibility to pathological condition in a subject. The protein is useful for identifying a binding partner. The nucleic acid is useful for diagnosing pathological condition or a susceptibility to pathological condition in a subject. The protein is useful as reagents for differential identification of the tissues or cell types present in a biological sample. The protein can be administered to pathological subject or the protein can be administered to pathological condition. In a subject. The protein can be administered to patients having absent or decreased levels of different polypeptides, e.g. haemoglobin S for hemographic e.g. insulin, to supplement absent or decreased levels of different polypeptides e.g. haemoglobin S for membrane bound receptor by competing inhibit the activity of membrane bound receptor by competing receptors used in reducing inflammation, or to bring about a desired response e.g. blood vessel growth inhibition, enhancement of immune response to prodiferative cells or tissues. The protein and the nucleic acid are useful for treating, preventing, detecting, diagnosing discasses. The protein and the nucleic acid are useful for treating diseases, disorders and or creating.

The protein the nucleic acid and antibodies are useful for treating increased in sortions of immune system involving diseases, disorders and or construct and an account and a second increased.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune system, hyperproliferative disorders including neoplasms, cardiovascular disorders (such as peripheral artery disease, limb ischaemia, arterio-arterial fistula, arteriovenous fistula, congenital heart defects, etc), neovascularisation disorders, wound healing and epithelial cell proliferation, neurological diseases (such as Alzheimer's disease, Parkinson's disease, Huntington's disease, mania, dementia, etc), infectious diseases caused by virus, bacteria, fungi, etc. The present sequence represents the amino acid sequence of a novel human secreted protein associated polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunosuppressive, antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antipheumatic; hepatotropic; cerebroprotective; antiinflammatory; antipallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                                                                      Novel human secreted proteins useful for treating and/or diagnosing disorders of immune system, cardiovascular disorders such as peripheral artery disease, neurological diseases such as Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
     Brewer LA, Janat F, Birse CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 4.18+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.le+02;
nes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human nervous system related polypeptide SEQ ID NO 4717.
  Yu G, Ni J, Rosen CA,
                                                                                                                                                                                                                    Disclosure; Page 15; 333pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB16060 standard; protein; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                     WPI; 2003-695903/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 KKTDKA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKTDKA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB16060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 190
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

Greene JM;

```
27-SEP-2000; 2000US-0235834P.
29-SEP-2000; 2000US-0235836P.
29-SEP-2000; 2000US-0235836P.
29-SEP-2000; 2000US-02353636P.
29-SEP-2000; 2000US-0235369P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-023630P.
02-OCT-2000; 2000US-0233630P.
02-OCT-2000; 2000US-0233937P.
02-OCT-2000; 2000US-0233937P.
02-OCT-2000; 2000US-023933P.
02-OCT-2000; 2000US-023933P.
02-OCT-2000; 2000US-023461P.
03-OCT-2000; 2000US-024617P.
03-OCT-2000; 2000US-024617P.
03-OCT-2000; 2000US-024617P.
03-OCT-2000; 2000US-024617P.
03-NOV-2000; 2000US-024617P.
03-NOV-2000; 2000US-024617P.
03-NOV-2000; 2000US-024617P.
03-NOV-2000; 2000US-024617P.
03-NOV-2000; 2000US-024617P.
03-NOV-2000; 2000US-024617P.
03-NOV-2000; 2000US-024617P.
03-NOV-2000; 2000US-024617P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 200US-0249218P.
03-NOV-2000; 2000US-0249218P.
03-NOV-2000; 2000US-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
       20000S-0180628P

20000S-0184664P

20000S-0189874P

20000S-0190076P

20000S-0190076P

20000S-0190076P

20000S-0190076P

20000S-0190076P

20000S-0190076P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

2000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

20000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-011813P

2000S-01813P

2000S-01813P

2000S-01813P

2000S-01813P

2000S-01813P

2000S-01813P

2000S-01813P

2000S-01813P

2000S-01813P

2000S-01813P

2000S-01813P

2000S-01813P

2000S-01813P

2000S-01813P

2000S-01813P

2000S-01813P

2000S-0181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0234997P.
2000US-0234998P.
2000US-0235484P.
                                                                                                                                             17-JAN-2001; 2001WO-US001334
                                              WO200159063-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-SEP-20000

06-SEP-20000

08-SEP-20000

08-SEP-20000

08-SEP-20000

08-SEP-20000

08-SEP-20000

08-SEP-20000

08-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

14-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15-SEP-20000

15
                                                                                                                                                                                                                                                              15-MAR-2000;

16-MAR-2000;

18-MAR-2000;

18-APR-2000;

19-MAY-2000;

28-JUN-2000;

30-JUN-2000;

30-JUL-2000;

11-JUL-2000;

11-JUL-2000;

11-JUL-2000;

14-JUL-2000;

14-MG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

14-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-AUG-2000;

11-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-SEP-2000; 2
01-SEP-2000; 2
05-SEP-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
  Homo sapiens
                                                                                                                                                                                           31-JAN-2000;
                                                                                            16-AUG-2001
```

```
ABG76643 standard; peptide; 29 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-NOV-2001; 2001WO-EP013663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-NOV-2000; 2000EP-00125693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                           Rosen CA, Barash SC,
                                                                                      WPI; 2001-541565/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 FEAFHV 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEAFHV 25
                                                                                                                  N-PSDB; ABA12386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200242455-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG76643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
PRINCE NEW YORK ON THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

```
Sequence 29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
         disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW15122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                The invention relates to novel genes (ABAl1004-ABA21534) and proteins (ABBHA678-ABBA18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The uncleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and owner and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune baset, gastrointestinal tract, liver, lung, or urogenital; (b) immune baset, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, theumatoid arthritis and ulcerative colifis; (c) and amenda, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, theumatoid arthritis and ulcerative colifis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suppressor of uncoupling protein 1; SOUP1; membrane stability; obesity; organalle function; mitrochondria; peroxisome; cellular metabolism; ROS; homeostasis; body weight; metabolic disorder; adipositas; cachexia; eating disorder; wasting syndrome; mitochondrial disorder; antilipaemic; pancreatic dysfunction; anorectic; immunomodulator; gene therapy; regulator of transporter molecule; modifier of mitochondrial protein; fruit fly; human; mouse; transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                            Claim 11; SEQ ID NO 4717; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wehr R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 4; Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human SOUP1 maximal transmembrane domain peptide MB-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ciossek T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Steuernagel A, Broenner G, Dohrmann C,
Rudolph B, Rudolph D;
```

```
The present invention relates to a new nucleic acid molecule, termed suppressor of uncoupling protein 1 (SOUPI), encoding a polypeptide contributing to membrane stability and/or function of organelles. The invention is useful for monitoring and/or controlling the function of gene and/or gene product which is influenced and/or modified by the SOUPI colypeptide, where the gene and/or gene product is expressed in corganelles such as mitochondria or peroxisome, or for identifying corganelles such as mitochondria or peroxisome, or for identifying a coll interacting with the polypeptide. The invention is also useful for identifying a polypeptide or substance(s) involved in cellular metabolism in an animal or capable of modifying homeostasis, or for identifying a polypeptide involved in the regulation of body weight or verifying a disorder in cells, cell masses, organs and/or subjects, where the disorder is a metabolic for treating, alleviating and/or preventing a disorder in cells, cell masses, organs and/or subjects, where the disorder is a metabolic disorder such as obesity, adipositas, eating disorder; wanting subjects, and disorders related to ROS production. The invention is useful for the detection of polypeptides capable of contributing to membrane stability and/or function in organelles, capable of modifying mitochondrial corders and contributing cellular metabolism. The present contribution of many peptide of the invention and sequence represents a SOUPI transmembrane domain peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "The side chain carboxyl group of Glu at position 19 forms a lactam bridge with the side chain amino group of Lys at position 22"
                                                                            New suppressor of uncoupling protein 1 polynucleotide encoding a polypeptide contributing to membrane stability and/or function of organelles, useful for treating metabolic disorders and mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corticotropin-releasing factor; CRF; analogue; agonist; antagonist; lipophilic; RT-PCR; ligand binding activity; treatment; astressin; depression; psychosomatic disease; therapeutic agent; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corticotropin-releasing factor (CRF) analogue IV (3Ala Astressin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 6; DB 5; Length 29; 100.0%; Pred. No. 4.9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Norleucine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW15122 standard; peptide; 33 AA.
                                                                                                                                                                                                                       Claim 15; Fig 5e; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label= Nle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                             WPI; 2002-599380/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 TVEYIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 TVEYIS 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
```

/note= "The side chain amino group of Lys at position 22

```
This 3Ala Astressin is a lipophilic corticotropin-releasing factor (CRF) analogue where some amino acids in the native h/rCRF (Astressin) have been replaced by alanine at positions 20, 25 and 32. The CRF analogue retains the CRF ligand binding activity. CRF is thought to integrate endocrine, autonomic, immune and behavioural responses to stress in the Central nervous system (CNS) through regulation of hypothalamus-pituitary-adrenal axis leading to glucocorticoids release after stress exposure, in which signal transduction is mediated through receptors. Analogues of CRF can intrate or block biological function of CRF (agonists or antagonists respectively), making them useful in investigation of peptidergic systems and as therapeutic agents e.g. in prevention or treatment of stress, depression, anxiety and other psychosomatic diseases. They can be used alone or with other agents and treatments. The analogues can easily pass through the blood-brain barrier due to their high affinity to CRF receptor and raised lipophilicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
forms a lactam bridge with the side chain amino group of
                                                                                                                                                                                                                                                                                                                                      Lipophilic corticotropin-releasing factor analogues - have increased ability to pass through the blood-brain barrier and are useful as therapeutic agents for treating e.g. stress and anxiety.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #10726 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 2; Length 33; ilarity 100.0%; Pred. No. 5.6e+02; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                      (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                   /note= "Norleucine"
                 Glu at position 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB43220 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 7; 14pp; English
                                                                                                                                                                     96WO-EP005010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US000669.
                                                                                                                                                                                                      95EP-00117940
                                                /label= Nle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                        Spiess J, Ruehmann A;
                                                                                                                                                                                                                                                                                                        WPI; 1997-289228/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 AQLAQE 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 AQLAQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 33 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157277-A2
                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ното варіелв.
                                                                                                                                                                    14-NOV-1996;
                                                                                                                                                                                                    14-NOV-1995;
                                                                                                  WO9718238-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                                                                                    22-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB43220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
```

```
o,
                                                                                                                                                                                                                                                                                  The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide #11097 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 35855; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 4; Length 34; 100.0%; Pred. No. 5.7e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe, microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W, Rank DR;
                                                                                                                                                   Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM37060 standard; protein; 34 AA.
            26-MAY-2000; 2000US-0207456P.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
27-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234539P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-0060408.
03-AUG-2000; 2000US-00633366.
21-SEP-2000; 2000US-0234687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
04-FEB-2000; 2000US-0180312P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US000663,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                  Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                             WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 TQPIVE 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TOPIVE 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM37060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 19
AAM37060
ò
```

٥;

0; Indels

```
The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human borne marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing
             Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                      The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       marrow expressed exon; gene expression analysis; probe; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human bone marrow expressed probe encoded protein SEQ ID NO: 37258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; SEQ ID NO 37258; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                   Score 6; DB 4; Length 34; Pred. No. 5.7e+02;
                                                                                                                                                                                                                                   1.8%; Score 6; DB 4
100.0%; Pred. No. 5.7
tive 0; Mismatches
                                                        Claim 27; SEQ ID NO 37329; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expression in human bone marrow.
                             gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                            AAM76952 standard; protein; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-0060B40B.
30-AUG-2000; 2000US-0063336C.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001; 2001WO-US000668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0180312P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000GB-00024263
                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100.00
Lham 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                       from human placenta. The
human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                  287 TOPIVE 292
                                                                                                                                                                                                                                                                                                                                TOPIVE 6
                                                                                                                                                                                                     Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM76952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn SG,
                                                                                                                                                                                                                                                                                                                                                                             RESULT 195
                                                                                                                                                                                                                                                                                                                                                                                               AAM76952
à
```

```
..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                               Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                    Human brain expressed single exon probe encoded protein SEQ ID NO: 36232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in human
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; SEQ ID NO 36232; 650pp + Sequence Listing; English.
                                         0; Indels
              Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Lenco. 5.7e+02;
             DB 4; Ler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
             1.8%; Score 6; DB 4
100.0%; Pred. No. 5.7
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 1.8%; Score 6; DB 4 Local Similarity 100.0%; Pred. No. 5.7 Les 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR;
                                                                                                                                                                 AAM64127 standard; protein; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG58614 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-2000; 2000US-0207456P.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532566.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023458PP.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US000667
                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000; 2000US-0180312P
Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483446/52.
                                                                  287 TQPIVE 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287 TQPIVE 292
                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TOPIVE 6
                                                                                              TOPIVE
                                                                                                                                                                                                                                                                                                                                                   WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                        05-NOV-2001
                                                                                                                                                                                            AAM64127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG58614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Penn SG,
                                                                                                                                     RESULT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                     AAM64127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG5861
                                                                   à
                                                                                            셤
                                                                                                                                                                                            à
```

```
The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. Lowprising one of 13109 defined nucleotide sequences given in the specification (or complements). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence but was obtained in electronic format directly from WIPO at the printed specification for this patent does not appear in the printed specification fire. WIPO: int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human peptide encoded by genome-derived single exon probe SEQ ID 35724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                            Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 4; Ler
100.0%; Pred. No. 5.7e+02;
rative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 37262; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene expression in human adult liver.
                                            Human liver peptide, SEQ ID No 37262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG46059 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                       26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023458PP.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                           2000US-0180312P
             25-FEB-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488898/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 TQPIVE 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TOPIVE 6
                                                                                                                                                          WO200157273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34 AA;
                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-AUG-2002
                                                                                                                                                                                            09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG46059;
                                                                                                                                                                                                                                                                                                                                                                                                                           Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
à
```

Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease;

```
The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes it the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung; comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung measuring the array with a measure mannal to each probe of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORP). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma; lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphanjoleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplacia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                     tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangiolelomyomtosis; Karagener syndrome; pulmonary alveolar proteinlosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spatially-addressable set of single exon nucleic acid probes, used to
familial idiopathic pulmonary fibrosis; neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27; SEQ ID NO 35724; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-2000; 2000US-0207456P
30-JUN-2000; 2000US-00608408.
03-MG-2000; 2000US-0033366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US000665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-OCT-2000; 2000GB-00024263
                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000; 2000US-0180312P
                                                                                                                                                        hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-114183/15.
                                                                                                                                                                                                                                                              WO200186003-A2
                                                                                                                                                                                                            Homo gapiens,
                                                                                                                                                                                                                                                                                                               15-NOV-2001
```

```
Sequence 39 AA;
                                       Key
Modified-site
                                                               Modified-site
                                                                                                                      20-MAY-1999;
                                                                                                                                       20-MAY-1998;
                        Unidentified
                                                                                       US6348568-B1
                                                                                                       19-FEB-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB67852;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADB67852
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                    The peptide is useful in a pharmaceutical composition as an antimicrobial compound for use in human and veterinary medicine and as an agent in agricultural, food science and industrial applications. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                              Purified beta-defensin peptide(s) - useful as antimicrobial agents in human and veterinary medicine.
                                       Gaps
                                                                                                                                                                                     Cattle; bovine; neutrophil; beta-defensin; antibiotic; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID No 1533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 2; Length 38; 100.0%; Pred. No. 6.3e+02; tive 0; Mismatches 0; Indels
                       1.8%; Score 6; DB 5; Length 34;
100.0%; Pred. No. 5.7e+02;
                                                                                                                                                                      Bovine neutrophil beta-defensin peptide BNBD-8.
                              Pred. No. 5.7
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE03026 standard; peptide; 39 AA.
                                                                                                               AAR63517 standard; peptide; 38 AA.
                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 5; 79pp; English.
                                                                                                                                                                                                                                                                              93US-00033873.
                               100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2004 (first entry)
                                                                                                                                                       (first entry)
                              Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                              Cullor JS;
                                                                                                                                               (revised)
                                                                                                                                                                                                                                                                                                                              WPI; 1994-316934/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 RRQIGT 111
                                                       287 TQPIVE 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RROIGT 28
                                                                      1 TOPIVE 6
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 38 AA;
        Sequence 34 AA;
                                                                                                                                                                                               pharmaceutical
                                                                                                                                                                                                                                                                              19-MAR-1993;
                                                                                                                                                                                                                              WO9421672-A1
                                                                                                                                              25-MAR-2003
22-JUN-1995
                                                                                                                                                                                                                                              29-SEP-1994
                                                                                                                                                                                                                                                                                                              Selsted ME,
                                                                                                                                                                                                              Bos taurus.
                                                                                                                              AAR63517;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE03026;
                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 200
                                                                                              RESULT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE03026
                                                                                                       AAR63517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XEXEXEX
XX SS
                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                       à
```

```
antiviral activity. The novel hybrid polypeptide is useful for decreasing viral infection and modulating intracellular processes involving coiled-
ool peptide interactions. The novel hybrid polypeptide comprises insulin or its fragment, so the core polypeptide is useful for ameliorating the symptoms of forms of diabetes. The novel hybrid polypeptide is also useful as a part of prognosis for preventing disorders including fusion events and viral infection that involves cell-cell and/or virus-cell fusion, and for diagnosis and in vivo imaging methods. This sequence represents an enhancer peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New hybrid polypeptide for modulating fusogenic events for e.g. antiviral activity, has enhancer peptide sequence derived from retroviral envelope protein sequences linked to core polypeptide e.g. therapeutic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel hybrid polypeptide comprising an enhancer peptide sequence linked to a core polypeptide. The enhancer peptide sequence comprises WQRWEQKI or WASLWEWF. The invention also includes novel peptides that exhibit anti-fusogenic activity, antiviral activity and/or ability to modulate intracellular processes. The novel hybrid polypeptide has virucide and antidiabetic activity. The enhancer peptide sequence enhances pharmacokinetic properties of any core polypeptide, for example, a polypeptide useful for the treatment or prevention of a disease, or an imaging agent useful for mediating tusegenic consecution in the novel when the core polypeptides and whibit antifusogenic or antiviral activity. The novel hybrid polypeptides are suseful for modulating fusogenic events and exhibit antifusogenic or antiviral activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
hybrid, enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;
pharmacokinetic; fusogenic; insulin; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                 'note= "Residue is modified by acetyl group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lambert DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 5; Length 39; 100.0%; Pred. No. 6.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lung specific protein sequence SEQ ID NO:135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merutka G, Anwer MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 1533; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "C-terminal amide"
                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB67852 standard; protein; 39 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-00315304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-00082279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barney S, Guthrie KI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TRIM-) TRIMERIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-424396/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 AQLAQE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 AQLAOE 20
```

```
The present invention describes human lung specific polypeptides (LSP, (I)) and lung specific nucleic acids (LSNA, (II)). Also described: (1) and lung specific nucleic acids (LSNA, in a sample: (2) a vector (III) comprising (III); (3) a host cell comprising (III); (4) a polypeptide (IV) comprising (III); (4) a polypeptide (IV) comprising (III); (4) a polypeptide (IV) encoded by (II); (5) production of (IV); (6) an antibody (V) or its fragment that specifically binds to an LSP; (7) determining (M2) the presence of an LSP in a sample; (8) a kit for detecting a risk of cancer or presence of (I) or (II) in a sample of the patient; and (9) a vaccine comprising (I) or (II). LSP and LSNA sequences have cytostatic actin inmune response. (I) and (II) can be used for diagnosing or monitoring the amount of the determined nucleic acid molecule or the polypeptide in the sample of the patient, and comparing the cample of the patient to the amount of the nucleic acid molecule or the polypeptide in the sample compared to the amount of the nucleic acid molecule or the polypeptide in the compared to the amount of the nucleic acid molecule or the polypeptide in the sample compared to the amount of the nucleic acid molecule or the polypeptide in the nucleic acid molecule or the polypeptide in the compared to the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of the amount of (I) or (I) induces an immune response against the amount of (I), and of the amount of (I), a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used in gene therapy, for producing transgenic animals and cells, and for producing engineered lung tissue for treatment and research. (II) is also useful for detecting or amplifying nucleic acid molecules that have similar or identical nucleic acid sequences compared to (II). (I) is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (II) can be
human; lung specific polypeptide; LSP; lung specific nucleic acid; LSNA; lung; cytostatic; vaccine; gene therapy; immune response; lung cancer; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                monitoring, staging, imaging and treating lung cancer and non-cancerous disease states in lung, for identifying lung tissue, and monitoring, identifying and/or designing agonists and antagonists of (I). (II) can b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel lung specific polypeptides and nucleic acids, useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous disease states in lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for producing engineered lung tissue. (\dot{V}) is useful for identifying (I). (II) is also useful for driving in vivo expression of (I). The present sequence represents a human LSP from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 6; DB 7; Length 39;
100.0%; Pred. No. 6.5e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 243; 263pp; English.
                                                                                                                                                                                                                                                                     29-AUG-2002; 2002WO-US027771.
                                                                                                                                                                                                                                                                                                                       31-AUG-2001; 2001US-0316260P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 100..
From 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sun Y, Liu C, Chen S;
                                                                                                                                                                                                                                                                                                                                                                             (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-300880/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 STFDIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 STFDIA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADB67946.
                                                                                                                                                          WO2003020899-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39 AA;
                                                                                                             Homo sapiens.
                                                                                                                                                                                                               13-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nvention.
```

```
The peptide is useful in a pharmaceutical composition as an antimicrobial compound for use in human and veterinary medicine and as an agent in agricultural, food science and industrial applications. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                              Purified beta-defensin peptide(s) - useful as antimicrobial agents in human and veterinary medicine.
                                                                                                           Cattle; bovine; neutrophil; beta-defensin; antibiotic; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cattle; bovine; neutrophil; beta-defensin; antibiotic; antimicrobial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 2; Length 40;
100.0%; Pred. No. 6.7e+02;
tive 0; Mismatches 0; Indels
                                                                                     Bovine neutrophil beta-defensin peptide BNBD-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine neutrophil beta-defensin peptide BNBD-9.
         AAR63516 standard; peptide; 40 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR63518 standard; peptide; 40 AA.
                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 5; 79pp; English.
                                                                                                                                                                                                                94WO-US003178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-US003178.
                                                                                                                                                                                                                                     93US-00033873
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100..
The footstrative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                  Selsted ME, Cullor JS;
                                                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003 (revised)
                                                                                                                                                                                                                                                                                                        WPI; 1994-316934/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 RRQIGT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 40 AA;
                                                                                                                       pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-1994;
                                                                                                                                                                   WO9421672-Al
                                                                                                                                                                                                              15-MAR-1994;
                                                                                                                                                                                                                                     19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9421672-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUN-1995
                                                                                                                                                                                          29-SEP-1994.
                                                     25-MAR-2003
                                                                22-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus.
                                                                                                                                             Bos taurus.
                              AAR63516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR63518;
AAR6351(
         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

; 0

. 0

```
ò
                                                                                                                                                                                                              a
                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Media comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds useful for the storage and preservation of organs prior to transplant.
                                                                                                                                      The peptide is useful in a pharmaceutical composition as an antimicrobial compound for use in human and veterinary medicine and as an agent in agricultural, food science and industrial applications. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                     Transplant, antimicrobial peptide; pore forming agent; cardioplegia; cell surface receptor binding compound; kidney transplant; cardioplegia; organ transplant; transplant rejection; defensin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes new transplant compositions comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds. The media is capable of extending the preservation period past 72 hours and can provide organs with increased functionality upon transplant, animals receiving kidneys stored in the
                                                                                      Purified beta-defensin peptide(s) - useful as antimicrobial agents in
                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                           1.8%; Score 6; DB 2; Length 40;
100.0%; Pred. No. 6.7e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Transplant media associated defensin peptide #28.
                                                                                                                                                                                                                                                                                                                       AAU91027 standard; peptide; 40 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mcanulty JF;
                                                                                                                     Disclosure; Fig 5; 79pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8; Page 29; 78pp; English.
                                                                                                   human and veterinary medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUL-2001; 2001WO-US023785.
         93US-00033873.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-2000; 2000US-0221632P.
17-NOV-2000; 2000US-0249602P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LS-MAY-2001; 2001US-0290932P
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                 6; Conservative
                            (REGC ) UNIV CALIFORNIA.
                                                Cullor JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reid TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-268995/31.
                                                                    WPI; 1994-316934/39
                                                                                                                                                                                                                                                    106 RRQIGT 111
                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MURP/) MURPHY C J.
                                                                                                                                                                                                                                                                       25 RROIGT 30
                                                                                                                                                                                        Sequence 40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200209738-A1.
         19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                               05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                Selsted ME,
                                                                                                                                                                                                                                                                                                                                           AAU91027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murphy
                                                                                                                                                                                                                                                                                                     204
                                                                                                                                                                                                                                                                                                  RESULT 2
```

```
receiving kidneys stored in We solution (defined in the specification) alone. Lower serum creatinine levels of less than half of those observed in control animal alone. Lower serum creatinine levels are indicative of healthier kidneys and a more preferable prognosis for the transplant patient. The media of the invention are useful for decreasing the incidence and/or severity of delayed graft function in patients receiving transplanted kidneys stored and/or treated in the media. The media may also be used in procedures such as cardioplegia. It is contemplated that transplant of healthier organs leads to a decrease in chronic rejection. This sequence represents an antimicrobial defensin peptide studied in the development of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Media comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds useful for the storage and preservation of organs prior to transplant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention describes new transplant compositions comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds. The media is capable of extending the preservation period past 72 hours and can provide organs with increased functionality upon transplant. animals receiving kidneys stored in the media of the present invention for either three or four days had serum creatinine levels of less than half of those observed in control animals receiving kidneys stored in UW solution (defined in the specification) and more preferable prognosis for the transplant patient. The media of the invention are useful for decreasing the incidence and/or severity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transplant, antimicrobial peptide, pore forming agent, cardioplegia; cell surface receptor binding compound; kidney transplant; cardioplegia; organ transplant; transplant rejection; defensin.
media of the present invention for either three or four days had serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 5; Length 40; 100.0%; Pred. No. 6.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transplant media associated defensin peptide #27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mcanulty JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU91026 standard; peptide; 40 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 29; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JUL-2001; 2001WO-US023785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-JUL-2000; 2000US-0221632P.
17-NOV-2000; 2000US-0249602P.
15-MAY-2001; 2001US-0290932P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reid TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-268995/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MURP/) MURPHY C J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 RROIGT 30
                                                                                                                                                                                                                                                                                                                                                                                                                          transplant media
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 40 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200209738-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murphy CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU91026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 205
```

```
delayed graft function in patients receiving transplanted kidneys stored and/or treated in the media. The media may also be used in procedures such as cardioplegia. It is contemplated that transplant of healthier organs leads to a decrease in chronic rejection. This sequence represents an antimicrobial defensin peptide studied in the development of the
                                                                                                                                        transplant media
8×338888×8
```

Sequence 40 AA;

```
.
0
                                0; Indels
   1.8%; Score 6; DB 5; Length 40;
100.0%; Pred. No. 6.7e+02;
live 0; Mismatches 0; Indels
                                 Conservative
                                                            106 RRQIGT 111
             Local Similarity
es 6; Conserv
                                                                                       25 RROIGT 30
Query Match
                             Matches
```

ö

```
Staphylococcus aureus antigenic protein #215.
    ADA89676 standard; protein; 41 AA.
            20-NOV-2003
        ADA89676;
RESULT 206
  ADA89676
```

antigenic protein, vaccine, Staphylococcus aureus; pathogenic organism; antibacterial; neuroprotective, immunosuppressive; antiinflammatory; antiuler; immunostimulant; ophthalmological, pathogenic microbe; bacteraemia; septic shock; organ infection; skin infection; bacterial basal colonisation; bacterial eye infection; septicaemia; tuberculosis; food poisoning; blood infection; peritonitis; endocarditis; sepsis; meningtis; pneumonia; stomach ulcer; gonorrhoea; toxic shock; necrotising fascitis; impetigo; histoplasmosis; Lyme disease; gastro-enteritis; dysentery; shigellosis; skin disorder.

WO2003011899-A2.

13-FEB-2003

02-AUG-2002; 2002WO-GB003606.

09-JAN-2002; 2002GB-00000349. 02-AUG-2001; 2001GB-00018825

(UYSH-) UNIV SHEFFIELD.

BIOSYNEXUS INC. (BIOS-)

Mcdowell P, Brummel K; Clarke S, Mond J, Foster S,

WPI; 2003-256434/25.

New antigenic polypeptides from Staphylococcus aureus or S. epidermidis, useful as a vaccine for immunizing humans against e.g. bacteremia, septic septicemia, tuberculosis, meningitis, pneumonia, gonorrhea or impetigo.

Claim 4; Page 163; 189pp; English.

The present invention describes an antigenic protein or its part, which is for use as a vaccine. The antigenic protein is encoded by an isolated DNA molecule of Staphylococcus aureus or S. epidermidis partial gene sequences (designated dnaSA and dna SB, respectively; and which encodes a protein expressed by a pathogenic organism. Also described: (1) a vaccine composition comprising at least one antigenic protein; (2) a method of immunishing an animal against a disease or condition caused by a pathogenic microbe by administering the antigenic protein or the vaccine; (3) an antibody or its binding part obtainable by the method above; (4) preparing a hybridoma cell line producing monoclonal antibodies; (5) a

The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe

```
ö
                                                                                                                                                                                                          fascitis, impetigo, histoplasmosis, Lyme disease, gastro-enteritis, dysentery, shigellosis, S. aureus-associated septicaemia, food-poisoning, skin disorders, S. epidermidis-associated septicaemia, peritonitis or endocarditis. The present sequence represents a S. aureus antigenic protein sequence from the present invention.
            opsonic antigeness expressed by a pathogenic microbe. The antigenic proteins have antibacterial, neuroprotective, immunosuppressive, antiinflammatory, antiulcer, immunostimulant and ophthalmological activities, and can be used in vaccines. The antigenic proteins or vaccines can be used for immunisting an animal (specifically a human) against a disease or condition caused by a pathogenic microbe, e.g. bacteraemia, septic shock, organ infection, skin infection, bacterial basal colonisation, bacterial eye infections, septicaemia, tuberculosis, bacteria-associated food poisoning, blood infections, peritonitis, endocarditis, sepsis, meningitis, pneumonia, stomach ulcers, gonorrhoea, strep throat, etreptococcal-associated toxic shock, necrotising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing
hybridoma cell line produced by the method of (4); and (6) identifying
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide #5824 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID NO 30953; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                          Length 41;
                                                                                                                                                                                                                                                                                                                                                     DB 6; Len
o. 6.8e+02;
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Fred. No. 6.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB38318 standard; peptide; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-0060B40B.
03-AUG-2000; 2000US-023366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US000669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000; 2000US-0180312P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-2000; 2000GB-00024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                           197 LVADFL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 LVADFL 41
                                                                                                                                                                                                                                                                                                                     Sequence 41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 207
ABB38318
 $$$$$$$$$$$$$$$$$$$$$$$$
                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

```
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                    format
                                                                                                                                                                                                                                                                                                                      Peptide #5794 encoded by probe for measuring placental gene expression.
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
of the invention. Note: The sequence data for this patent did not part of the printed specification, but was obtained in electronic directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                        DB 4; בייב
אס. 7e+02;
O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                 Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Le
                                                                                1.8%; Score 6; DB 4
100.0%; Pred. No. 7e+
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.8%; Score 6; DB 4
Best Local Similarity 100.0%; Pred. No. 7e+
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; SEQ ID NO 32026; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W, Rank DR;
                                                                                                                                                                                                                                   AAM31757 standard; protein; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US000663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0207456P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0180312P
                                                                   Query Match
Best Local Similarity 100...
6; Conservative
                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488897/53
                                                                                                                                         36 DKASEE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 DKASEE 31
                                                                                                                                                                  26 DKASEE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 DKASEE 41
                                                                                                                                                                                                                                                                                                                                                             genetic disorder
                                                         Sequence 42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157272-A2.
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-2000;
                                                                                                                                                                                                                                                                                          17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
                                                                                                                                                                                                                                                                AAM31757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn SG,
                                                                                                                                                                                                            RESULT 208
                                                                                                                                                                                                                                                               SSSSSS
```

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a single exon nucleic acid probe (SENP) [1] for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification for complements fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. [1] may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                             Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 4; Length 42;
100.0%; Pred. No. 7e+02;
ive 0; Mismatches 0; Indel8
                                                                                                                                                                              hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID NO 31804; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W, Rank DR;
                                                                                                                              Human liver peptide, SEQ ID No 31804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM14123 standard; protein; 43 AA.
                              ABG53156 standard; peptide; 42 AA.
                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-003466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US000664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488898/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 DKASEE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 DKASEE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 42 AA;
                                                                                                                                                                                                                                            WO200157273-A2.
                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
                                                                                              25-FEB-2003
                                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM14123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 210
RESULT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM14123
                 ABG53156
                                ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

```
The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide #567 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 25703; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.8%; Score 6; DB 4; Length 43; Best Local Similarity 100.0%; Pred. No. 7.1e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                     Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                          gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM26530 standard; protein; 43 AA.
                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                 03-AUG-2000; 2000US-0063236C.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468TP.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                             26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
30-JAN-2001; 2001WO-US000669,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
                                         2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US000663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-OCT-2001 (first entry)
                                                                                                                                                                                                                                                     Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                            WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 GLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 GLLVTL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157272-A2
                                         04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 212
AAM26530
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical sepithalial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing
               Peptide #557 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                  Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide #574 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 4
100.0%; Pred. No. 7.11
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 18949; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB33068 standard; peptide; 43 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                               03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
7-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US000670.
                                                                                                                                                                                                                                                                                    2000US-0180312P.
2000US-0207456P.
2000US-00608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.8
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 GLLVIL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 GLLVTL 40
                                                                             cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 43 AA;
                                                                                                                                                            WO200157278-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157277-A2
                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                        04-FEB-2000;
                                                                                                                                                                                                                                                                                                        26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001.
                                                                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB33068;
```

ò

ö

Gaps

ó

0; Indels

```
35
                                          ABB27896;
                                                                                                                                                                                                            Penn SG,
g
```

```
07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
                                                                                                                                                                                                                                                                                                                           21-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L4-AUG-2000
                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                       AAM94970
     ₽
                                                                                                                                                                                                                                                                                            ö
                           Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                               The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placents. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                 Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the
                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                            Peptide #547 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID NO 10864; 327pp + Sequence Listing; English.
                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                1.8%; Score 6; DB 4; Length 43; 100.0%; Pred. No. 7.1e+02;
                                                                                                                                                                                      100 0%; Prec. ...
                                                           Claim 27; SEQ ID NO 26799; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W, Rank DR;
                                        gene expression in human placenta.
                                                                                                                                                                                                                                                                                             ABB27896 standard; peptide; 43 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-00632366.
2000US-0234687P.
2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US000662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000; 2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0207456P.
2000US-00608408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2000; 2000GB-00024263
                                                                                                                                                                  Query Match
Best Local Similarity 100.00
Lhes 6; Conservative
                                                                                                                                                                                                                                                                                                                                       01-FEB-2002 (first entry)
                                                                                                                                     human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-496933/54.
                                                                                                                                                                                                                       77 GLLVTL 82
                                                                                                                                                                                                                                            GLLVTL 40
                                                                                                                                                         Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157271-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
```

```
0;
                are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed sequence by the second of the invention of the printed of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; reproductive system related antigen; reproductive system disorder;
expression of regions of genomic DNA predicted to encode proteins. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human reproductive system related antigen SEQ ID NO: 3628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Length 43;
                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Lenco. 7.1e+02;
                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 4
100.0%; Pred. No. 7.1.
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM94970 standard; protein; 43 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-2000; 2000US-0179065P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-FEB-2000; 2000US-0184664P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-2001; 2001WO-US001339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-2000; 2000US-0189874P
17-MAR-2000; 2000US-0190076P
18-APR-2000; 2000US-0198123P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0205515P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0209467P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0214886P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0215135P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0216647P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0216880P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0217487P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0217496P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0218290P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0220963P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0225266P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-2000; 2000US-0225447P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0224518P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0224519P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 GLLVTL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 GLLVTL 82
                                                                                                                                                                                                                                                                                                                                                   Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200155320-A2.
```

```
2000US-0231242P

2000US-0231244P

2000US-0231244P

2000US-0231244P

2000US-0231414P

2000US-023166P

2000US-023196B

2000US-023298P

2000US-023239P

2000US-023239P

2000US-023240P

2000US-023240P

2000US-023240P

2000US-023240P

2000US-023240P

2000US-023240P

2000US-023240P

2000US-023240P

2000US-023240P

2000US-023240P

2000US-023240P

2000US-0233064P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0234274P
2000US-0234997P
2000US-0234998P
2000US-0235484P
2000US-0235834P
2000US-0235834P
2000US-0235834P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0236367P.
2000US-0236368P.
2000US-0236369P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0236370F
2000US-0236370F
2000US-0237037F
2000US-0237039F
2000US-0237039F
2000US-0237039F
2000US-0239937F
2000US-0249960F
2000US-024128F
2000US-024178F
2000US-024178F
2000US-024178F
2000US-024178F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0246475P.
2000US-0246476P.
2000US-0246477P.
2000US-0246478P.
                                                                                                                                                                                                                       2000US-0229345P.
                                                                                                                                                                                                                                                                               2000US-0230437P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0244617P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           000US-0246523P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0246524P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0246528P.
2000US-0246532P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0246609P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-OCT-2000; 2
02-OCT-2000; 2
02-OCT-2000; 2
02-OCT-2000; 2
13-OCT-2000; 2
13-OCT-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 20 08-NOV-2000; 2
                                                                                                                                                         01-SEP-2000;
                                                          22-AUG-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                   -SEP-2000;
                                                                                                                                                                                                                   01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-OCT-2000;
```

```
Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein #516 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID NO 3628; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.8%; Score 6; DB 4; Length 43; Best Local Similarity 100.0%; Pred. No. 7.1e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB18537 standard; protein; 43 AA.
08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-02496611P.
17-NOV-2000; 2000US-0249209P.
17-NOV-2000; 2000US-0249209P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024930P.
17-NOV-2000; 2000US-024930P.
17-NOV-2000; 2000US-024930P.
17-NOV-2000; 2000US-024930P.
17-NOV-2000; 2000US-025199P.
05-DEC-2000; 2000US-0251499P.
06-DEC-2000; 2000US-025189P.
08-DEC-2000; 2000US-025189P.
08-DEC-2000; 2000US-025189P.
08-DEC-2000; 2000US-025189P.
08-DEC-2000; 2000US-025189P.
08-DEC-2000; 2000US-025189P.
08-DEC-2000; 2000US-025189P.
08-DEC-2000; 2000US-025189P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA, Barash SC, Ruben SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JAN-2001; 2001US-0259678P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-465570/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 FLSSFQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 FLSSFO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAL00940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB18537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB18537
     ò
```

. 0

```
30-JAN-2001; 2001WO-US000668.
       09-AUG-2001,
                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 217
                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM53865
                                                                                                                                                                                                                                                                                                                                             Beat
       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                         measuring human gene expression in a sample derived from human heart (see MaA21552-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, human heart and vascular system e.g. cardiovascular diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o;
                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human bone marrow expressed probe encoded protein SEQ ID NO: 26559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
         Human; gene expression; heart; microarray; vascular system;
cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 4; Length 43;
100.0%; Pred. No. 7.1e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                    Claim 15; SEQ ID NO 20307; 530pp; English.
                                                                                                                                                                                                                                     Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM66253 standard; protein; 43 AA.
                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                   2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
                                                                                                                                                          03-AUG-2000; 2000US-00632366
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                           30-JAN-2001; 2001WO-US000666
                                                                                                                                2000US-0180312P
                             congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                   Hanzel DK,
                                                                                                                                                                                                                                                       WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 GLLVTL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 GLLVTL 82
                                                                    WO200157274-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157276-A2
                                                  Homo sapiens,
                                                                                                                                                    30-JUN-2000;
                                                                                                                              04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                          26-MAY-2000;
                                                                                        09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
                                                                                                                                                                                                                                  Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphona, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human brain expressed single exon probe encoded protein SEQ ID NO: 25970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO 26559; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 1.8%; Score 6; DB 4; Length 43; Local Similarity 100.0%; Pred. No. 7.18+02; les 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM53865 standard; protein; 43 AA.
04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0207456P.
30-UJX-2000; 2000US-00608408
03-AUG-2000; 2000US-00632366.
21-SFE-2000; 2000US-023468PP.
21-SEP-2000; 2000US-023458PP.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                    Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FBB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-UJN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023468PP.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US000667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                 Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 GLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 GLLVTL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
```

```
·
                                                                                                            The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring buman gene expression in a sample derived from human adult liver. comprising one of 13109 defined nucleotide sequences given in the specification (or complements). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression
                                         Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
                                                                                                                                                                                                                                                                                                   .
                                                                                  Example 4; SEQ ID NO 25970; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                DB 4; Length 43;
                                                                                                                                                                                                                                                                                 7.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                            100.0%; Pred. No. 7.1 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; SEQ ID NO 26566; 658pp; English.
                                                                                                                                                                                                                                                                  Score 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human liver peptide, SEQ ID No 26566.
                                                                                                                                                                                                                                                                                                                                                                                                                       ABG47918 standard; peptide; 43 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-00608408.
2000US-00632366.
2000US-0234687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0207456P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0236359P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000GB-00024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                             Conservative
               WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                       77 GLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488898/53
                                                                                                                                                                                                                                                                                                                                                 35 GLLVTL 40
                                                                                                                                                                                                                                 Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2000;
                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-AUG-2001
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penn SG,
                                                          brains.
                                                                                                                                                                                                                                                                                          Matches
à
                                                                                                                                                                                                                                                                                                                                                                                                                                      엄
```

```
in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                        Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic.
                                                                                                                                                                   Gaps
                                                                                                                                                                   ;
0
                                                                                                                                                                0; Indels
                                                                                                                                       1.8%; Score 6; DB 4; Length 43; 100.0%; Pred. No. 7.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   Human testicular antigen SEQ ID NO: 1064.
                                                                                                                                                                                                                                                                           ABB95680 standard; protein; 43 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-2001; 2001WO-US001329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0179065P.
2000US-0180628P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0184664P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0186350P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0190076P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAY-2000; 2000US-0205515P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-2000; 2000US-0209467P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1000; 2000US-0214886P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0216647P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0216880P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0217496P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0218290P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0220964P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0224518P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0225759P
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                Conservative
                                                                                                                                               Local Similarity
                                                                                                                                                                                       GLLVTL 82
                                                                                                                                                                                                               35 GLLVTL 40
                                                                                                                Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200155317-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-2000; 2
17-MAR-2000; 2
18-APR-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                          21-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-AUG-2001.
                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2000
                                                                                                                                                                                                                                                                                                   ABB95680;
                                                                                                                                                                                       17
                                                                                                                                      Query Match
Best Local (
                                                                                                                                                                                                                                                   RESULT 219
                                                                                                                                                              Matches
     8888888888
                                                                                                                                                                                                             qq
```

```
2000US-0229343P
2000US-0229344P
2000US-0229513P
2000US-0229513P
2000US-0230431P
2000US-0230431P
2000US-0231243P
2000US-0231243P
2000US-0231243P
2000US-0231444P
2000US-0231444P
2000US-0231944P
2000US-0231944P
2000US-0231944P
                        2000US-0227182P.
2000US-0227009P.
2000US-0228924P.
2000US-0229287P.
                                                                                                                                                                                                   2000US-0232398P
2000US-0232401P
2000US-0233401P
2000US-023365P
2000US-023365P
2000US-023365P
2000US-023423P
2000US-023423P
2000US-023429P
2000US-023499P
2000US-023499P
2000US-023499P
2000US-023499P
2000US-023499P
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0241786P.
2000US-0241787P.
2000US-0241808P.
2000US-0241809P.
2000US-0241826P.
                                                                                                                                                                                                                                                                                                                                                     2000US - 0236369
2000US - 0236370
2000US - 02370812P
2000US - 0237031P
2000US - 0237031P
2000US - 0237040P
2000US - 0239935P
2000US - 0239935P
2000US - 0239937P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0244617P.
2000US-0246474P.
2000US-0246475P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0246476P.
2000US-0246477P.
2000US-0246478P.
2000US-0246523P.
2000US-0226279P
                                                                                                                                                                                                                                                                                                                             2000US-0236327P.
2000US-0236367P.
2000US-0236368P.
                                                                                                                                                                                                                                                                                                                                                                                                                                            0000US-0241221P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     000US-0246524P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0246525P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0246526P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0246610P.
2000US-0246611P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0246527P
                                                 01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
                                                                                            05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
                                                                                                                                       08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-2000; 2
08-NOV-2000; 2
08-NOV-2000; 2
08-NOV-2000; 2
08-NOV-2000; 2
08-NOV-2000; 2
08-NOV-2000; 2
08-NOV-2000; 2
08-NOV-2000; 2
08-NOV-2000; 2
08-NOV-2000; 2
                                                                                                                                                                         08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                       21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
                        22-AUG-2000;
          22-AUG-2000;
22-AUG-2000;
                                                                                                                      08-SEP-2000;
                                                                                                                                                                                                                      14-SEP-2000;
                                                                                                                                                                                                                              14-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                               14-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                  21-SEP-2000;
                                                                                                                                                                                                                                                                                                           27-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                              29-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                       29-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2000;
13-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-OCT-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                02-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                          13-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                   20-OCT-2000;
```

```
The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide #543 encoded by probe for measuring human breast gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 43;
. 7.1e+02;
ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 4
100.0%; Pred. No. 7.1
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; SEQ ID NO 1064; 766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM01861 standard; protein; 43 AA.
08-NOV-2000; 2000US-0246613P.
17-NOV-2000; 2000US-0249207P.
17-NOV-2000; 2000US-0249203P.
17-NOV-2000; 2000US-0249203P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-024924FP.
17-NOV-2000; 2000US-025198FP.
0S-DEC-2000; 2000US-025198FP.
0S-DEC-2000; 2000US-025186FP.
0S-DEC-2000; 2000US-025186FP.
0S-DEC-2000; 2000US-025186FP.
0S-DEC-2000; 2000US-025186FP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA, Barash SC, Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-DEC-2000; 2000US-0251990P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-DEC-2000; 2000US-0254097P 05-JAN-2001; 2001US-0259678P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-483232/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 FLSSFQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLSSFQ 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 43 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM01861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM01861
    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX BX BX BX
```

ô

```
The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic inflammationsy diseases include: breast canner, disorders of development, breast disease and non-carcinoma tumours. Note: The sequence data for obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                             Novel single exon nucleic acid probe used to measuring gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human peptide encoded by genome-derived single exon probe SEQ ID 25565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome;
pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 4; Length 43;
100.0%; Pred. No. 7.18+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 10601; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                     Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG35900 standard; peptide; 43 AA.
                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                           2000US-0207456P.
2000US-00608408.
2000US-00632366.
                                                                                                                                                                                                                                                      21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                            29-JAN-2001; 2001WO-US000661.
                                                                                                                                                                                           2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                  Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77 GLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 GLLVTL 40
                                                                                             WO200157270-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                               a human breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 43 AA;
                                                                   Homo gapiens.
                                                                                                                                                                                                                                    03-AUG-2000;
                                                                                                                                                                                                                                                    21-SEP-2000;
                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                                                                                           26-MAY-2000;
                                                                                                                                                                                                                         30-JUN-2000;
                                                                                                                              09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-2002
                                                                                                                                                                                                                                                                                                                                                    Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG35900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
```

```
The interior Teatace to a spatially-addressable set of single exon mucleic acid probes for measuring gene expression in a sample derived from the mann lung comprising single exon nucleic acid probes for measuring gene expression in the specification, or their complements or the 1337 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridises at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample carried from human lung, comprising (a) contacting the array with a sample carray; identifying exons in a enkaryotic genome, comprising (a) contacting the array with a caray; identifying exons in a enkaryotic genome, comprising (a) and long from human lung measuring the label detectably bound to each probe of the enkaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from enkaryote lung mRNA, to a single exon probe, the enkaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from enkaryote lung mRNA, to a single exon probe, the above mentioned microarray; assigning exons to a single exon probe, in the above mentioned microarray; assigning exons to a single exon in the above mentioned microarray; assigning exons to a single exon in classus and/or cell types using hybridisation to a single exon microarray having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types using hybridisation to a single exon microarray having a probes of itsuses and/or cell types using hybridisation to a single expression captured mRNA and for the struct probes of itsuses and for identifying exons in a gene; particularly using human lung diseases such as asthma, lung derived mRNA and for the struct pulmonary disease (LDD), interstital lung cancer, chronic obstructive pulmonary disease (LDD), interstital lung cancer, chronic obstructive pulmonary places are used for gene expression of the summon structure pulmo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; SEQ ID NO 25565; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                               30-JAN-2001; 2001WO-US000665.
                                                                                                                                                                                                                                                                                   03-AUG-2000; 2000US-00632366
21-SEP-2000; 2000US-0234687P
                                                                                                                                                                                                                                                                                                                            2000US-0236359P.
2000GB-00024263.
                                                                                                                                                                                                                       04-FEB-2000; 2000US-0180312P
                                                                                                                                                                                                                                                                  2000US-00608408
                                                                                                                                                                                                                                                                                                                                                                                                                            Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-114183/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 43 AA;
                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                     27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                              30-JUN-2000;
                                                                                                                                          15-NOV-2001.
```

1.8%; Score 6; DB 5; Length 43; 100.0%; Pred. No. 7.1e+02;

Query Match Best Local Similarity

```
990S-0139456P.
990S-0139456P.
990S-0139463P.
990S-0139461P.
990S-0139461P.
990S-0139461P.
990S-0139462P.
990S-013949P.
990S-013963P.
990S-014083P.
990S-014299P.
990S-014299P.
990S-014299P.
990S-014299P.
990S-014299P.
990S-014299P.
990S-014293P.
990S-014299P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-014433P.
990S-0144688P.
990S-014433P.
990S-014468P.
990S-014468P.
990S-014468P.
990S-014468P.
990S-014468P.
990S-014468P.
990S-014468P.
990S-014468P.
990S-014468P.
990S-014468P.
990S-014468P.
990S-014468P.
                   99US-0139492P.
99US-0139454P.
99US-0139455P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9905-0147260P.
9905-0147303P.
9905-0147416P.
9905-014793P.
9905-0148171P.
9905-0148319P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0145918P
99US-0145919P
99US-0146386P
99US-0146388P
99US-0147038P
99US-0147703P
99US-0147703P
99US-0147703P
                18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 70N - 1999

18 - 7
                                                                                                                                                                                     21-JUN-1999;
22-JUN-1999;
23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-1999;
02-AUG-1999;
02-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03 - AUG-1999;
04 - AUG-1999;
05 - AUG-1999;
05 - AUG-1999;
06 - AUG-1999;
06 - AUG-1999;
06 - AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-AUG-1999;
11-AUG-1999;
12-AUG-1999;
                                                                                                                                                                                                                                        24-JUN-1999
                                                                                                                                                                                                                                                                  29-JUN-1999
      0
                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
      Gaps
     ..
    Indels
    .
0
                                                                                                                                                                                           Zea mays protein fragment SEQ ID NO: 20258.
  0; Mismatches
                                                                                                                 AAG18732 standard; protein; 44 AA.
                                                                                                                                                                                                                                                                                                                                                                          990S-0121825P.
990S-0123180P.
990S-0125748P.
990S-0126748P.
990S-01267462P.
990S-0128744P.
990S-0128744P.
990S-0128744P.
990S-0138449P.
990S-0138449P.
990S-0138449P.
990S-0138447P.
990S-0132447P.
990S-0132447P.
990S-0132447P.
990S-0132447P.
990S-0132468P.
990S-0132468P.
990S-0132468P.
990S-0132468P.
990S-0132468P.
990S-0132468P.
990S-0132468P.
990S-0134941P.
990S-0134941P.
990S-0134228P.
990S-0134228P.
990S-0134234P.
990S-0134234P.
990S-0134234P.
990S-0134234P.
990S-0134234P.
990S-0134234P.
990S-0134341P.
990S-0136782P.
990S-0136782P.
990S-0136782P.
                                                                                                                                                                                                                                                                                                                                                   25-FEB-2000; 2000EP-00301439
                                                                                                                                                               17-OCT-2000 (first entry)
6; Conservative
                                                                                                                                                                                                                                                                        Zea mays subsp. mays.
                                        ||||||
GLLVTL 40
                        77 GLLVTL 82
                                                                                                                                                                                                                                                                                                  EP1033405-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-APR-1999;
19-APR-1999;
21-APR-1999;
23-APR-1999;
23-APR-1999;
28-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-1999;
14-MAY-1999;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAY-1999;
28-MAY-1999;
01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUN-1999;
04-JUN-1999;
07-JUN-1999;
08-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUN-1999;
14-JUN-1999;
16-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-1999;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                            06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                             25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAY-1999
05-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-1999
21-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAY-1999
25-MAY-1999
                                                                                                                                         AAG18732;
                                                  35
                                                                                       RESULT 222
Matches
                                                                                                      AAG18732
                                                                                                                 g
                         8
```

```
99US-0151066P.
99US-0151080P.
99US-0151303P.
99US-015130P.
99US-0152303P.
                                  99US-0149722P.
99US-0149723P.
99US-0149929P.
                                                                                                                                         990S-0153758P

990S-015403P

990S-015403P

990S-0155486P

990S-0155486P

990S-015548P

990S-015548P

990S-015628P

990S-015717P

990S-015717P

990S-015727P

990S-015823P

990S-015823P

990S-015823P

990S-015823P

990S-015823P

990S-015923P

990S-015923P

990S-015923P

990S-016976P

990S-016976P

990S-016098P

990S-016098P

990S-016098P

990S-016098P

990S-016098P

990S-016098P

990S-016098P

990S-016098P

990S-016098P

990S-016098P

990S-016098P

990S-016098P

990S-016098P

990S-016098P

990S-0161405P
                                                                            99US-0150884P.
99US-0151065P.
                      99US-0149175P.
99US-0149426P.
                                                        99US-0149902P.
                                                                                                                                                                                                                                                                                                                                                                                                       99US-0161360P.
99US-0161361P.
99US-0161920P.
                                                                      99US-0150566P.
                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0161992P
                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0162142P
                            18-AUG-1999
                                               20-AUG-1999
23-AUG-1999
                                                                                                                                                                                                                                                                                                                          21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                            22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
25-0CT-1999;
                                                                                                                           07-SEP-1999,
                                                                                                                                   10-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                       26-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-1999
```

```
Gaps
                                           .
0
              1.8%; Score 6; DB 3; Length 44; 100.0%; Pred. No. 7.3e+02; Live 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.0
```

```
ö
```

à

```
Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage.
                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 600; 894pp; English.
                   AAU14265 standard; protein; 44 AA.
                                                                                                                                                                                                                                                25-JAN-2001; 2001WO-US002623.
                                                                                                                                                                                                                                                                                                           Fang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                   25-JAN-2000; 2000US-00491404.
                                                                                Human novel protein #136.
                                                                                                                                                                                                                                                                                                                                WPI; 2001-451939/48.
                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAS22570.
                                                                                                                                                                                                       WO200155437-A2.
                                                                                                                                                                                   Homo sapiens.
                                                            24-OCT-2001
                                                                                                                                                                                                                           02-AUG-2001.
                                       AAU14265;
RESULT 223
            AAU14265
```

The invention relates to polymucleotides encoding novel human proteins or taised against the polypeptides, polymucleotides and antibodies traised against the polypeptides are used in a method of treatment of a marmal and prevention of disorders caused by the aberrant protein mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight care used to identify compounds which bind to the polypeptides.

CC expression or activity. The polypeptides can be used as probes and primers, for are used to identify compounds which bind to the polypeptides.

CC encombinant proteins, and in generating anti-ense but or argued the invention can be used to target drugs to a therapy. Polypeptides of the invention can be used to target drugs to a cumour, in assays to determine pological activity, to raise therapy. Polypeptides of the invention can be used to target drugs to a cumour, in assays to determine pological activity, to raise antibodies/elicit an immune response, to determine quantitative protein can be useful in treating platelet disorders, set me cell disorders, regenerating bone, cartilage, tendon, contraceptive, treating osteoporosis and osteoarthritis, anamamia, contraceptive, treating osteoporosis and osteoarthritis, anamamia, allery, asthma, graft-oversus-host disease, eczema, haemphilia, thrombosis, anti-inflammatory contraceptive inflammatory contraceptive appropriation of the invention.

C fungal infection or from autoinmunity, cancer, allery, artical accement eaquence contraceptive inflammatory contraceptive appropriation of the invention.

Sequence 44 AA;

. Ouery Match 1.8%; Score 6; DB 4; Length 44; Best Local Similarity 100.0%; Pred. No. 7.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels

ö

Gaps

ð

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

WO200175067-A2.

11-OCT-2001.

Novel human diagnostic protein #9878.

13-FEB-2002 (first entry)

```
The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AA019310) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce cytokine, cell proliferation or cell differentiation or which may induce cytokine, of other cytokines in other cell populations. The production of other cytokines in other cell populations. The polypeptides have various cytokine-like activities, cell growth factor activity, haematopoiesis regulating cativity, tissue growth factor activity, immunomodulatory activity and citivity, immunomodulatory activity and citivity, immunomodulatory activity and citivity in the diagnosis and/or citiammation. Note: The sequence data for this patent did not form part cof the printed specification, but was obtained in electronic format directly from MIPO at fitp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 18600; 1399pp + Sequence Listing; English.
                                                                                    AAO04708 standard; protein; 45 AA.
                                                                                                                                                                                               Human polypeptide SEQ ID NO 18600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                                                                                                                           06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-514838/56.
36 KIILFS 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAI84639.
                                                                                                                                                                                                                                                                                                                                                                  WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45 AA;
                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                  07-SEP-2001.
                                                                                                                          AA004708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                     RESULT 224
```

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

biodiversity.

Tang YT;

WPI; 2001-639362/73. N-PSDB; AAS74074. Drmanac RT, Liu C, (HYSE-) HYSEQ INC.

```
ö
                         Gaps
                         .;
                      Indels
   DB 4; Length 45;
            7.4e+02;
1.8%; Score 6; DB 4;
100.0%; Pred. No. 7.4¢
tive 0; Mismatches
       Local Similarity 100.0
                                      228 SLKLLG 233
                                                          19 SLKLLG 24
                                                                                        RESULT 225
                 Matches
```

ABG09887 standard; protein; 45 AA.

ABG09887

ABG09887;

```
The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain creattion (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used can in recombinant production of (II). The polymucleotides are also used genes. (I) is useful in gene therapy techniques to restore normal crivity of (II) or totreat disease states involving (II). (II) is useful in gene therapy techniques to restore normal crivity of (II) or totreat disease states involving or quantitating a setul for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating of supplement. (II) and (II) are useful in medical imaging of supplement. (II) and (II) are useful for treating disorders of supplement. (II) and (II) are useful for treating disorders of involving aberrant protein expression or biological activity. The copynyphide and polymucleotide sequences have applications in capponishing for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cond sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this coptent format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 4; Length 45;
100.0%; Pred. No. 7.4e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID NO 40246; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW92823 standard; protein; 46 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LFSKSH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 LFSKSH 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAR-2003
14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW92823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           axxxaa
```

```
WPI; 2000-136702/12.
                                                                                                                                                                                                                  230 KLLGEL 235
                                                                                                                                                                                                                                    15 KLLGEL 20
                                                                                                                                                              Sequence 46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         WO200155314-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2000;
                                             sclerosis
                                                                                                                                                                                                                                                                                                 AAM92813;
                                                                                                                                                                                                                                                                        AAM92813
         원
                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                           This sequence represents a human transaldolase (TAL-H) protein fragment. This protein fragment can be used in methods to raise antibodies for detecting human transaldolase-mediated neurodegenerative autoimmune diseases, especially multiple sclerosis. The protein has neuroprotective properties and is a proliferation, cytotoxicity and binding inhibitor. (Updated on 20-MAR-2003 to correct PF field.)
                                                                                                                                                                                                       Isolated human transaldolase gene - useful for raising antibodies for detecting neurodegenerative autoimmune diseases, especially multiple
                        Transaldolase, TAL-H; autoantigen; human; antibody; neuroprotector; neurodegenerative autoimmune disease; multiple sclerosis; detection; proliferation inhibitor; cytotoxicity inhibitor; binding inhibitor.
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; transaldolase; autoantigen; multiple sclerosis; diagnosis;
neurodegenerative disease; neuroprotective; TAL-H.
                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 2; Length 46;
100.0%; Pred. No. 7.6e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human transaldolase protein (TAL-H) peptide SEQ ID NO:21.
       Human transaldolase TAL-H protein fragment #6.
                                                                                                                                                   (UYNY ) UNIV NEW YORK STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYNY ) UNIV NEW YORK STATE RES FOUND.
                                                                                                                                                                                                                                          Claim 5; Col 59-60; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY68326 standard; peptide; 46 AA.
                                                                                                                   98US-00057762,
                                                                                                                                    94US-00326119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-00326119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-00326119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                      WPI; 1999-203948/17.
                                                                                                                                                                                                                                                                                                                                                                               230 KLLGEL 235
                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                KilGEL 20
                                                                                                                                                                                                                                                                                                                           Sequence 46 AA;
                                                             Homo sapiens.
                                                                                                                 09-APR-1998;
                                                                                                                                  19-OCT-1994;
                                                                               US5879909-A.
                                                                                               09-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US6018021-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2000
                                                                                                                                                                                                                           sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                15
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY68326;
                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                     Perl A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perl A;
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 227
                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY68326
```

```
;
0
                                                                                                                                       The present invention describes a human transaldolase protein molecule (TAL-H). Peptides (1) derived from TAL-H which comprise at least 1 T cell epitope or at least 1 B cell/antibody epitope are also described. TAL-H or (1) induce a transaldolase-specific immune response. TAL-H (I) and antibodies to TAL-H or (1) are useful for diagnosing and treating multiple sclerosis and other human immune-related neurodegenerative diseases. The present sequence represents a specifically example of a TAL-H peptide, from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, digestive system antigen, gene therapy; cancer; appendicitis,
ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
digestive system disorder; Meckel's diverticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Transaldolase proteins and peptides, useful for diagnosing multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human digestive system antigen SEQ ID NO: 2162.
                                                                                 Claim 4; Col 11-12; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM92813 standard; protein; 47 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2001; 2001WO-US001324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0179065P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-FEB-2000; 2000US-0184664P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAR-2000; 2000US-0186350P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-2000; 2000US-0189874P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAR-2000; 2000US-0190076P.
18-APR-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0205515P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0205515P.
2000US-0209467P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0214886P.
2000US-0215135P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0225213P.
2000US-0225214P.
2000US-0225266P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0216880P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0217487P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0217496P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0220963P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0220964P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0224518P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0224519P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001 (first entry)
```

```
14-AUG-2000; 2000US-022526FP.
14-AUG-2000; 2000US-022526FP.
14-AUG-2000; 2000US-022547PP.
14-AUG-2000; 2000US-022547PP.
14-AUG-2000; 2000US-022578FP.
14-AUG-2000; 2000US-022578FP.
14-AUG-2000; 2000US-022578FP.
14-AUG-2000; 2000US-022578FP.
22-AUG-2000; 2000US-022578FP.
22-AUG-2000; 2000US-022578FP.
23-AUG-2000; 2000US-02266BP.
23-AUG-2000; 2000US-02266BP.
23-AUG-2000; 2000US-022984P.
01-SEP-2000; 2000US-022984P.
01-SEP-2000; 2000US-022984FP.
01-SEP-2000; 2000US-022984FP.
05-SEP-2000; 2000US-022984FP.
06-SEP-2000; 2000US-022984FP.
06-SEP-2000; 2000US-022984FP.
06-SEP-2000; 2000US-022984FP.
06-SEP-2000; 2000US-023144FP.
08-SEP-2000; 2000US-023144FP.
08-SEP-2000; 2000US-023144FP.
08-SEP-2000; 2000US-023144FP.
08-SEP-2000; 2000US-023144FP.
08-SEP-2000; 2000US-023144FP.
08-SEP-2000; 2000US-023144FP.
08-SEP-2000; 2000US-023144FP.
08-SEP-2000; 2000US-023144FP.
08-SEP-2000; 2000US-023144FP.
08-SEP-2000; 2000US-023144FP.
08-SEP-2000; 2000US-023144FP.
08-SEP-2000; 2000US-023146FP.
08-SEP-2000; 2000US-023146FP.
08-SEP-2000; 2000US-023146FP.
08-SEP-2000; 2000US-023146FP.
08-SEP-2000; 2000US-023146FP.
08-SEP-2000; 2000US-023146FP.
08-SEP-2000; 2000US-023146FP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0232397P

2000US-0232397P

2000US-0232401P

2000US-0233063P

2000US-0233063P

2000US-0233063P

2000US-0233063P

2000US-023424P

2000US-0234298P

2000US-0234298P

2000US-0234298P

2000US-0234298P

2000US-0234298P

2000US-0234298P

2000US-0234298P

2000US-0234298P

2000US-0234298P

2000US-0234298P

2000US-0234298P

2000US-0234298P

2000US-0234298P

2000US-0234298P

2000US-023429P

2000US-02363P

2000US-02363P

2000US-0237039P

2000US-0237039P

2000US-0237039P

2000US-0237039P

2000US-0237039P

2000US-0237039P

2000US-0237039P

2000US-0237039P

2000US-0237039P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P

2000US-023703P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0246525P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-2000; 27-SEP-2000; 27-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SEP-2000; 20-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-0CT-2000; 2
02-0CT-2000; 2
02-0CT-2000; 2
02-0CT-2000; 2
13-0CT-2000; 2
13-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-SEP-2000;
14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
20-0CT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-2000;
```

```
The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer. Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a digestive system antigen of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; SEQ ID NO 2162; 986pp; English.
08-NOV-2000; 2000US-0246526P.
08-NOV-2000; 2000US-0246527P.
08-NOV-2000; 2000US-0246527P.
08-NOV-2000; 2000US-0246609P.
08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-0246613P.
17-NOV-2000; 2000US-0249209P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249248P.
17-NOV-2000; 2000US-0249248P.
17-NOV-2000; 2000US-0249248P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
18-DEC-2000; 2000US-025198P.
08-DEC-2000; 2000US-025198P.
08-DEC-2000; 2000US-025198P.
08-DEC-2000; 2000US-025198P.
08-DEC-2000; 2000US-025198P.
08-DEC-2000; 2000US-025198P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.8
Best Local Similarity 100.
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-502630/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAK88586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 47 AA;
```

Gaps

. 0

1.8%; Score 6; DB 4; Length 47; 100.0%; Pred. No. 7.7e+02; Live 0; Mismatches 0; Indels

102 NNILRR 107 NNILRR 25

à g

20

```
The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activity, activity, tissue growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and extined may be useful in the diagnosis and/or tradtment of cancer, leukaemia, nervous system disorders, arthitis and tradtment of cancer, leukaemia, nervous system disorders, arthitis and ciffammation. Note: The sequence data for this patent did not form part directly from WIPO at ftp.wipo.int/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                        Human; cytokine; cell proliferation; cell differentiation; gene therapy;
vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID NO 19124; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 4; Length 47;
100.0%; Pred. No. 7.7e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human colon associated polypeptide #201.
                                                                                                                           Human polypeptide SEQ ID NO 19124.
                          AAO05232 standard; protein; 47 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU22668 standard; protein; 47 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                    26-FEB-2001; 2001WO-US004927
                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 SLKLLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAI85163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 SLKLLG 8
                                                                                                                                                                                                                                                                      WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 47 AA;
                                                                                                                                                                                                                                        Homo sapiens.
                                                                                          06-NOV-2001
                                                                                                                                                                                                                                                                                                      07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2001
                                                            AAO05232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
RESULT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 230
               AA005232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU22668
                               SEX PX PX BX
```

```
Fuman; colon cancer; congenital abnormality; infection; colitis;
inflammatory bowel disease; IBD; neoplastic disorder; gene therapy;
intestinal inflammatory disorder; malabsorption syndrome; gastric;
sigmoid disease; antibacterial; antiviral; antiinflammatory; cytostatic.
                                                                                                                                                                                                                                                                                                                               14-AUG-2000) 2000US-0225213P.
14-AUG-2000) 2000US-0225214P.
14-AUG-2000) 2000US-022526F.
14-AUG-2000) 2000US-022526F.
14-AUG-2000) 2000US-0225268P.
14-AUG-2000) 2000US-022526P.
                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-2000; 2000US-0225757P.
14-AUG-2000; 2000US-0225758P.
14-AUG-2000; 2000US-0225758P.
18-AUG-2000; 2000US-0226279P.
22-AUG-2000; 2000US-0226681P.
22-AUG-2000; 2000US-0226681P.
                                                                                                                                        2000US-0180628P.
2000US-0184664P.
2000US-0186350P.
                                                                                                           17-JAN-2001; 2001WO-US001240
                                                                                                                                                                     2000US-0189874P.
                                                                                                                                                                                 2000US-0190076P.
                                                                                                                                                                                          000US-0198123P
                                                                                                                                                                                                                                                                                2000US-0218290P.
2000US-0220963P.
2000US-0220964P.
                                                                                                                                                                                                                        2000US-0214886P
                                                                                                                                                                                                                                         000US-0216647P
                                                                                                                                                                                                                                                                                                             2000US-0224518P.
2000US-0224519P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-SEP-2000; 2000US-022937P.
01-SEP-2000; 2000US-0229343P.
01-SEP-2000; 2000US-0229344P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-2000; 2000US-0227182P.
23-AUG-2000; 2000US-0227009P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0228924P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-SEP-2000; 2000US-0229345P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-SEP-2000; 2000US-0229509P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-SEP-2000; 2000US-0229513P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0231242P.
2000US-0231243P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0230438P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0231968P
                                                                   WO200155302-A2.
                                                  Homo sapiens.
                                                                                                                                                                    16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                        07-JUL-2000;
                                                                                                                                                                                                                                                                    11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-2000;
30-AUG-2000;
                                                                                        02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-SEP-2000;
```

oʻ

Gaps .; o

```
2000US-023499B
2000US-0235484P
2000US-0235834P
2000US-0235836P
2000US-023637P
2000US-023636P
2000US-023636P
                                                                                                                                                                                                    2000US-0236369P.
2000US-0236370P.
2000US-0236802P.
                                                                                                                                                                                                                                                                   2000US-0237037P.
2000US-0237038P.
2000US-0237039P.
2000US-0237040P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0241787P.
2000US-0241808P.
2000US-0241809P.
2000US-0241826P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0246524P.
2000US-0246525P.
2000US-0246526P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0251868P.
2000US-0251869P.
2000US-0251989P.
                                                                                                                                                                                                                                                                                                                                                     2000US-0239935P.
2000US-0239937P.
2000US-0240960P.
                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0241221P.
2000US-0241785P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0241786P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0000US-0246474P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1000US-0246476P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              000US-0244617P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0246478P.
2000US-0246523P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0246527P.
2000US-0246528P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-NOV-2000; 2000US-0246613P
17-NOV-2000; 2000US-0249207P
17-NOV-2000; 2000US-0249208P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0246532P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0246609P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0249208P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    000US-0249211P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0249245P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0249299P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2000; 20
17-NOV-2000; 20
17-NOV-2000; 20
                                                                                                                    27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208-DEC-2000; 208
                                                                                                                                                                                                                                                                                                                                                                                          20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-0CT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-2000;
```

```
The present invention relates to the isolation of novel human colon seasociated polypeptides, and the cDNA (AAS19148-AAS19591) and genomic sequences encoding for them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders of the colon including colon cancer, congenital abnormalities (e.g. atresia and stenosis), bacterial and viral infections, inflammatory bowel disease (IBD), neoplastic cell disorders (e.g. polyps and adenomas, intestinal inflammatory disorders, colitis, colonic inflammatory of arrhoea and dysentery, malabsorption syndromes (e.g. lactose intolerance), intestinal obstruction and sigmoid diseases. The polymocleotides sequences of the invention can also be used in gene therapy. AAU22468-AAU22701 represent the novel human colon associated polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed set form, with was obtained in electronic format directly from WIPO at fire, with was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                    Isolated polypeptide for treating, preventing and/or prognosing disorders related to the colon including colon cancers and also for testing and detection e.g. diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy, cancer; liver disorder; hepatitis; neural disorder; Alzheimer's disease; human; colon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.8%; Score 6; DB 4; Length 47; Best Local Similarity 100.0%; Pred. No. 7.7e+02; Matches 6; Conservative 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human novel colon related polypeptide SEQ ID NO 445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                            Claim 11; SEQ ID NO 445; 562pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB32508 standard; protein; 47 AA.
                                                                                                            Rosen CA, Barash SC, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0186350P.

2000US-0189874P.

2000US-0190076P.

2000US-0198123P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-2001; 2001US-00764872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-2000; 2000US-0179065P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180628P.
2000US-0184664P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-2003 (first entry)
                                                                                                                                               WPI; 2001-465567/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 NNILRR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 NNILRR 25
                                                                                                                                                                 N-PSDB; AAS39548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2003050231-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2000; 2
16-MAR-2000; 2
17-MAR-2000; 2
18-APR-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB32508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB32508
   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
```

```
07-JUN-2000; 2000US-0209467P.
38-JUN-2000; 2000US-02154886P.
38-JUN-2000; 2000US-02154886P.
10-JUL-2000; 2000US-0216880P.
11-JUL-2000; 2000US-0216880P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
14-JUC-2000; 2000US-0217496P.
14-JUC-2000; 2000US-02218290P.
26-JUL-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-022568P.
14-JUC-2000; 2000US-02259P.
14-JUC-2000; 2000US-0223144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-SEP-2000; 2000US-023144P.
16-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0239937P.
2000US-0240960P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0241221P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-OCT-2000;
20-OCT-2000;
20-OCT-2000;
```

```
New nucleic acid molecule, useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g. cancer, liver disorders or neural disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0249217P
2000US-0249218P
2000US-0249244P
2000US-0249264P
2000US-0249264P
2000US-0249264P
2000US-0249297P
2000US-0249297P
2000US-0249297P
2000US-0249297P
2000US-0250391P
2000US-0250391P
2000US-0250391P
2000US-0250391P
2000US-0250391P
2000US-0250391P
2000US-0250391P
2000US-0250391P
2000US-0241785P.
2000US-024186FP.
2000US-0241809P.
2000US-0241809P.
2000US-0241809P.
2000US-0246474P.
2000US-0246474P.
2000US-0246477P.
2000US-0246477P.
2000US-0246477P.
2000US-0246477P.
2000US-0246477P.
2000US-0246478P.
2000US-024652P.
2000US-024652P.
2000US-024652P.
2000US-024652P.
2000US-024652P.
2000US-024652P.
2000US-024652P.
2000US-024652P.
2000US-024652P.
2000US-024652P.
2000US-024652P.
2000US-024652P.
2000US-024652P.
2000US-024652P.
2000US-024652P.
2000US-024652P.
2000US-024653P.
2000US-024653P.
2000US-024653P.
2000US-024653P.
2000US-024920P.
2000US-024920P.
2000US-024921P.
2000US-024921P.
2000US-024921P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0251990P.
2000US-0254097P.
2001US-0259678P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0251869P.
2000US-0251989P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROSEN C A.
RUBEN S M.
BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-625420/59
N-PSDB; ADB32274.
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT-2000; 2
20-0CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-2000;
01-DBC-2000;
05-DBC-2000;
05-DBC-2000;
05-DBC-2000;
06-DBC-2000;
08-DBC-2000;
08-DBC-2000;
08-DBC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-DEC-2000;
11-DEC-2000;
05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ROSE/) I
(RUBE/) I
(BARA/) I
    CCXXSXY
```

The invention relates to an isolated nucleic acid molecule encoding a polypeptide. The nucleic acid is useful for preparing a medicament for

Claim 12; SEQ ID NO 445; 216pp; English.

```
This invention relates to novel nucleic acid molecules, and encoded proteins thereof, which are present in normal and neoplastic endometrial cells. Specifically, it refers to the use of these endometrial specific nucleic acids (ESNAs), as well as suitable antibodies, agonists and antagonists that are useful for the identification, diagnosis and menitoring of endometrial cancer. The present invention describes a method for monitoring the presence of an endometrial specific protein in a sample (potentially representing metastases) that comprises contacting the sample with a reagent and detecting the intensity of this interaction. Accordingly, via gene therapy, these ESNAs are useful for preparing a cytostatic composition for diagnosing or treating endometrial specific composition for diagnosing or treating endometrial polypeptide of the invention.
                                                                                                                                                                                                                      ö
preventing, treating or ameliorating a medical condition e.g. cancer, liver disorders such as hepatitis or neural disorders such as Alzheimer's disease. The present sequence represents the amino acid sequence of a human novel colon related polypeptide. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endometrial specific protein identified as DEX0379_20_aa_1 (SeqID 169).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid, useful for preparing a composition for diagnosing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neoplastic; endometrial cell; endometrial specific nucleic acid; ESNA; cancer; metastasis; gene therapy; cytostatic; human.
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                        0;
                                                                                                                                                                                   1.8%; Score 6; DB 7; Length 47;
100.0%; Pred. No. 7.7e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 169; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         ADE78262 standard; protein; 48 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-DEC-2001; 2001US-0343134P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-DEC-2002; 2002WO-US041175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating endometrial cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2004 (first entry)
                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-569441/53.
                                                                                                                                                                                                                                                                102 NNILRR 107
                                                                                                                                                                                                                                                                                                    20 NNILRR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADE78367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003055982-A2
                                                                                                                                                      Sequence 47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUL-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                              ADE78262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sun Y,
                                                                                                                                                                                                                                                                                                                                                          RESULT 232
                                                                                                                                                                                                                                                                                                                                                                           ADE78262
                                                                                                                                                                                                                                                                                                                                                                                              8888888888
                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                  g
```

```
The invention relates to the isolation of genes AAC59624-C59669 encoding the human secreted proteins AAB34439-B34484. This sequence represents a perticular fragment homologous to the protein encoded by the gene isolated in the present invention. The sequence is used as a query sequence for in the present invention. The sequence is used as a query sequence for doing BiASIX searches to determine homologous sequence to the protein. The apenes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antiagonists of specification in the diagnosis, treatment and prevention of: (a) cancer, c.g. breast and ovarian cancer, and other cancers of the adrenal gland, c.g. breast and ovarian cancer, and other cancers of the adrenal gland, c.g. breast and ovarian cancer, and other cancers of the adrenal gland, c.g. urogenital; (b) immune disorders e.g. Addison's disease, allergies, c.g. autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, c.g. colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and c.g. epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                              Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiuleer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                         Human secreted protein BLAST search protein SEQ ID NO: 132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 3; Length 49; 100.0%; Pred. No. 8e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 368; 384pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen CA, Ruben SM, Komatsoulis
                                                                                                                                       AAB34514 standard; protein; 49 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L6-MAR-2000; 2000WO-US006828.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAR-1999; 99US-0125358P.
08-DEC-1999; 99US-0169616P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epilepsy; and (f) infect:
and parasitic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 SLKLLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-602216/57
80
                                      35 SSGLLV 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200056767-A1.
SSGLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-SEP-2000.
                                                                                                                                                                                                                           02-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                      AAB34514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                     RESULT 233
                                                                                                                            AAB3451
                                                                                                                                                                 ð
                                  셤
```

0; Gaps

Indels

Query Match
1.8%; Score 6; DB 7; Length 48;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels

SLKLLG 23

18

g

```
Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                             Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                              Human colon cancer antigen protein SEQ ID NO:6106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU45565 standard; protein; 50 AA.
               AAG75342 standard; protein; 50 AA
                                                                                                                                                  28-SEP-2000; 2000WO-US026524.
                                                                                                                                                                  99US-0157137P.
99US-0163280P.
                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                              (first entry)
                                                                                                                                                                                                         Ruben SM, Barash SC,
                                                                                    colorectal carcinoma.
                                                                                                                                                                                                                        WPI; 2001-235357/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 TEAVAQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEAVAO 20
                                                                                                                                                                                                                                 N-PSDB; AAH34747.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50 AA;
                                                                                                                   WO200122920-A2
                                                                                                    Homo sapiens.
                                                                                                                                                                  29-SEP-1999;
03-NOV-1999;
                                              03-SEP-2001
                                                                                                                                   05-APR-2001
                               AAG75342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU45565
ID AAU4
XX
RESULT
                     ð
```

```
cancer-associated nucleic acid molecules (N) and proteins notion cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome cyptession by rectifying mutations or deletions in a patient's genome consupplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
                                                                                                                            AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
Claim 11; Page 7564; 9803pp; English.
```

Gaps ., 0; Indels 1.8%; Score 6; DB 4; Length 50; 100.0%; Pred. No. 8.2e+02; tive 0; Mismatches 0; Indels Query Match 1.8 Best Local Similarity 100. Matches 6; Conservative

AAU45565;

Propionibacterium acnes immunogenic protein #6461.

(first entry)

27-FEB-2002

SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uvaitis; endopthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.

Propionibacterium acnes.

WO200181581-A2

01-NOV-2001

20-APR-2001; 2001WO-US012865.

21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P.

(CORI-) CORIXA CORP.

Bhatia A; Persing DH, Mitcham JL, Wang SS, JJ, Zhang Y, Jen S, Carter D; L'maisonneuve J, Skeiky YAW,

WPI; 2001-616774/71. N-PSDB; AASS9526.

Rosen CA;

Birse CE,

Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.

Example 1; SEQ ID NO 6760; 1069pp; English.

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by a canes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgatical. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies opecific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as therefore treat P. acnes infections. The antibodies may also be used as dayanostic agents for determining P. acnes presence, for example, by conzyme linked immunosorbent assay (ELISA). Note: The sequence data for this parent did not form part of the printed specification, but was the construction of the printed specification, but was the construction of the printed specification, but was the construction of the printed specification, but was the construction of the printed specification, but was the construction of the printed specification, but was the construction of the printed specification, but was the construction of the printed specification, but was the construction of the printed specification, but was the construction of the printed specification, but was the construction of the printed specification, but was the construction of the printed specification, but we can be constructed the construction of the printed specification of the printed specification of the printed of the pri ftp.wipo.int/pub/published_pct_sequences 

Sequence 50 AA;

Gaps ö Query Match
1.8%; Score 6; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels

ö

ò

0;

RESULT 236

AAU42299 standard; protein; 50 AA.

AAU42299 ID AAU4 XX

(first entry)

```
27-FEB-2002 (first entry)
                            Propionibacterium acnes.
                                                                        2001-616774/71.
                                                            (CORI-) CORIXA CORP
                                                                           N-PSDB; AAS59516.
                                                                    L'maisonneuve J,
                                 WO200181581-A2.
                                                                                                                                                        Sequence 50 AA;
                                       01-NOV-2001.
                                                                 Skeiky YAW,
AAU42299;
```

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteonyellitis), uvetis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies polypeptides may be used as antigens in the production of antibodies polypeptides and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used at diagnostic agents for determining P. acnes presence, for example, by charmed inked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at

```
Gарв
                                      ö
 1.8%; Score 6; DB 4; Length 50;
100.0%; Pred. No. 8.2e+02;
vative 0; Mismatches 0; Indels
                                   6; Conservative
                   Best Local Similarity
Query Match
                                   Matches
```

78 LLVTLI 83

```
ABM42084 standard; protein; 50 AA.
RESULT 237
ABM42084
ID ABM420
XX
```

21 LLOSEN 26

임

```
New Propionibacterium acnes polypeptides and polynucleotides encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                       Propionibacterium acnes predicted ORF-encoded polypeptide #6760.
                                                                                  Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 6760; 1481pp; English.
                                                                                                immunostīmulant; immune response; vaccine
                                                                                                                                                                                                                                                                                                                      Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                 11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                           .5-OCT-2001; 2001US-00978825.
                                                                                                                                                                                                                                                                                                      Mitcham JL, Skeiky YAW,
                                                                                                                             Propionibacterium acnes.
                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-381789/36.
                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ACF64455
                                                                                                                                                          WO2003033515-A1.
                         20-OCT-2003
                                                                                                                                                                                     24-APR-2003.
%XCCCCCCCCCCCCCCCCCCCCCCCCCCCCX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                             SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                            Persing DH, Mitcham JL, Wang SS, Bhatia A; ve J, Zhang Y, Jen S, Carter D;
                                                   Propionibacterium acnes immunogenic protein #3195.
                                                                                                                           dermatological; osteopathic; neuroprotectant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 3494; 1069pp; English.
                                                                                                                                                                                                                                                                     21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                         20-APR-2001; 2001WO-US012865.
```

Maisonneuve JL; Jones R, Carter D;

Persing DH, Bhatia A, Lodes MJ, Benson DR,

```
The invention relates to an isolated polymucleotide (ACF64435-ACF64733)
encoding a Propionibacterium acnes protein. The invention also relates to
polympoptides encoded by the polymucleotides. The invention
additionally encompasses expression vectors and host cells comprising a
additionally encompasses expression vectors and host cells comprising a
polymucleotide of the invention; antibodies against polympoptides of the
invention; funion proteins comprising a polympoptide of the invention; a
configuration of the invention; and an isolated T cell population comprising T cells prepared
control this method; a vaccine composition (comprising T cells prepared
configuration cells that express the polympoptide; and an isolated
configuration of the capter of the populations, or
configuration of the capter of the polympoptide; and an isolated
configuration of the capter of the polympoptides, and the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of the capter of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 6; DB 6;
100.0%; Pred. No. 8.2e+(
ilve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 LLQSEN 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ઠે
```

|||||| 2 LLVTLI

d

```
Propionibacterium acnes polypeptides and polynucleotides encoding the
                                                                                                                                                                                                                                                     polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                    Propionibacterium acnes predicted ORF-encoded polypeptide #3494.
                                                                   Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
                                                                              immunostimulant; immune response; vaccine
       ABM38818 standard; protein; 50 AA.
                                                                                                                                                                                               Zhang Y, Wang S, Jen S, Lod
Barth B, Vallieve-Douglass J;
                                                                                                                                         11-OCT-2002; 2002WO-US032727.
                                                                                                                                                        15-OCT-2001; 2001US-00978825
                                                                                                                                                                                Mitcham JL, Skeiky YAW, I
                                     (first entry)
                                                                                            Propionibacterium acnes
                                                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                     WPI; 2003-381789/36.
                                                                                                                                                                                                                             N-PSDB; ACF64445
                                                                                                          WO2003033515-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50 AA;
                                      20-OCT-2003
                                                                                                                          24-APR-2003.
                       ABM38818;
ABM38818
```

Maisonneuve JL; Jones R, Carter D;

Bhatia A, Benson DR,

Persing DH, Lodes MJ,

invention relates to an isolated polynucleotide (ACF64435-ACF64733) Example 1; SEQ ID NO 3494; 1481pp; English.

```
The inventor branch to an Isolated polymorecorde (ACK64435, ACK64433)

conciding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polymorecordes (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a colymposition of the invention; anniholdies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; an immune response specific for a P. acnes

Co polymposition proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes

Co polymposition and an isolated T cell population comprising P. acnes polypeptides, antibodies, fusion proteins, T cell populations, or a trism method and kit confidence of the acnes in a selecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and method for inhibiting the development of P. acnes in collypeptides are useful for diagnosing, preventing or treating acceptations or antigen-presenting cells that express the polympositions or antigen-presenting cells that express the collypeptides are useful for diagnosing, preventing or for treating acceptations of an immune response against P. acnes, or for treating acceptation of an immune response against P. acnes, or for treating acceptance adainst P. acnes polymposited by an ORF (open reading frame) contained within the P. acnes polymuclectides of the princed specification, which in the P. acnes polymuclectides of the princelly of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince of the prince
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from WIPO at ftp.wipo.int/pub/published_pct_sequences
```

0 0; Indels 1.8%; Score 6; DB 4; Length 51; 100.0%; Pred. No. 8.3e+02; cive 0; Mismatches 0; Indels AAB34389 standard; protein; 52 AA. 6; Conservative Local Similarity 228 SLKLLG 233 SLKLIG 44 Sequence 51 AA; 39 AAB34389; Query Match 240 Matches AAB34389 ò EXXX ó: Gaps

ò

1.8%; Score 6; DB 6; Length 50; 100.0%; Pred. No. 8.2e+02; cive 0; Mismatches 0; Indels

6; Conservative

78 LLVTLI 83

Best Local Similarity

Query Match Matches

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to oytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell proulations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammalopoidsis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, indubin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form the directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                  Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptidde therapy; etem cell growth factor; haematopoiesis; tissue growth factor; immunomedulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID NO 18272; 1399pp + Sequence Listing; English.
AA004380 standard; protein; 51 AA.
                                                                                                                 Human polypeptide SEQ ID NO 18272.
                                                                                                                                                                                                                                                                                                                                                               26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAI84311.
                                                                                                                                                                                                                                                                                     WO200164835-A2.
                                                                           06-NOV-2001
                                                                                                                                                                                                                                                                                                                           07-SEP-2001.
                                     AAC04380;
```

```
Human; secreted protein; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; and antibacterial; gene therapy; detection; cancer; chromosome marker; chromosome identification; neural disorder; immune disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; wound healing; infectious disease; preservative;
                                                                                                                                                                                                                                                                                                                                                                                        Human secreted proteins and gene sequences encoding them, useful for detecting, preventing, and treating disorders such as cancer, neurological disorders and immune system disorders.
                       Human secreted protein sequence encoded by gene 23 SEQ ID NO:150.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 406; 429pp; English.
                                                                                                                                                                                                                                                                                                                                         Komatsoulis G;
                                                                                                                                                                                                                                                  16-MAR-2000; 2000WO-US006822.
                                                                                                                                                                                                                                                                           99US-0126054P.
                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
26-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                        Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-587666/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 52 AA;
                                                                                                                                                                                                WO200056883-A1.
                                                                                                                                                 food additive
                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                           23-MAR-1999;
                                                                                                                                                                                                                                                                                       10-DEC-1999;
                                                                                                                                                                                                                         28-SEP-2000.
```

human secreted proteins given in AAC59566 to AAC59614 encode the human secreted proteins given in AAB34299 to AAB34347. AAB34348 to AAB343437 represent human secreted polypeptide sequences and proteins considered by the proteins and colored by the proteins have activities based on the tissues invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Example of activities include: convergorective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; and antibacterial. The polynucleotides can be used for the detection of various disorders such as cancer, chromosome cidentification, as chromosome markers, and for numerous other diagnostic or research purposes. The secreted proteins can be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmanary, cardiovascular, remai, and proliferative disorders, wound healing, and infectious diseases. The proteins can also be used as a food additive or preservative to increase or decrease sequences used in the exemplification of the present invention

1.8%; Score 6; DB 3; Length 52; 100.0%; Pred. No. 8.5e+02; ative 0; Mismatches 0; Indels Conservative 228 SLKLLG 233 Query Match Best Local Similarity . 9 Matches

.; 0

Gaps

.. 0

AAU53123 standard; protein; 53 AA. SLKLLG 27 RESULT 241

AAU53123;

22

d

ABM49642 standard; protein; 53 AA.

RESULT 242

**ABM49642** 

ABM49642;

a x y x

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by p. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. C. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The colypeptides may be used as antigens in the production of antibodies placing the amount of bound protein in the sample. The colypeptides may be used as antigens in the production of antibodies of therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes proteins. The acnes polypeptides and ctivity of P. acnes polypeptides may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was ö SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; polypeptides and nucleic acids useful for diagnosing infections, especially useful for Gaps · 0 Mitcham JL, Wang SS, Bhatia A; , Jen S, Carter D; 0; Indels 1.8%; Score 6; DB 4; Length 53; 100.0%; Pred. No. 8.7e+02; ive 0; Mismatches 0; Indels Propionibacterium acnes immunogenic protein #14019. dermatological; osteopathic; neuroprotectant. Example 1; SEQ ID NO 14318; 1069pp; English. ftp.wipo.int/pub/published_pct_sequences L'maisonneuve J, Zhang Y, Jen S, 21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P. 20-APR-2001; 2001WO-US012865. 27-FEB-2002 (first entry) Skeiky YAW, Persing DH, 6; Conservative Propionibacterium acnes. Propionibacterium acnes vaccinating against and treating acne vulgaris. (CORI-), CORIXA CORP. WPI; 2001-616774/71. 136 POIALR 141 Local Similarity 42 PQIALR 47 N-PSDB; AAS59558. Sequence 53 AA; WO200181581-A2. 01-NOV-2001. Query Match Best Loc Matches 

AAO12979 standard; protein; 54 AA.

```
The invention relates to an isolated polymucleotide (ACF64435-ACF64733) encoding a Propionibacterium acres protein. The invention also relates to encoding a Propionibacterium acres protein. The invention also relates to polypeptides encoded by the polymucleotides (ABM35624-ABM64536) and to additionally encompasses expression vectors and host cells comprising a diditionally encompasses expression vectors and host cells comprising a polypeptide of the invention; and misclated T cell population comprising T cells prepared invention; the invention; and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising T cells prepared via this method; a vaccine composition (comprising T cells proputides, polymucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P, acres in a patient; and a method for inhibiting the development of P, acres in a patient. The P, acres polypeptides, polymucleotides, antibodies, fusion protein. The P, acres polypeptides, preventing cells that express the polymucleotides can also be used as probes or priners for outlears, or for stimulations or antigen-presenting cells that express the protein. The polymucleotides can also be used as probes or priners for nucleic acid hybridisation. The vaccine composition is useful for the simmune response against P, acres polymucleotides can also be used as probes or priners for cucleic acid hybridisation. The vaccine composition is useful for performing a diagnostic assay. The present conding frame) contained within the P, acres polymucleotides of the printed specification, but was obtained in electronic format directly the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Propionibacterium acnes polypeptides and polymucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                               Propionibacterium acnes predicted ORF-encoded polypeptide #14318.
                                                                                              Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitcham JL, Skeiky YAW, Persing DH, Bhatia A,
Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR,
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 14318; 1481pp; English.
                                                                                                                                                                                                                                                                                                           11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                          15-OCT-2001; 2001US-00978825
  20-OCT-2003 (first entry)
                                                                                                                                                                     Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003-381789/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ACF64487
                                                                                                                                                                                                                WO2003033515-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 53 AA;
                                                                                                                                                                                                                                                               24-APR-2003.
```

Maisonneuve JL; Jones R, Carter D;

```
0; Gaps
1.8%; Score 6; DB 6; Length 53;
100.0%; Pred. No. 8.7e+02;
Live 0; Mismatches 0; Indels
                                  6; Conservative
Query Match
Best Local Similarity
                                  Matches
```

ó

RESULT 243 AA012979

```
The invention relates to human polynucleotides (AAI19941-AAI93841) and the encoded proteins (AA000010-AA01910) that exhibit activity elating to Oytokine. Call proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammanomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leuksemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                           Human; cytokine; cell proliferation; cell differentiation; gene therapy; accine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 26871; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 4; Length 54; 100.0%; Pred. No. 8.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes immunogenic protein #8234.
                                                                                                          Human polypeptide SEQ ID NO 26871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU47338 standard; protein; 54 AA.
                                                                                                                                                                                                                                                                                                                                               26-FEB-2001; 2001WO-US004927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                    06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 SLKLLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 SLKLLG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAI92910.
                                                                                                                                                                                                                                                                         WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 54 AA;
                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                             07-SEP-2001.
                                  AA012979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU47338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 244
AAU47338
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAKEXEXEX EXEXE
```

```
Sequences AMOSIVO-AMOSIVI. TERPLEBER. PROPIOLIZACTERIUM acutes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by a conse. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and costcomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central carvance system, however it is particularly involved in the inflammatory lesions system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a cample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The capt and determining as antigens in the production of antibodies polypeptides may be used as antigens in the production of antibodies con perceit for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes presence, for example, by enzylengence treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzylenged immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was constanted in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                          Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 4; Length 54;
100.0%; Pred. No. 8.8e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                        Mitcham JL, Wang SS,
, Jen S, Carter D;
                   dermatological; osteopathic; neuroprotectant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ORFX protein sequence SEQ ID NO:15004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 8533; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP07511 standard; protein; 54 AA.
                                                                                                                                                                                                                           21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                 20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                                                                                                                                                                 Persing DH, M:
ve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                           Propionibacterium acnes,
                                                                                                                                                                                                                                                                                                                                                                                                              2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 LRECIR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 LRECIR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AASS9538.
                                                                                                                                                                                                                                                                                                                                                                           L'maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 54 AA;
                                                                                                WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 9
                                                                                                                                            01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                     Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP07511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

```
(referred to as open reading frame, ORFX, where X is 1-11491 processed in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polymucleotide sequences can be used in Gene therapy. ORFX sequences can be used in the reading disorders, cirrhosis of liver, psoriamis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders mellitus, systemic transplantation, cardiovascular diseases mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage diseases, various immune deficiencies and disorders, infectious diseases, autoimmune thyroiditis, myaethenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ·.
                      cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertensibo; hypothyroidiam; cholseserol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes substantially purified human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
degenerative disorder; osteoarthritis; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 5; Length 54;
100.0%; Pred. No. 8.8e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 15004; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABM43857 standard; protein; 54 AA.
                                                                                                                                                                                                                                                                                                                    30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                              29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                  (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 LAKIIL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                          myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-106308/
N-PSDB; ABN23263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 LAKIIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 54 AA;
                                                                                                                                                                                          WO200192523-A2.
                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                            Shimkets RA,
                                                                                                                                                                                                                                    06-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABM43857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM43857
  à
```

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;

termination sequence.

Arabidopsis thaliana protein fragment SEQ ID NO: 10297,

(first entry)

17-OCT-2000

AAG11542;

AAG11542 standard; protein; 55 AA.

```
Propionibacterium acnes predicted ORF-encoded polypeptide #8533.
                           Acne vulgaris, antiseborrhoeic, dermatological, antibacterial, immunostimulant; immune response, vaccine.
                                                                                                                                 Mitcham JL, Skeiky YAW, Persing DH, Bhatia A,
Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR,
                                                                                                                                                                                                             Example 1; SEQ ID NO 8533; 1481pp; English.
                                                                                                                                          Wang S, Jen S, Lod
Vallieve-Douglass J;
                                                                                         11-OCT-2002; 2002WO-US032727.
                                                                                                       15-OCT-2001; 2001US-00978825
20-OCT-2003 (first entry)
                                                 Propionibacterium acnes
                                                                                                                                                              2003-381789/36.
                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                              WPI; 2003-381789/
N-PSDB; ACF64467.
                                                             WO2003033515-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 54 AA;
                                                                            24-APR-2003.
                                                                                                                                          Zhang Y,
Barth B,
```

```
ö
                                Gaps
                                 .
0
                           0; Indels
1.8%; Score 6; DB 6; Length 54;
100.0%; Pred. No. 8.8e+02;
ive 0; Mismatches 0; Indels
                             6; Conservative
                                                    146 LRECIR 151
          Sest Local Similarity
                        Matches
```

12 LRECIR 17

RESULT 247

AAG11542

```
99US-0130891P.
99US-0131449P.
99US-0132048P.
99US-0132407P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    990S-0134370P.
990S-0134768P.
990S-0134941P.
990S-0135124P.
                                                                                                                                                                                                                                                                                                                                                                                                                99US-0126785P.
99US-0127462P.
99US-0128234P.
                                                                                                                                                                                                                                                                                                                                                                 99US-0123548P.
99US-0125788P.
99US-0126264P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0129845P.
99US-0130077P.
99US-0130449P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0132486P.
99US-0132487P.
99US-0132863P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0134218P.
99US-0134219P.
99US-0134221P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0135629P.
99US-0136021P.
99US-0136392P.
99US-0136782P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0137222P.
99US-0137528P.
99US-0137502P.
                                                                                                                                                                                                                                                                                                 25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0128714P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0130510P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0132484P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0134256P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0137724P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0138847P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0138540P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0139453P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0139492P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0139452P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0139455P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0139458P
99US-0139459P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0139460P
                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                  EP1033405-A2.
                                                                                                                                                                                                                                                                 06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-APR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -NDD-87
The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to encoding a Propionibacterium acnes protein. The invention also relates to collypoptides and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a diditionally encompasses expression vectors and host cells comprising a polypeptide of the invention, antibodies against polypeptides of the invention; any polynuclectide of the invention; and immune response specific for a P. acnes parts polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising T cells prepared to polynuclectides, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a protein. The P. acnes polypeptides, preventing cells that express the collypeptides are useful for indigen-presenting cells that express the polynucleotides can also be used as probes or primers for nucleic acid hybridistation. The vaccine composition is useful for the simmulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present content of the printed specification, but was obtained in electronic format directly the printed specification, but was obtained in electronic format directly contents.
                                                                                                                                                                                                                                                                                                                                                                                                                         New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                               Maisonneuve JL;
Jones R, Carter D;
```

Page 158

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9e+02;
\cream 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 3 Similarity 100.0%; Pred. No. 9e+6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ORFX protein sequence SEQ ID NO:2386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP01202 standard; protein; 55 AA
                                                                                                                                                                                                                                                  9905.0155486P
9905.0155659P
9905.0156659P
9905.015717P
9905.015763P
9905.015763P
9905.0158629P
9905.0158629P
9905.0158232P
9905.0158232P
9905.0159234P
9905.0159234P
9905.0159234P
9905.0159234P
9905.0159234P
9905.0159234P
9905.0159234P
9905.0159634P
9905.0159634P
9905.0160741P
9905.0160741P
9905.0160741P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0161404P.
99US-0161405P.
99US-0161359P.
99US-0161360P.
99US-0161361P.
99US-0161361P.
99US - 0149930P
99US - 0150566P
99US - 0151065P
99US - 0151066P
99US - 0151080P
99US - 0151303P
99US - 0151338P
99US - 0151338P
99US - 015133P
99US - 01530P
99US - 01530P
99US - 01530P
99US - 0154018P
99US - 0154018P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0161992P.
99US-0161993P.
99US-0162142P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 LSSFOK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSSFOK 24
23-AUG-1999;
25-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
32-SEP-1999;
32-SEP-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AUG-1999;
33-AU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S:
Matches 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP01202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP01202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BXHXHXB
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             엄
```

ö

```
Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                          Novel human polypeptides and polymucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                       Disclosure, SEQ ID NO 2386; 1037pp; English.
                                                                                                                                                                                                30-MAY-2000; 2000US-0206132P. 29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                           29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                            WPI; 2002-106308/14.
                                                                                   myasthenia gravis.
                                                                                                                                                                                                                                                                                       N-PSDB; ABN16954.
                                                                                                                                WO200192523-A2.
                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                    Shimkets RA,
                                                                                                                                                      06-DEC-2001,
```

Leach MD;

```
The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1) in the specification). ABM15762 to ABM27525 encode the human ORFX proteins given in ABB000010 to ABP11500. ORFX proteins are useful for proteins given in ABB000010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polymucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, intending or transplantation, cardiovascular disorders, disorders related to organ cransplantation, cardiovascular disorders, disorders, infectious disease, various immune deficiencies and disorders, infectious disease, various immune deficiencies and disorders, infectious disease, varioummune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also cuseful for treating burns, inforisons, ulcers, for treating obsceporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from cytokine damage. NB. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic correction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 55 AA;
```

```
Score 6; DB 5; Length 55;
Pred. No. 9e+02;
0; Mismatches 0; Indels
1.8%; Scc. No. ...
100.0%; Pred. No. ...
                                      6; Conservative
       Query Match
Best Local Similarity
Matches 6; Conserv
```

128 MLLKGY 133

ABP25762 standard; protein; 55 AA. RESULT 249 ABP25762 ID ABP2

```
Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
                                                                                                                                                                                       Grandi G, Fraser C;
                                                     group A streptococcus, Streptococcus pyogenes, antibacterial, antiinflammatory, infection, vaccine, meningitis, gene therapy.
                                                                                                                                                                                       Masignani V, Margarit Y RosI,
                                  Streptococcus polypeptide SEQ ID NO 700.
                                                                                                                                     27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                       29-OCT-2001; 2001WO-GB004789.
                    (first entry)
                                                                             Streptococcus agalactiae.
                                                                                                                                                                        INST GENOMIC RES.
                                                                                                                                                                 (CHIR-) CHIRON SPA
                                                                                           WO200234771-A2.
                   02-JUL-2002
                                                                                                                                                                                    Telford J, I
Tettelin H;
                                                                                                         02-MAY-2002
      ABP25762;
                                                                                                                                                                         (GENO-)
```

New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.

2002-352536/38.

N-PSDB; ABN66393.

Claim 1; Page 3222; 4525pp; English.

streptococcus/GBS (Streptococcus adalactise) or group A streptococcus/GBS (Streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiniflammatory activity. (I), nucleic acids encoding (I), ABM66044-ABM71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromography, immunoassays, and distinguishing/identifying The invention relates to a protein (ABP25413-ABP30895) from group B Streptococcus proteins

DB 5; Length 55; o. 9e+02; tches 0; Indels 1.8%; Score 6; DB 5 100.0%; Pred. No. 9e+ iive 0; Mismatches 6; Conservative Local Similarity Sequence 55 AA; Query Match Matches

. 0

Gaps

ö

ò

ö

Gaps

..

AAM94423 standard; protein; 56 AA. 250 AAM94423

AAM94423; EXXX

```
21-58F-2000) 2000US-0234397P

25-58F-2000) 2000US-0234397P

26-58F-2000) 2000US-0235434P

27-58F-2000) 2000US-0235434P

27-58F-2000) 2000US-0235434P

27-58F-2000) 2000US-0235434P

27-58F-2000) 2000US-0235434P

29-58F-2000) 2000US-0235434P

29-58F-2000) 2000US-0235434P

29-58F-2000) 2000US-0235434P

29-58F-2000) 2000US-0236363P

29-58F-2000) 2000US-0236363P

29-58F-2000) 2000US-0236363P

20-0CT-2000) 2000US-0236363P

20-0CT-2000) 2000US-0236363P

20-0CT-2000) 2000US-0236363P

20-0CT-2000) 2000US-0236363P

20-0CT-2000) 2000US-0236363P

20-0CT-2000) 2000US-0236363P

20-0CT-2000) 2000US-0236363P

20-0CT-2000) 2000US-0236363P

20-0CT-2000) 2000US-024647P

20-0CT-2000) 2000US-024647P

20-0CT-2000) 2000US-024647P

20-0CT-2000) 2000US-024652P

20-0CT-2000) 2000US-024652P

20-0CT-2000) 2000US-024652P

20-0CT-2000) 2000US-024652P

20-0CT-2000) 2000US-024652P

20-0CT-2000) 2000US-024652P

20-0CT-2000) 2000US-024652P

20-0CT-2000) 2000US-024652P

20-0CT-2000) 2000US-024652P

20-0CT-2000) 2000US-024652P

20-0CT-2000) 2000US-024652P

20-0CT-2000) 2000US-024652P

20-0CT-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

17-NOV-2000) 2000US-024921P

10-NOS-024921P

10-NOS-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0251479P.
2000US-0251856P.
2000US-0251868P.
  14 - SEP - 2000; 2 14 - SEP - 2000; 2 14 - SEP - 2000; 2 17 - SEP - 2000; 2 25 - SEP - 2000; 2 25 - SEP - 2000; 2 25 - SEP - 2000; 2 27 - SEP - 2000; 2 29 - SEP - 2000; 2 29 - SEP - 2000; 2 29 - SEP - 2000; 2 29 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 2000; 2 20 - SEP - 20
       Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy.
                                            Human reproductive system related antigen SEQ ID NO: 3081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-025515P

2000US-0205467P

2000US-021486F

2000US-021486F

2000US-021486P

2000US-021486P

2000US-021486P

2000US-021486P

2000US-021486P

2000US-021486P

2000US-021486P

2000US-021486P

2000US-022564P

2000US-022526P

2000US-022526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02526P

2000US-02529P

2000US-02529P

2000US-02529P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P

2000US-0259P
                                                                                                                                                                                                                                                                                                                                                           2000US-0180628P.
2000US-0184664P.
2000US-0186350P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0231242P.
2000US-0231244P.
2000US-023144P.
2000US-0231414P.
2000US-0232080P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0232400P.
2000US-0232401P.
2000US-0233063P.
                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0189874P.
2000US-0190076P.
2000US-0198123P.
                                                                                                                                                                                                                                                                                           17-JAN-2001; 2001WO-US001339
                                                                                                                                                                                                                                                                                                                                        2000US-0179065P
21-NOV-2001 (first entry)
                                                                                                                                                                                                 WO200155320-A2
                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
24-FEB-2000;
16-MAR-2000;
11-MAR-2000;
11-MAY-2000;
19-MAY-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
20-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 - JUL-2000;
14 - AUG-2000;
14 - AUG-2000;
14 - AUG-2000;
14 - AUG-2000;
14 - AUG-2000;
14 - AUG-2000;
14 - AUG-2000;
14 - AUG-2000;
14 - AUG-2000;
16 - AUG-2000;
17 - AUG-2000;
18 - AUG-2000;
18 - AUG-2000;
18 - AUG-2000;
18 - AUG-2000;
19 - AUG-2000;
22 - AUG-2000;
23 - AUG-2000;
23 - AUG-2000;
26 - SEP-2000;
26 - SEP-2000;
26 - SEP-2000;
26 - SEP-2000;
27 - AUG-2000;
28 - AUG-2000;
28 - AUG-2000;
29 - AUG-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - SEP-2000;
20 - S
                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-SEP-2000;
                                                                                                                                                                                                                                              02-AUG-2001
```

us-10-025-730-1.oligo.rag

```
0
                                                                                                                                                                                                                       Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                      Claim 11; SEQ ID NO 3081; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.8%; Score 6; DB 4; Length 56; Best Local Similarity 100.0%; Pred. No. 9.1e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                       Rosen CA, Barash SC, Ruben SM;
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                    WPI; 2001-465570/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 VKILKD 11
                                                                                                                                                                                         N-PSDB; AAL00393.
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 56 AA;
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
```

Search completed: April 12, 2004, 10:35:23 Job time : 75 secs

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

April 12, 2004, 10:36:54; Search time 46 Seconds (without alignments) 1926.306 Million cell updates/sec

US-10-025-730-1 337 Title: Perfect score:

1 MKKMPLFSKSHKNPAEIVKI........RADEKNYLIKQIRDLKKTAP 337

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

Sequence:

1073127 seqs, 262937947 residues Searched:

0 Word size :

1073127 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 300 summaries

Database :

Published Applications AA:*

| cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Secure 1 secure 1	i m	Segment A Applia	ìu	Segmence 4 Applia		, ,	Segrence 100/2, A	Semiona 140For	Sequence 149393,	Segretate 88/1, Ap	deducine passa, A	sedneuce 271// A	Sequence 55961, A	Semience 13726 a	Sequence 23, Appl
SUMMARIES	ΩI	US-10-025-730-1	US-10-025-730-3	US-10-239-079-5	US-10-239-079-6	US-10-025-730-4	US-10-025-730-5	US-10-425-114-48872	US-10-424-599-224185	US-10-424-599-149595	US-10-369-493-8871	US-10-425-114-54669	118-10-425-114-53177	1177 177 177 177 177 177 177 177 177 17	US-10-475-114-25961	US-10-369-493-13726	US-09-862-027-23
	DB	14	14	14	14	14	14	12	12	12	15	12	12	,	77	15	9
	Match Length DB	337	341	496	552	339	377	342	339	184	307	412	446	000	7 2 2	649	923
مه و د	Match	100.0	6.8	6.8	6.8	4.5	4.2	3.0	2.7	2.4	2.4	2.4	2.4	2 4		4.	2.4
	Score	337	23	23	23	15	14	10	6	80	60	80	80	α	•	20	<b>6</b> 0
Result	No.	г	7	m	4	S	9	7	ω	σ	10	11	12	13		4.	12

aquence 1453, aquence 1450, aquence 1450, aquence 140, aquence 140, aquence 1413, aquence 22167, aquence 22167, aquence 22167, aquence 22167, aquence 22167, aquence 22167, aquence 240, aquence 173625, aquence 18325, aquence 18325, aquence 173629, aquence 173629, aquence 173629, aquence 173629, aquence 173629, aquence 173629, aquence 173629, aquence 173629, aquence 173629, aquence 173609, aquence 2522, aquence 2522, aquence 2522, aquence 27387, aquence 173206, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence 27387, aquence	quence 37583 quence 859, quence 7310, quence 10, A quence 110, A quence 173, quence 173, quence 22038 quence 22038 quence 22038 quence 1163, quence 1163, quence 1163, quence 1163, quence 14077 quence 14077 quence 1261, quence 1261, quence 1261, quence 1261, quence 1261, quence 1261, quence 1261, quence 1261, quence 1261, quence 1261, quence 1261, quence 1261, quence 1261, quence 1261, quence 1261, quence 1261,
US-10-238-075-1 US-10-424-599-2. US-10-424-599-2. US-10-424-599-1. US-10-424-599-1. US-10-424-599-1. US-10-10-6-698-5. US-10-16-698-5. US-10-16-698-5. US-10-16-698-5. US-10-16-698-5. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-10-424-599-2. US-10-10-424-599-2. US-10-10-424-599-2. US-10-10-424-599-2. US-10-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-424-599-2. US-10-425-114-41. US-10-425-114-41. US-10-425-114-41.	US-10-425-114-3758 US-10-0238-075-859 US-10-0238-075-859 US-10-032-585-7310 US-10-424-599-2210 US-10-425-114-3825. US-09-952-464A-10 US-09-952-464A-8 US-10-944-633-173 US-09-952-464A-8 US-10-244-633-32 US-09-803-245-2221 US-10-389-566-1163 US-10-389-566-1163 US-10-389-566-1261 US-10-389-566-1261 US-10-389-566-1261 US-10-389-566-1261 US-10-389-566-1261 US-10-389-566-1261 US-10-389-566-1261 US-10-389-566-1261 US-10-389-566-1261 US-10-389-566-1261 US-10-389-566-1261 US-10-389-566-1261 US-10-389-566-1261 US-10-389-566-1261 US-10-407-866-93 US-10-425-114-66877 US-10-425-114-66877
44444994444444444444444444444444444444	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
11111111111111111111111111111111111111	4 4 4 4 4 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0
11111120222222222222222222222222222222	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

us-10-025-730-1.oligo.rapb

Sequenc Sequenc Sequenc Sequenc Sequenc Sequenc Sequenc Sequenc	equence equence Sequence Sequence Sequence Sequence	Sequence 24566, A Sequence 245645, Sequence 186473, Sequence 1603, Ap Sequence 1603, Ap Sequence 153190,	Sequence 165968, Sequence 251249, Sequence 8935, Ap Sequence 257, App Sequence 268688, Sequence 268688, Sequence 268688,	Sequence 163560, Sequence 186702, Sequence 188262, Sequence 280571, Sequence 20671, Sequence 8758, Ap Sequence 157298, Sequence 157298, Sequence 157298,	Sequence 256649, Sequence 23412, Ap. Sequence 234125, Sequence 282678, Sequence 28907, Sequence 147796, Sequence 17796, Sequence 17066, Sequence 17066, Sequence 18660, Sequence 18660, Sequence 1868, Sequence 1868,	Sequence 1868, Ap Sequence 3692, App Sequence 36923, Sequence 76, Appl Sequence 478, Appl Sequence 478, Appl Sequence 117, Appl Sequence 216376, Sequence 20671, Sequence 20671, Sequence 20671, Sequence 17878, Sequence 17878, Sequence 17878, Sequence 17878, Sequence 17878, Sequence 17878, Sequence 17878, Sequence 6796, Appl Sequence 6796, Appl Sequence 71923, Sequence 71923, Sequence 71923, Sequence 71923, Sequence 258409,
US-10-424-599-244014 US-10-425-114-37263 US-10-425-114-56749 US-09-864-408h-2574 US-09-864-550-574 US-10-424-599-162228 US-10-424-599-162228 US-10-424-599-162228	US-09-738-626-4641 US-09-88-664A-32 US-09-764-877-1643 US-10-697-265-33 US-10-242-515-1643 US-09-764-891-3412 US-10-424-599-231338	US-09-864-761-37566 US-10-424-599-245645 US-10-424-599-186473 US-09-925-301-1603 US-09-864-406A-8152 US-09-864-406A-8152	US-10-424-599-165968 US-10-424-599-165968 US-10-135-97-8935 US-10-073-961-257 US-10-424-599-268688 US-10-335-977-8936 US-09-882-277-114	US-10-424-599-163560 US-10-424-599-186702 US-10-424-599-188702 US-10-424-599-206791 US-10-424-599-206794 US-10-424-599-206798 US-10-424-599-157298 US-10-424-599-151299 US-10-424-599-151299	US-10-24-599-256499 US-10-335-977-8937 US-10-424-599-234125 US-10-424-599-282678 US-10-424-599-14796 US-10-424-599-154660 US-10-424-599-164813 US-10-424-599-164813	US-09-082-302-852 US-09-864-761-36927 US-09-864-761-36927 US-09-867-550-76 US-09-731-872-478 US-09-731-872-478 US-09-731-872-478 US-09-731-872-478 US-09-731-872-478 US-09-731-872-478 US-09-731-872-478 US-09-731-872-478 US-10-424-599-200671 US-10-424-599-200671 US-10-424-599-178787 US-10-424-599-178787 US-10-424-599-178787 US-10-424-599-178787 US-10-424-599-178787 US-10-424-599-178787 US-10-424-599-178787
ннанопанан	2004444	94449449	, – – – – – –	++++++++++	ченененененене	
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~		യ മാമാമാമാമാമാമ	) <b>න න න න න න න</b> න	ானன்னைன்னைன்?	, , , , , , , , , , , , , , , , , , ,	100 1003 1004 1004 1004 1005 1007 1008 1008 1009 1009
	νουυυνα	νουουουο		νφοσοσοσοσο	• ๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗ ๗	<i>୰</i> ୰୰୰୰୰୰୰୰୰୰୰୰୰୰୰୰୰
162 163 164 165 166 170 171	172 174 175 176 176 178	179 181 182 183 184 185	188 188 189 190 191 192	1995 1995 1998 1999 2000	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2011 2011 2011 2011 2011 2011 2011 2011
ৰ ন উল্লেখ ক কিন্তুল বিধাৰ জ						
Sequence 72475, Sequence 8, Appl Sequence 2071, Sequence 80, Appl Sequence 33, Appl Sequence 33, Appl Sequence 6986, Sequence 6986, Sequence 69548, Sequence 806, R	Sequence Seq	Sequence Seq Sequence Sequence Sequence Sequence Sequence Sequence Sequence	Sequence 46961, A Sequence 33835, A Sequence 3628, Ap Sequence 372, App Sequence 157183, Sequence 159316, Sequence 445, App	Sequence 188181, Sequence 26967, Sequence 174437, Sequence 186215, Sequence 23354, Sequence 249890, Sequence 15079, A Sequence 15079, A	Sequence 149472, Sequence 182688, Sequence 49022, A Sequence 3081, Ap Sequence 267396, Sequence 278427, Sequence 278627, Sequence 27862, A Sequence 27862, A Sequence 278627, Sequence 278627, Sequence 278627, Sequence 195329,	Sequence 211257, Sequence 21257, Sequence 47397, Sequence 159823, Sequence 159823, Sequence 15800, Ap Sequence 115600, Sequence 115600, Sequence 114751, Sequence 114751, Sequence 212560, Sequence 212560, Sequence 212560, Sequence 242460, Sequence 242460, Sequence 242, App Sequence 242, App Sequence 242, App Sequence 242, App Sequence 242, App Sequence 242, App Sequence 242, App Sequence 242, App Sequence 242, App
1-425-114-72475 Sequen 1-086-464-8 Sequen 1-369-493-2071 Sequen 1-312-088-34 Sequen 1-312-088-34 Sequen 1-312-088-33 Sequen 1-312-088-33 Sequen 1-3282-122A-69986 Sequen 1-334-143-27 Sequen 1-369-493-3006 Sequen 1-369-493-3006 Sequen 1-369-493-3006 Sequen	-833-245-222 Sequention of the control of the contr	1774-639-312 Sequent 1-969-730-239 Sequent 1-621-33-239 Sequent 1-621-33-239 Sequent 1-621-33-239 Sequent 1-24-599-230826 Sequent 917-340-63 Sequenc	864-761-46661 Sequenc 864-761-3835 Sequenc -764-891-3628 Sequen -291-265-372 Sequen -424-599-15916 Sequen -764-872-445 Sequence	-424-599-188181 Sequent-424-599-188181 Sequent-424-599-174437 Sequent-424-599-186215 Sequent-424-599-223354 Sequent-424-599-223354 Sequent-424-599-22699 Sequent-424-599-2699 Sequent-424-599-22699 Sequent-424-599-22699 Sequent-424-599-22699 Sequent-424-599-22699 Sequent-424-599-22699 Sequent-424-599-22699 Sequent-424-599-22699 Sequent-424-599-22699 Sequent-424-599-22699	424-599-149472 Sequent -424-599-182688 Sequenc 864-761-4902 Sequenc 764-891-3081 Sequenc -764-891-3081 Sequenc -764-891-3081 Sequenc -424-599-267396 Sequenc -029-386-27862 Sequenc -127-641-59 -127-641-59-195329 Sequenc -424-599-195329 Sequenc	424-599-211257 Sequent 424-599-210529 Sequent 424-599-210556 Sequent 424-599-1159823 Sequent 424-599-115980 Sequent 424-599-11560 Sequent 424-599-11683 Sequent 424-599-11683 Sequent 424-599-11683 Sequent 424-599-11683 Sequent 424-599-11683 Sequent 424-599-11683 Sequent 424-599-1264 Sequent 424-599-20246 Sequent 424-599-20246 Sequent 424-599-20246 Sequent 424-599-20246 Sequent 424-599-20346 Sequent 424-599-20346 Sequent 424-599-20346 Sequent 424-599-20346 Sequent 424-599-20346 Sequent 424-599-20346 Sequent 424-599-20319 Sequent
US-10-425-114-72475 Sequen US-10-086-464-8 Sequen US-10-369-493-2071 Sequen US-10-312-088-34 Sequen US-10-176-306-80 Sequen US-10-176-306-80 Sequen US-10-312-088-33 Sequen US-10-382-122A-69986 Sequen US-10-282-122A-69548 Sequen US-10-282-122A-69548 Sequen US-10-39-493-3006 Sequen US-09-800-729-89	1 US-09-833-245-222 Sequents US-09-744-807-2 Sequents US-09-764-853-554 Sequents US-10-399-385-5 Sequents US-10-261-798-51 Sequents US-10-261-798-51 Sequents US-10-399-385-4 Sequents US-09-385-4 Sequents US-09-385-4460 Sequents US-09-864-761-46460 Sequents US-09-864-761-761-761-761-761-761-761-761-761-761	US-09-774-639-312 Sequent US-09-969-730-239 Sequent US-10-621-363-239 Sequent US-09-864-761-45850 Sequent US-09-917-340-63 Sequent US-09-917-340-63 Sequence	US-09-864-761-46961 Sequenco US-09-864-761-38335 Sequenco US-09-64-891-3628 Sequenco US-10-291-265-372 Sequenco US-10-424-599-159316 Sequenco US-09-764-872-445 Sequenco US-09-764-872-445	US-110-424-599-188181 Sequent 2 US-110-424-599-186667 Sequent US-110-424-599-186215 Sequent US-10-424-599-186215 Sequent US-10-424-599-223354 Sequent US-10-424-599-249890 Sequent US-110-424-599-249890 Sequent US-110-424-599-249890 Sequent US-110-424-599-249890 Sequent US-110-424-599-247013 Sequent	US-10-424-599-149472 Sequent US-09-908-111-83 Sequent US-09-864-761-49022 Sequenc US-09-864-891-3081 Sequenc US-09-768-891-3081 Sequenc US-00-764-891-3081 Sequenc US-10-424-599-178427 Sequent US-10-22-386-27862 Sequent US-10-127-641-59-195329 Sequent US-10-424-599-195329 Sequent US-10-424-599-195329 Sequent US-10-424-599-195329 Sequent	US-10-424-599-211257 Sequent US-10-424-599-211257 Sequent US-00-424-599-21556 Sequent US-09-864-761-47397 Sequent US-10-324-599-159823 Sequent US-10-424-599-15980 Sequent US-10-424-599-15660 Sequent US-10-424-599-191683 Sequent US-10-424-599-191683 Sequent US-10-424-599-191683 Sequent US-10-424-599-195946 Sequent US-10-424-599-195946 Sequent US-10-424-599-202460 Sequent US-10-424-599-202460 Sequent US-10-231-172-242 Sequent US-10-231-172-242 Sequent US-10-231-172-243 Sequent US-10-231-172-243 Sequent US-10-231-172-243 Sequent US-10-244-599-203199 Sequent US-10-244-599-203199 Sequent US-10-244-599-203199 Sequent
637 12 US-10-425-114-72475 Sequen 731 13 US-10-369-493-2071 Sequen 752 15 US-10-369-493-2071 Sequen 875 14 US-10-312-088-34 Sequen 873 14 US-10-176-306-80 Sequen 878 15 US-10-312-088-33 Sequen 878 15 US-10-282-122A-69986 Sequen 893 15 US-10-334-143-27 Sequen 893 15 US-10-369-493-306 Sequen 745 9 US-02-89-493-306 Sequen 8745 9 US-02-89-89 Sequen	45 11 US-09-833-245-222 Sequent 62 13 US-09-833-245-222 Sequent 63 US-09-764-885-54 Sequent 11 12 US-10-399-385-5 Sequent 14 14 US-10-399-385-5 Sequent 15 12 US-10-399-385-6 Sequent 18 14 US-10-399-385-6 Sequent 18 12 US-10-399-385-6 Sequent 18 19 US-09-864-76-46460 Sequent	10 US-09-774-639-312 Sequent US-09-774-639-312 Sequent US-09-969-730-239 Sequent US-10-621-363-239 Sequent US-10-621-363-239 Sequent US-10-424-599-230826 Sequency US-09-917-340-63 Sequency US-09-917-340-63 Sequency US-09-917-340-63 Sequency	9 US-09-864-761-46961 Sequence US-09-864-761-3835 Sequence US-09-864-891-3628 Sequence US-09-764-891-3628 Sequence US-10-424-599-157183 Sequence US-10-424-599-159316 Sequence US-09-764-872-445 Sequence US-09-764-872-445	12 US-10-424-599-188181 Sequent 12 US-10-424-599-26967 Sequent 12 US-10-424-599-17437 Sequent 12 US-10-424-599-186215 Sequent 14 US-10-424-599-186215 Sequent 12 US-10-424-599-23354 Sequent 12 US-10-424-599-249890 Sequent 14 US-10-424-599-249890 Sequent 12 US-10-424-599-249890 Sequent 12 US-10-424-599-249890 Sequent 12 US-10-424-599-249890 Sequent	12 US-10-424-599-149472 Sequent 12 US-10-424-599-182688 Sequent 9 US-09-08-41-49022 Sequenc 10 US-09-864-761-49022 Sequenc 10 US-09-764-891-3081 Sequenc 12 US-10-424-599-267396 Sequenc 12 US-10-424-599-178427 Sequenc 14 US-10-029-386-27862 Sequenc 14 US-10-424-599-195229 Sequenc 12 US-10-424-599-195229 Sequenc 12 US-10-424-599-195229 Sequenc 12 US-10-424-599-195229 Sequenc 12 US-10-424-599-195229 Sequenc	US-10-424-599-211257 Sequent US-10-424-599-211257 Sequent US-10-424-599-211257 Sequent US-10-424-599-159956 US-10-424-599-159823 Sequent US-10-424-599-159823 Sequent US-10-424-599-15980 Sequent US-10-424-599-11560 Sequent US-10-424-599-11683 Sequent US-10-424-599-11683 Sequent US-10-424-599-11683 Sequent US-10-424-599-11683 Sequent US-10-424-599-202460 Sequent US-10-21-172-242 Sequent US-10-21-172-242 Sequent US-10-21-172-242 Sequent US-10-21-172-242 Sequent US-10-21-172-243 Sequent US-0-864-408A-998
1 637 12 US-10-425-114-72475 Sequen 31 US-10-425-114-72475 Sequen 731 13 US-10-66-464-8 Sequen 752 15 US-10-369-493-2071 Sequen 1 855 15 US-10-312-088-34 Sequen 1 873 14 US-10-312-088-33 Sequen 1 891 12 US-10-312-088-33 Sequen 1 891 12 US-10-384-143-27 Sequen 1 1053 12 US-10-343-143-27 Sequen 1 1053 12 US-10-369493-306 Sequen 1 1745 9 US-10-36-493-306 Sequen 1 1745 9 US-09-800-722-89	1 1745 11 US-09-833-245-2222 Sequent 1762 13 US-10-044-807-2 Sequent 1 1762 13 US-10-047-803-554 Sequent 1 1 US-10-399-385-5 Sequent 1 1 US-10-399-385-5 Sequent 1 1 US-10-399-385-5 Sequent 1 1 US-10-399-385-5 Sequent 1 1 US-10-399-385-6 Sequent 1 1 US-10-261-798-51 Sequent 1 1 US-10-399-385-6 Sequent 1 1 US-10-399-385-7 Sequent 1 US-10-399-385-7 Sequent	. 24 10 US-09-774-639-312 Sequence 24 10 US-09-969-339 Sequence 3 24 10 US-09-969-330-239 Sequence 3 34 9 US-09-864-761-45850 Sequence 3 38 12 US-10-424-599-230826 Sequence 3 38 12 US-10-424-599-230826 Sequence 3 40 9 US-09-917-340-63 Sequence 3 38 12 US-10-340-63 Sequence 3 38 12 US-10-340-63 Sequence 3 38 10 US-09-917-340-63 Sequence 3 38 10	.8 42 9 US-09-864-761-46961 Sequence Construction of the Construct	8 48 12 US-10-424-599-188181 Sequents 12 US-10-424-599-188181 Sequents 12 US-10-424-599-188181 Sequents 12 US-10-424-599-174437 Sequents 12 US-10-424-599-186215 Sequents 12 US-10-424-599-186215 Sequents 12 US-10-424-599-24384 Sequents 12 US-10-424-599-248898 Sequents 12 US-10-424-599-18689 Sequents 13 12 US-10-424-599-12489 Sequents 13 US-10-424-599-24809 Sequents 13 US-10-424-599-247013 Sequents 13 US-10-424-599-247013 Sequents 13 US-10-424-599-247013 Sequents 13 US-10-424-599-247013 Sequents 15 US-10-424-599-247013 Seque	.8 54 12 US-10-424-599-149472 Sequent 18 55 12 US-10-424-599-18688 Sequent 18 56 9 US-09-864-761-49022 Sequent 18 56 10 US-09-864-761-49022 Sequent 18 56 10 US-09-864-891-3081 Sequent 18 57 12 US-10-424-599-267396 Sequent 18 57 12 US-10-424-599-178427 Sequent 18 57 12 US-10-424-599-178427 Sequent 18 50 12 US-10-424-599-195229 Sequent 18 60 12 US-10-424-599-195229 Sequent 18 60 12 US-10-424-599-195229 Sequent 18 60 12 US-10-424-599-195229 Sequent 18 60 12 US-10-424-599-195229	62 12 US-10-424-599-211257 Sequent (S. 12 US-10-424-599-211257) Sequent (S. 12 US-10-424-599-211257) Sequent (S. 12 US-10-424-599-285560 Sequent (S. 12 US-10-424-599-18682) Sequent (S. 12 US-10-424-599-18682) Sequent (S. 12 US-10-424-599-18682) Sequent (S. 12 US-10-424-599-18682) Sequent (S. 12 US-10-424-599-18682) Sequent (S. 12 US-10-424-599-18682) Sequent (S. 12 US-10-424-599-18682) Sequent (S. 12 US-10-424-599-18682) Sequent (S. 12 US-10-424-599-18682) Sequent (S. 12 US-10-424-599-18682) Sequent (S. 12 US-10-424-599-18642) Sequent (S. 12 US-10-424-599-264462) Sequent (S. 12 US-10-424-599-264462) Sequent (S. 12 US-10-211-172-242) Sequent (S. 12 US-10-211-172-242) Sequent (S. 13 US-10-282-1224-76423) Sequent (S. 13 US-10-424-599-203219) Se
2.1 637 12 US-10-425-114-72475 Sequen 2.1 731 13 US-10-66-464-8 Sequen 2.1 752 15 US-10-369-493-2071 Sequen 2.1 762 15 US-10-369-493-2071 Sequen 2.1 873 14 US-10-312-088-34 Sequen 2.1 8873 14 US-10-176-306-80 Sequen 2.1 891 12 US-10-312-088-33 Sequen 2.1 891 12 US-10-38-122A-69986 Sequen 2.1 893 15 US-10-38-142-27 Sequen 2.1 1053 12 US-10-369-493-306 Sequen 2.1 1745 9 US-10-369-493-306 Sequen 2.1 1745 9 US-10-369-493-306 Sequen 2.1 1745 9 US-10-369-493-306	2.1 1745 11 US-09-833-245-2222 Sequent 2.1 1762 13 US-09-483-854 Sequent 2.1 1762 13 US-09-764-883-554 Sequent 1.8 11 12 US-10-399-385-5 Sequent 1.8 14 US-10-399-385-5 Sequent 1.8 12 US-10-399-385-5 Sequent 1.8 18 19 US-10-261-798-51 Sequent 1.8 18 19 US-10-399-385-4 Sequent 1.8 18 9 US-09-864-767-46460 Sequent 1.8 18 9 US-09-864-767-46460 Sequent 1.8 18 9 US-09-864-767-46460 Sequent 1.8 18 9 US-09-864-767-46460 Sequent 1.8 18 9 US-09-864-767-46460 Sequent 1.8 18 9 US-09-864-767-46460 Sequent 1.8 18 9 US-09-864-767-46460 Sequent 1.8 18 9 US-09-864-767-46460 Sequent 1.8 18 9 US-09-864-767-46460 Sequent 1.8 18 9 US-09-864-767-46460 Sequent 1.8 18 9 US-09-864-767-46460 Sequent 1.8 18 9 US-09-864-767-46460 Sequent 1.8 18 9 US-09-864-767-46460 Sequent 1.8 18 9 US-09-864-767-46460 Sequent 1.8 18 9 US-09-864-767-46460 Sequent 1.8 18 9 US-09-864-767-767-764-764-764-764-767-767-767-7	1.8 24 10 US-09-774-639-312 Sequence 1.8 24 10 US-09-969-730-239 Sequence 1.8 24 16 US-10-621-363-239 Sequence 1.8 34 9 US-09-864-761-45850 Sequence 1.8 38 12 US-10-641-599-230826 Sequence 1.8 40 9 US-09-917-340-62 Sequence 1.8 40 9 US-09-917-340-63 Sequence 1.	1.8 42 9 US-09-864-761-46961 Sequence 1.8 43 10 US-09-864-761-3835 Sequence 1.8 44 15 US-09-764-891-3628 Sequence 1.8 45 12 US-10-291-265-372 Sequence 1.8 45 12 US-10-424-599-157183 Sequence 1.8 46 12 US-10-424-599-159316 Sequence 1.8 47 10 US-09-764-872-445 Sequence 1.8 47 10 US-09-764-872-445	1.8 48 12 US-10-424-599-188181 Sequentis 48 12 US-10-424-599-188181 Sequentis 49 12 US-10-424-599-174437 Sequentis 49 12 US-10-424-599-174437 Sequentis 50 14 US-10-424-599-186215 Sequentis 51 12 US-10-424-599-223354 Sequentis 52 12 US-10-424-599-249890 Sequentis 52 12 US-10-424-599-249890 Sequentis 53 12 US-10-424-599-124099 Sequentis 53 12 US-10-424-599-247013 Sequentis 53 12 US-10-424-599-247013 Sequentis 53 12 US-10-424-599-247013 Sequentis 53 12 US-10-424-599-247013 Sequentis 53 12 US-10-424-599-247013 Sequentis 53 12 US-10-424-599-247013 Sequentis 53 12 US-10-424-599-247013 Sequentis 53 12 US-10-424-599-247013 Sequentis 53 12 US-10-424-599-247013 Sequentis 53 12 US-10-424-599-247013 Sequentis 53 12 US-10-424-599-247013 Sequentis 53 12 US-10-424-599-247013 Sequentis 53 12 US-10-424-599-247013 Sequentis 53 US-10-424-599-247013 Sequentis 53 US-10-424-599-247013 Sequentis 53 US-10-424-599-247013 Sequentis 53 US-10-424-599-247013 Sequentis 54 US-10-424-499-248010 Sequentis 54 US-10-424-499-248010 Sequentis 54 U	1.8 54 12 US-10-424-599-149472 Sequent 1.8 55 12 US-10-424-599-149472 Sequent 1.8 56 9 US-09-864-761-49022 Sequent 1.8 56 10 US-09-864-761-49022 Sequent 1.8 56 10 US-09-764-891-3081 Sequent 1.8 57 12 US-10-424-599-177427 Sequent 1.8 57 12 US-10-424-599-177427 Sequent 1.8 57 12 US-10-424-599-177427 Sequent 1.8 57 14 US-10-424-599-195329 Sequent 1.8 60 12 US-10-424-599-195329 Sequent 1.8 60 12 US-10-424-599-195329 Sequent 1.8 60 12 US-10-424-599-195329	62 12 US-10-424-599-211257 Sequent 63 12 US-10-424-599-211257 Sequent 64 9 US-10-424-599-285560 Sequent 64 12 US-10-424-599-15823 Sequent 64 12 US-10-424-599-15820 Sequent 65 12 US-10-424-599-15880 Sequent 65 12 US-10-424-599-11560 Sequent 66 12 US-10-424-599-11560 Sequent 67 12 US-10-424-599-11561 Sequent 67 12 US-10-424-599-11670 Sequent 69 12 US-10-424-599-11264 Sequent 69 12 US-10-424-599-12640 Sequent 69 12 US-10-424-599-12640 Sequent 69 12 US-10-424-599-12640 Sequent 69 12 US-10-424-599-26440 Sequent 71 12 US-10-21-172-242 Sequent 72 12 US-10-21-172-242 Sequent 73 11 US-10-282-1224-76423 Sequent 73 11 US-10-424-599-203219 Sequent

Sequence 1, Application No. US20; GENERAL INFORMATION APPLICANT: Targ, Y APPLICANT: Coteley, APPLICANT: Coteley, Applicant	TITLE OF INVENTION FILE REFERENCE: PF: CURRENT APPLICATION CURRENT FILING DATE PRIOR APPLICATION PRIOR FILING DATE PRIOR FILING DATE	ACTION FILE OF THE STATE OF THE	; OTHER INFORMATION. US-10-025-730-1 Query Match Best Local Similarit Matches 337; Conse	Oy 1 MKKOMPLER Db 1 MKKOMPLER OY 61 PPTEAVAC Db 61 PPTEAVAC	Oy 121 AHPHILEN Db 121 AHPHILEN OY 181 SDAFATER Db 181 SDAFATER OY 241 NFAIMTKO Db 241 NFAIMTKO	Qy 301 LIBFLSSI 	Sequence 3, Applicat Publication No. 1082, BAPLICANT: Tang, Y. APPLICANT: Guegles APPLICANT: COLLEY, APPLICANT: GORGONS, TITLE OF INVENTION, FILE REPERENCE: PF. CURRENT APPLICATION, CURRENT FILING DATE, PRIOR PELLING DATE, PRIOR FILING DATE; NUMBER OF SEQ ID N
00000	Sequence 347, App. Sequence 347, App. Sequence 42612, A. Sequence 50, App. Sequence 240972, Sequence 271118,	Sequence 175359, Sequence 186519, Sequence 243645, Sequence 48848, A Sequence 264673, Sequence 264673, Sequence 264673,	2314, Ap 2314, Ap 5472, A 181434, 673, App 30, App	204501, 204501, 554, App 66566, A 194879, 55006, A	Sequence 1832, Ap Sequence 273732, Sequence 178546, Sequence 17579, A Sequence 19556, Sequence 223050, Sequence 987, App Sequence 987, App Sequence 59233, A Sequence 737, App	מ ומ 0.	Sequence 808, App Sequence 1129, Ap Sequence 1129, Ap Sequence 211, App Sequence 211, App Sequence 67031, A Sequence 67031, A Sequence 8569, A Sequence 8642, Ap Sequence 8642, Ap
12 US-10-424-599-266911 12 US-10-424-599-273101 12 US-10-424-599-181030 12 US-10-424-599-186662 12 US-10-424-599-186662 1 US-10-424-599-23529 9 US-09-864-761-37175	9 US-09-99-347 12 US-10-425-114-42612 14 US-10-278-087A-50 12 US-10-424-599-240972 12 US-10-424-599-272118 9 US-09-893-737-26	12 US-10-424-599-175359 12 US-10-424-599-186519 12 US-10-424-599-243645 9 US-09-864-761-48848 15 US-10-24-4-06-38 12 US-10-424-599-264673 15 US-10-108-260A-3137	444444	12 US-10 - 424-599-284501 10 US-09-809-391-554 10 US-09-882-171-554 12 US-10-425-114-6656 15 US-10-080-334-26 12 US-10-424-599-194879 12 US-10-424-599-194879	11 US-09-864-408A-1832 12 US-10-424-599-273732 12 US-10-424-599-178546 9 US-09-764-869-987 12 US-10-424-599-199536 12 US-10-424-599-199536 14 US-10-424-599-199536 15 US-10-027-574-987 15 US-10-227-577-987 12 US-10-227-577-987 12 US-10-424-599-199815 9 US-10-424-599-199815 9 US-10-424-599-199815	12 US-10-282-123-79 12 US-10-424-599-155068 12 US-10-424-599-155068 14 US-10-44-649A-13 14 US-10-144-649A-13 12 US-10-282-122A-76902 12 US-10-424-599-238754 15 US-10-264-237-1997	9 US-09-764-868-808 11 US-09-764-868-808 14 US-09-764-875-1129 15 US-09-774-659-304 10 US-09-96-730-231 12 US-10-425-114-67031 14 US-10-282-122A-5899 15 US-10-282-122A-78668 16 US-10-282-122A-78668 17 US-10-282-122A-78668 18 US-10-291-851-89
		6 1 1 8 1 2 5 6 1 1 8 1 2 5 6 1 1 8 1 2 5 6 6 1 1 8 1 2 5 6 6 1 1 8 1 2 5 6 6 1 1 8 1 2 8 6 6 1 1 8 1 2 8 6 6 1 1 8 1 2 8 6 6 1 1 8 1 2 8 6 6 1 1 8 1 2 8 6 6 1 1 8 1 2 8 6 6 6 1 1 8 1 2 8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	, , , , , , , , , , , , , , , , , , ,	,			4 4 4 4 4 4 4 5 5 5 5 5 5 6
235 234 238 238 240 241	2442 2443 2443 246 247	2 2 2 2 2 2 2 3 2 3 2 3 3 3 3 3 3 3 3 3	255 256 258 259 261 261		. 222222222222222222222222222222222222	1	3 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2

ALIGNMENTS

```
ò
                                                                                                                                                                                                                                                                                                       AQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVBYIS 120
                                                                                                                                                                                                                                                                                                                                            FMLLKGYBAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIA 180
                                                                                                                                                                                                                                                                                                                                                                                  KYISKPENLKIMMNILRDKSPNIQFBAFHVFKVFVASPHKTQPIVBILLKNQPK 300
                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                             FSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKE 60
                                                                                                                                                                                                                                                                 FSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKE
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                           100.0%; Score 337; DB 14; Length 337; ity 100.0%; Pred. No. 0; Servative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFOKERTDDEOFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Y. Tom
gler, Karl J.
lley, Meil C.
gone, Gina A.
ION: CALCIUM BINDING PROTEIN
PF-0635 US
TION NUMBER: US/10/025,730
DATE: 2001-12-18
ON NUMBER: US/09/190,965
TE: 1998-11-13
D NOS: 5
ation US/10025730
20030045466A1
                                                                                                                                                                                                N: 3734805
                                                                                                                                                                               apiens
```

```
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377
    RESULT 5
US-10-025-730-4
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      o;
                                                                                                                              ö
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence: Lexa-ANIC-BP-1; OTHER INFORMATION: fusion protein US-10-239-079-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Gal4-ANIC-BP-1; OTHER INFORMATION: fusion protein US-10-239-079-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                    Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 6.8%; Score 23; DB 14; Length 496; 1 Similarity 100.0%; Pred. No. 2.6e-14; 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
6.8%; Score 23; DB 14; Length 552;
Best Local Similarity 100.0%; Pred. No. 2.8e-14;
Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                             Score 23; DB 14; L
; Pred. No. 1.9e-14;
                                                                                Query Match
6.8%; Score 23; DB .
Best Local Similarity 100.0%; Pred. No. 1.9
Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                          US-10-239-079-5
Sequence 5, Application US/10239079
FULDIcation No US20030148446A1
GENERAL INFORMATION:
APPLICANY: Merock Patent GmbH
TITLE OF INVENTION: ANIC-BP1-ligand
FILE REFERENCE: ANIC-BP1-ligand
CURRENT APPLICATION NUMBER: US/10/239,079
CURRENT FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SSEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ANIC-BF1-ligand
FILE REFERENCE: ANIC-BF1-ligand
FILE REFERENCE: ANIC-BF-1-ligand
CURRENT PEDILGATION NUMBER: US/10/239,079
CURRENT FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 IMTKYISKPENLKLMMNLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456 IMTKYISKPENLKLMMNLLRDKS 478
                                                                                                                                                                    244 IMTKYISKPENLKLMMNLLRDKS 266
                                                                                                                                                                                                              245 IMTKYISKPENLKLMMNLLRDKS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 IMTKYISKPENLKLMMNLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 IMTKYISKPENLKUMMNLLRDKS 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 6, Application US/10239079; Publication No. US20030148446A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
; FEATURE: -
; OTHER INFORMATION: G262934
US-10-025-730-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-239-079-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
4.5%; Score 15; DB 14; L
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.2%; Score 14; DB 14; L
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 14; Conservative 0; Mismatches 0;
                                                                   APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Meil C.
APPLICANT: Gorgone, Gina A.
TITLE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REFERENCE: PF-055 US
CURRENT APPLICATION NUMBER: US/10/025,730
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US/09/190,965
PRIOR APPLICATION NUMBER: US/09/190,965
NUMBER OF SEQ ID NOS: 5
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorley, Meil C.
APPLICANT: Gorgone, Gina A.
TITLE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REFERENCE: PF-0635 US
CURRENT APPLICATION NUMBER: US/10/025,730
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US/09/190,965
PRIOR FILING DATE: 1998-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-425-114-48872
; Sequence 48872, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-025-730-5
, Sequence S, Application US/10025730
; Publication No. US20030045466A1
; GENERAL INFORMATION:
; Sequence 4, Application US/10025730; Publication No. US20030045466A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 LRRQIGTRSPTVEYI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 LRROIGTRSPTVEYI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 LRRQIGTRSPTVEY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 LRRQIGTRSPTVEY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: 91794137
US-10-025-730-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE: -
; OTHER INFORMATION: g1255838
US-10-025-730-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL Program
SEQ ID NO 5
```

; 0

Gaps

; 0

Length 184; 0; Indels

```
Query Match
2.4%; Score 8; DB 12;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 149595
                                                                                                                                                                                                                                                                                                                                                                  145 MLRECIRH 152
                                                                                                                                                                                                                                                                                                                                                                                                                  140 Mireciri 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 LVTLIADL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 LVTLIADL 86
                                                                                                                                            ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-425-114-54669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-369-493-8871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 54669
LENGTH: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 224185, Application US/10424599
Sequence 224185, Application US/10424599
Sublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRESENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 149595, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cou Vihua
APPLICANT: Zhou Yihua
APPLICANT: Zo Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                 APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 48872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.0%; Score 10; DB 12; Length 342;
100.0%; Pred. No. 0.25;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
2.7%; Score 9; DB 12; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT3847_44468C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: LIB3637-244-El_FLI.pep
US-10-425-114-48872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
....nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 AFHVFKVFVA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 AFHVFKVFVA 292
  Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 CGIMLRECI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 CGIMLRECI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-424-599-224185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-10-424-599-149595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-424-599-224185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 224185
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
```

```
US-10-369-493-8871

US-10-369-493-8871

Sequence 8871, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Chor, Yongwell

APPLICANT: Glodman, Barry S.

APPLICANT: Chen, Xianfeng

TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

TITLE OF INVENTION: PLANTS WITH IMPROVED

FILE REFERENCE: 38-10 (52052)

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 47374

LEMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Chou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Can, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.4%; Score 8; DB 15; Length 307; ilarity 100.0%; Pred. No. 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 54669, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Chloroflexus aurantiacus
```

```
US-09-862-027-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
                                                                                                                                                                        ठ
                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Sourist David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaeka, Jack E
APPLICANT: Tabaeka, Jack E
APPLICANT: Tabaeka, Jack E
APPLICANT: Tabaeka, Jack E
APPLICANT: Tabaeka, Jack E
APPLICANT: Tabaeka, Jack E
APPLICANT: Sourist Succession Sourist Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession Succession S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313) B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 55961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                               Query Match
2.4%; Score 8; DB 12; Length 412;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.4%; Score 8; DB 12; Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: LIB3912-007-H10_FLI.pep
US-10-425-114-52177
                                                                                OTHER INFORMATION: Clone ID: LIB3069-003-D7 FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: 701125903_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.4%; Score 8; DB 12
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 55961, Application US/10425114
Publication No. US20040034868A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack
APPLICANT: Tabaska, Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 52177, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 MLRECIRH 266
                                                                                                                                                                                                                                                                                                                                                                                 145 MLRECIRH 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 MLRECIRH 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 MLRECIRH 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Zea mays
ORGANISM: Zea mays
                                                                                                               US-10-425-114-54669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-425-114-52177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-425-114-55961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-425-114-55961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Gao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILLE REPERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR PILLING DATE: 2003-02-28
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEG ID NOS: 47374
                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                       Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hodge, Martin R.

TITLE OF INVENTION: No. US20020142428Alel Kinases and Uses Thereof FILE REFRENCE: 35800/234662
CURRENT APPLICATION NUMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR PILING DATE: 1999-06-30
WUMBER OF SEQ ID NOS: 82
SOFTWARE: FASELSQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.4%; Score 8; DB 15; Length 649; Best Local Similarity 100.0%; Pred. No. 46; Matches 8; Conservative 0; Mismatches 0; Indels
                          Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 923;
                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                        DB 12;
5. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.4%; Score 8; DB 9;
100.0%; Pred. No. 62;
ative 0; Mismatches
                        2.4%; Score 8; DB 1.
100.0%; Pred. No. 36;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                  Sequence 13726, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/09862027
Patent No. US20020142428A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Pseudomonas fluorescens
US-10-369-493-13726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Drosophila melanogaster US-09-862-027-23
Ouery Match
Best Local Similarity 100...
Best Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 RQSLKLLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 ROSLKLLG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 SSGLLVTL 456
                                                                                                                                                                  202 DKASEEVS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 SSGLLVTL 82
                                                                                                                   36 DKASEEVS 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                            US-10-369-493-13726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 16
US-10-238-075-1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 13726
LENGTH: 649
```

.. 0

Gaps

```
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REPERSINCE: 38-21(3523)B
CURRENT APPLICATION WUNBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 165543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.1%; Score 7; DB 12; Length 83; Best Local Similarity 100.0%; Pred. No. 75; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12; Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT_MRT3847_120500C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)..(87)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: 700959026_FLI.pep
US-10-425-114-44450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.1%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 44450
LENGTH: 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 165543, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 220733, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 EAFHVFK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 LEKODKK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 EAFHVFK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 LEKODKK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-424-599-165543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-424-599-220733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-424-599-165543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 220733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                  TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolar IITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of their FILE REFERENCE: BLANDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Est Rosa Thomas J
APPLICANT: About K
APPLICANT: About Solution David K
APPLICANT: About Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 44450, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Stou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 14; Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.1%; Score 7; DB 12; Length 63; Best Local Similarity 100.0%; Pred. No. 59; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_50302C.1.pep US-10-424-599-230655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
2.1%; Score 7; DB 14
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                               CURRENT FILING DATE: 2002-09-10
FRIOR APPLICATION NUMBER: US/10/238,075
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 0003145
FRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: Patentin version 3.1
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 230655, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
Sequence 1453, Application US/10238075
Publication No. US20030148324A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Escherichia coli
                                                                                                                     APPLICANT: I.N.S.E.R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 EAFHVFK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 EILLKNQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 EILLKNÓ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 EAFHVFK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-424-599-230655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-425-114-44450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-238-075-1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
```

ö

Gaps

Gaps

```
Sequence 5213, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide:
FILE REFERENCE: PA005P1
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 194131, Application US/10424599
Sequence 194130, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: About Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICANT: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 194139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (12) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.1%; Score 7; DB 12; Length 102; Best Local Similarity 100.0%; Pred. No. 90; Matches 7; Conservative 0; Mismatches 0; Indels
                                                         2.1%; Score 7; DB 10; Length 99;
100.0%; Pred. No. 88;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_17335C.1.pep US-10-424-599-194139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)..(102)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT PERSONAL FACUS 1970, 106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US/10/106,698
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
SEQ ID NO 5213
LENGTH: 113
                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 HKNPAEI 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 HKNPAEI 17
                                                                                                                                                                                                    59 KEPPTEA 65
                                                                                                                                                                                                                                                                    87 KEPPTEA 93
                                                                                         Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 24
US-10-106-698-5213
US-09-876-997-430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT
                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 430. Application US/09731872

Factor Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
TITLE OF INVENTION FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
CURRENT APPLICATION NUMBER: US/09/876,997
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 1099-12-08
NUMBER OF SEQ ID NOS: 482
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                2.1%; Score 7; DB 12; Length 95; 100.0%; Pred. No. 84; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 99;
                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_41352C.1.pep
US-10-424-599-220733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 9;
100.0%; Pred. No. 88;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 430, Application US/09876997
Publication No. US20030152921A1
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
                                                                                                                                                                                                                         Query Match
Best Local Similarity 100."
Matches 7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens US-09-731-872-430
                                TYPE: PRT ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 KEPPTEA 65
                                                                                                                                                                                                                                                                                                                                                                               77 GLLVTLI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 KEPPTEA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                            67 GLLVTLI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 21
US-09-731-872-430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-876-997-430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Pat
SEQ ID NO 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 430
LENGTH: 99
   LENGTH: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

ö

Gaps

```
RESULT 28
US-10-425-114-56304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                       LOCATION: (13) COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: MISC FEATURE LOCATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATION: (49) COTHER INFORMATIO
                                                                                                                                                                                                                            ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-106-698-5213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ٥;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
2.1%; Score 7; DB 14; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 14; Length 113; 100.0%; Pred. No. 99; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8084, Application US/10156761
| Publication No. US20030119018A1
| GENERAL INFORMATION:
| APPLICANT: OWURA, SATOSHI
| APPLICANT: ISHIKAWA, UNN
| APPLICANT: ISHIKAWA, UNN
| APPLICANT: SHIRAW, HROSHI
| APPLICANT: SHIRAW, HROSHI
| APPLICANT: SHIRAW, HROSHI
| APPLICANT: HATTORY XOSHIYUKI
| APPLICANT: SHIRA, TADAYOSHI
| APPLICANT: HATTORY NOVEL POLYNUCLEOTIDES
| TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
| TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
| TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
| TITLE OF INVENTION: NOVER POLYNUCLEOTIDES
| TITLE OF INVENTION: NOVER: 202-262
| CURRENT FILING DATE: 2001-05-30
| PRIOR FILING DATE: 2001-05-30
| PRIOR FILING DATE: 2001-06-30
| PRIOR FILING DATE: 2001-06-30
| PRIOR FILING DATE: 2001-06-30
| NUMBER OF SEQ ID NOS: 15109
| SEQ ID NO 8084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: ELITRA.014A
CURRENT APPLICATION NUMBER: US/10/282,122A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 59346, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Olsen, Kari
APPLICANT: Zyskind, Undith
APPLICANT: Tyskind, Undith
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Streptomyces avermitilis US-10-156-761-8084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carr, Grant
Yamamoto, Robert
Forsyth, R.
Xu, H.
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 7; Conservative
NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 EEVSKSL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 VAQLAQE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 EEVSKSL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 VAÇLAÇE 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 26
US-10-282-122A-59346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-156-761-8084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
```

```
Sequence 222167, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cov Youngwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION: VANDER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PLICATION NUMBER: 60/200,848
PRIOR PILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2001-02-22
PRIOR PELING DATE: 2001-02-22
PRIOR PELING DATE: 2001-02-22
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PELING DATE: 2001-02-06
PRIOR PELING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PELING DATE: 2001-02-16
PRIOR PELING DATE: 2001-02-16
PRIOR PELING DATE: 2001-02-16
PRIOR PELING DATE: 2001-02-16
PRIOR PELING DATE: 2001-02-16
PRIOR PELING DATE: 2001-03-09
PRIOR PELING DATE: 2001-03-09
PRIOR PELING DATE: 2001-03-09
PRIOR PELING DATE: 2001-03-09
PRIOR PELING DATE: 2001-03-09
PRIOR PELING DATE: 2001-03-09
PRIOR PELING DATE: 2001-03-09
PRIOR PELING DATE: 2001-03-09
PRIOR PELING DATE: 2001-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
2.1%; Score 7; DB 12; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.1%; Score 7; DB 12; Length 147; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_42646C.1.pep
US-10-424-599-222167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 AEIVKIL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 AEIVKIL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32 DKKTDKA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 DKKTDKA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-424-599-222167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-282-122A-59346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 222167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 59346
LENGTH: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 27
```

```
Sequence 173625, Application US/10424599
Publication No US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Avoalic David K
APPLICANT: An William Soy Mucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Mucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 173625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Expansion by the APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Can You we in the APPLICANT: Can You we in the APPLICANT: Can You we in the APPLICANT: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILIS PREPERSION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
                         APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 70029
LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.1%; Score 7; DB 12; Length 165; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_73847C.1.pep
US-10-424-599-256726
                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: UC-ZMFLB73031E03_FLI.pep US-10-425-114-70029
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
2.1%; Score 7; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-424-599-256726
; Sequence 256726, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
     Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 EAFHVFK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 EAFHVFK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 LLVTLIA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 LLVTLIA 73
                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 32
US-10-424-599-173625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 256726
                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 234035, Application US/10424599

Sequence 234035, Application US/10424599

Sequence 234035, Application US/2040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
CAO YOUGH
APPLICANT:
CAO YOUGH
TITLE OF INVENTION:
Plants and Uses Thereof for Plant Improvement
FILE REFREENCE: 32-1(53233)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 234035

LENGTH: 157
                                                                    APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٥;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.1%; Score 7; DB 12; Length 151; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 12; Length 157; 100.0%; Pred. No. 1.38+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Clone ID: PAT_MRT3847_53358C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: 700975650_FLI.pep US-10-425-114-56304
                                                                                                                                                                                                                                                                                          FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 56304
LENGTH: 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-425-114-70029

Sequence 70029, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Screen, Steven E

APPLICANT: Screen, Screen
Sequence 56304, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 DKASEEV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 RHEPLAK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 DKASEEV 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 RHEPLAK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 29
US-10-424-599-234035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-424-599-234035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
```

g ð

```
Merberg, David
Treacy, Maurice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wong, Gordon G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clark, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        272 EAFHVFK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 EAFHVFK 114
                                                                                      151 RHEPLAK 157
                                                                                                                               88 RHEPLAK 94
                                                                                                                                                                                                                        US-10-424-599-158029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-729-674-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-729-674-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                 RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                        ð
                                                                                                                               엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 38325, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Edu, Yihua

APPLICANT: Edu, Vihua

APPLICANT: Cao, Yongwei

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

ITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Dlants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/425,114

WUMBER OF SEQ ID NOS: 73128

SEQ ID NO 38225

LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 221069, Application US/10424599
Sequence 221069, Application US/10424599
Publication No US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Apolic David K
APPLICANT: Can Vinua
APPLICANT: Can Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 221069
LENGTH: 168
                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.1%; Score 7; DB 12; Length 168; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                  2.1%; Score 7; DB 12; Length 168; 100.0%; Pred. No. 1.4e+02; tive 0; Mismatches 0; Indels
                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_127802C.1.pep
US-10-424-599-173625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Clone ID: PAT_MRT3847_41655C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: LIB3242-311-C1_FLI.pep
US-10-425-114-38325
                                                                                                                                                  Query Match
Best Local Similarity 100.(
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Glycine max
LENGTH: 168
TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                             302 IEFLSSF 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 RHEPLAK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 RHEPLAK 94
                                                                                                                                                                                                                                                                                    7 IEFLSSF 13
                                                                                                                                                                                                                                                                                                                                                     RESULT 33
US-10-424-599-221069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-424-599-221069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 34
US-10-425-114-38325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                         요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

```
PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 00048.US1
Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wood, Linda S.
APPLICANT: Parodi, Luis
APPLICANT: Parodi, Luis
APPLICANT: Lind, Peter
TITLE OF INVENTION: No. U
PILE REFERENCE: 00048.US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                      65 AVAQLAQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 AVAQLAQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 LAQELYS 75
                                                                                                                                                                                                                                   ORGANISM: Zea mays
                                                                                                                                                                                          204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 185
                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gарв
                                                           ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                            Sequence 4437, Application US/10108260A;
Publication No. US20040005560A1;
GENERAL INPORMATION:
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA;
FILE REFERENCE: H1-A0106;
CURRENT APPLICATION NUMBER: US/10/108,260A;
CURRENT FILING DATE: 2002-03-27;
NUMBER OF SEQ ID NOS: 5458;
SOFTWARE: Patentin Ver. 2.1;
SEQ ID NO 4437;
LENGTH: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 38
US-10-108-260A-4032
US-10-108-260A-4032
Sequence 4032, Application US/10108260A
Fublication No. US20040005560A1
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 4032
LENGTH: 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.1%; Score 7; DB 15; Length 197; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.1%; Score 7; DB 15; Length 199; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
           Query Match 2.1%; Score 7; DB 9; Length 176; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 45029, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: liu, Jingdong
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-108-260A-4437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4032
                                                                                                231 LIGELIL 237
                                                                                                                                         98 Ligerir 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 ILEKODK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 ILEKODK 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 LYSSGLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 LYSSGLL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 39
US-10-425-114-45029
                                                                                                                                                                                                          RESULT 37
US-10-108-260A-4437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
```

```
THE CONTROL TO TABLES AND AGE E

THE CONTROL TO TABLES AND AGE E

THE CONTROL TO TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES AND TABLES
```

```
TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 EKLLQSE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 EKLLÖSE 119
                                                                                                                                                                                                                                                          211 EAVAQLA 217
                                                                                                                                                                                                                64 EAVAOLA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 44
US-10-424-599-179206
                                                                                                                                                                                                                                                                                                                                             US-10-424-599-203478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 179206
LENGTH: 245
    SEQ ID NO 8653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                      LENGTH:
                                                                                                                                                                                                                                                                                                                         RESULT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 7; DB 15; Length 217; 100.0%; Pred. No. 1.8e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NAGAL KEILCHI
APPLICANT: TAMGALI KEILCHI
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAGHIKO
APPLICANT: OCHIKAMA, TSUTOMU
APPLICANT: OCHIKAMA, TSUTOMU
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHORI, NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: 06/350,435
PRIOR APPLICATION NUMBER: 06/350,435
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2002-01-14
PRIOR FILING DATE: 2001-09-14
NUMBER: OF SEQI DI NOS: 3381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: BHIRAM, HIROSHI
APPLICANT: SHIRAM, HIROSHI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: SAKAKI, YOSHIVUKI
APPLICANT: BATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: UP 2001-272697
PRIOR PRILING DATE: 2001-06-30
PRIOR PRILING DATE: 2001-06-30
PRIOR PRILING DATE: 2001-06-30
PRIOR PRILING DATE: 2001-06-30
PRIOR PRILING DATE: 2001-06-30
PRIOR PRILING DATE: 2001-06-30
PRIOR PRILING DATE: 2001-06-30
PRIOR PRILING DATE: 2001-06-30
                                                                                                                        Sequence 2522, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8653, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
                                                                                                                                                                                                         SUGIYAN, TOMOYASU
OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOYO, JUN-ICHI
ISONO, YUUKO
HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2522
LENGTH: 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   OTSUKA, KAORU
                                                                                                                                                                                            APPLICANT: ISOGAI, TAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 NLAILEK 27
||||||||
21 LAQELYS 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 42
US-10-156-761-8653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-094-749-2522
                                                                                                         US-10-094-749-2522
                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                           APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                      g
```

```
DepLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Experiment David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Indua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
UURBER PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                         .,
                                                                                                                           Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
2.1%; Score 7; DB 12; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
COTHER INFORMATION: Clone ID: PAT_MRT3847_13283C.1.pep US-10-424-599-179206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Clone ID: PAT_MRT3847_25767C.1.pep
US-10-424-599-203478
                                                                                                                     Query Match
2.1%; Score 7; DB 14; Le
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)..(243)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 179206, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 203478, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8653
```

ó;

Gaps

.; 0

```
Sequence 328, Application US/10080170
Publication No. US20030129601A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT PILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.1%; Score 7; DB 14; Length 275; Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT PEPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PEPLICATION NUMBER: 06/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-29
PRIOR PILING DATE: 2000-10-29
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 52103, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Manney, Liangsu
APPLICANT: Malnow, Chery1
APPLICANT: Haeelbeck, Robert
APPLICANT: Haeelbeck, Robert
APPLICANT: Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Mycobacterium leprae
                                Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.1
                                                                   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 ILKDNLA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 ILKDNLA 80
                                                                                                                                                                                                    87 QAMKEIL 93
                                                                                                                                    47 QAMKEIL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-282-122A-52103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-080-170-328
                                                                                                                                                                                                                                                                                                                                            US-10-080-170-328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                       à
                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 151467, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                       ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: POLYNUCLECTIDE ENCODING AN ACTIVATED HUMAN
TITLE OF INVENTION: T-LYMPHOCYTE-DERIVED PROTEIN RELATED TO UBIQUITIN
TITLE OF INVENTION: T-LYMPHOCYTE-DERIVED PROTEIN RELATED TO UBIQUITIN
TITLE OF INVENTION: CONJUGATING ENZYME
FILE REFERENCE: D00341p
CURRENT APPLICATION NUMBER: US/10/005,549
CURRENT FILING DATE: 2001-10-29
PRIOR PELING DATE: 2001-07-30
PRIOR PELING DATE: 2000-10-30
PRIOR PILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-30
SOFTWARE: PACHICLIN VOS: 5:
SOFTWARE: PACHICLIN VOS: 5:
SEQ ID NO 17
IVPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                       Gaps
                                                                                                                                       ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 14; Length 245; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 12; Length 251;
                                                                2.1%; Score 7; DB 12; Length 245; 100.0%; Pred. No. 2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_107798C.1.pep
US-10-424-599-151467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 38-21(5323) B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 15:467 LENGTH: 251
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 17, Application US/10005549; Publication No. US20030190613A1; GENERAL INFORMATION:
APPLICANT: BOWEN, MICHAEL A.
APPLICANT: WU, YULI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: YANG, WEN-PIN
APPLICANT: FINGER, JOSHUA
APPLICANT: CARROLL, PAMELA
APPLICANT: FEDER, JOHN
                                Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100...
Fines 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 NLAILEK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 NLAILEK 30
                                                                                                                                                                                                           17 IVKILKD 23
                                                                                                                                                                                                                                                             21 IVKILKO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-424-599-151467
                                                                                                                                                                                                                                                                                                                                                                                RESULT 45
US-10-005-549-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-005-549-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                               δ
```

```
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: And Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short Short S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 72787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.1%; Score 7; DB 12; Length 338; Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_53767C.1.pep
US-10-424-599-234484
                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: LIB3354-066-B6_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 2.1%; Score 7; DB 12; Le Local Similarity 100.0%; Pred. No. 2.6e+02; Pred. 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 234484, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 51574, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 LEKODKK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 VSKSLQA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 VSKSLQA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 LEKQDKK 34
                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-282-122A-51574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-424-599-234484
                                                                                                                                                                                                                                                                                                                                                                                                        US-10-425-114-72787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Show Yihua
APPLICANT: Can Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 209662
LENGTH: 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING.DATE: 2000-12-22
PRIOR FILING.DATE: 2000-12-22
PRIOR PRICHATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
LENGTH: 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 12; Length 282; 100.0%; Pred. No. 2.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.1%; Score 7; DB 12; Length 337 Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_31352C.1.pep
US-10-424-599-209662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (1)..(337)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 209662, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 72787, Application US/10425114 ; Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100. Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 ROSLKLL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 EAFHVFK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 EAFHVFK 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 ROSLKLL 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-424-599-209662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-282-122A-52103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-425-114-72787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 50
```

```
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhou, Yibhua Shavid K.
APPLICANT: Zhou, Yibhua Shavid K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 73128
LENGTH: 351
LENGTH: 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
             CURRENT FILING DATE: 2003-02-0
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-05-07
PRIOR PILING DATE: 2000-05-07
PRIOR PILING DATE: 2000-10-27
PRIOR PLING DATE: 2000-10-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2001-12-27
PRIOR PLING DATE: 2001-12-27
PRIOR PLING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 12; Length 351; 100.0%; Pred. No. 2.7e+02; ttive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.1%; Score 7; DB 12; Length 344 Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: Clone ID: 700170954_FLI.pep
US-10-425-114-46025
CURRENT APPLICATION NUMBER: US/10/282,122A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 46025, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Clostridium acetobutylicum US-10-282-122A-51574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 FDIASDA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 FDIASDA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      335 EIVKILK 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 EIVKILK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 53
US-10-425-114-46025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
```

```
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT PELICAND NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 7; DB 12; Length 360; 100.0%; Pred. No. 2.8e+02; Arive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_79416C.1.pep
US-10-424-599-262896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
2.1%; Score 7; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: 700865271_FLI.pep
US-10-425-114-41971
                                               ; Sequence 262896, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-425-114-47953

Sequence 47953, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-425-114-41971
Sequence 41971, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 SLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325 SLKLLGE 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 SLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 SLKLLGE 327
RESULT 54
US-10-424-599-262896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 41971
```

us-10-025-730-1.oligo.rapb

Page 17

```
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Grack Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 68619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COTATION: (25)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEX: MISC FEATURE
LOCATION: (38)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-4458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.1%; Score 7; DB 12; Length 391; Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.1%; Score 7; DB 14; Length 374; Best Local Similarity 100.0%; Pred. No. 2.9e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: UC-ZMFLMO17048B05_FLI.pep
                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patentin Ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 68619, Application US/10425114; Publication No. US20040034888A1
GENERAL INFORMATION: APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 37084, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou, Yihua
Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 NLAILEK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 AQLAQEL 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 AQLAQEL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-425-114-68619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-425-114-68619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 60
US-10-425-114-37084
                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 4458
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4458, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: PO02-03-27
PRIOR PILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
ug-10-025

APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Baska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Gao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 47953
LENGTH: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Greven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianteng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFIEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: 2003-02-28
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

2.1%; Score 7; DB 15; Length 373;
Best Local Similarity 100.0%; Pred No. 28e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.1%; Score 7; DB 12; Length 360; Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: 700909018_FLI.pep
US-10-425-114-47953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 42
LENGTH: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 42, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Aquifex aeolicus
US-10-369-493-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 SLKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 PKLIEFL 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 SLKLLGE 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 58
US-10-106-698-4458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-369-493-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

ö

Gaps

ö

Gaps

```
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With FITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313) B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128 SEQ ID NO 37084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: YANG, WEN-PIN
APPLICANT: FINGER, JOSHUA
APPLICANT: RINGER, JOSHUA
APPLICANT: NADLER, STEVEN
APPLICANT: CARROLL, PAMELA
APPLICANT: CARROLL, PAMELA
APPLICANT: CARROLL, PENER, JOSH
TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING AN ACTIVATED HUMAN
TITLE OF INVENTION: T-LYMPHOCYTE-DERIVED PROTEIN RELATED TO UBIQUITIN
TITLE OF INVENTION: CONJUGATING ENZYME
TITLE OF INVENTION: CONJUGATING ENZYME
TITLE OF INVENTION: CONJUGATING ENZYME
CURRENT APPLICATION NUMBER: US/10/005,549
PRIOR APPLICATION NUMBER: 60/308,706
PRIOR PLILING DATE: 2001-07-30
PRIOR PLILING DATE: 2001-07-30
PRIOR PLILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 14; Length 422;
100.0%; Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                     2.1%; Score 7; DB 12; Length 399; 100.0%; Pred. No. 3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: LIB3242-059-D4_FLI.pep US-10-425-114-37084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10307928A

Publication No. US20030229016A1

GENERAL INFORMATION:

APPLICANT: Anderson, David W.

APPLICANT: Boldog, Ferenc L.

APPLICANT: Burgess, Catherine E.

APPLICANT: Catterton, Elina

APPLICANT: Edinger, Shlomit R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10005549; Publication No. US20030190613A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BOWEN, MICHAEL A. APPLICANT: WU, YULI
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 NLAILEK 232
                                                                                                                                                                                                                                                                                                                                                                                                               151 RHEPLAK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 RHEPLAK 325
                                                                                                                                                                                       TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE.
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-307-928A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-005-549-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-005-549-2
                                                                                                                                                                 LENGTH: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
APPLICATION NUMBER: 05/341,477
PRIOR FILING DATE: 2001-12-17
PRIOR FILING DATE: 2001-12-17
PRIOR PLICATION NUMBER: 60/341,477
PRIOR PLILING DATE: 2001-12-17
PRIOR PLILING DATE: 2001-12-17
PRIOR PLILING DATE: 2001-12-17
PRIOR PLILING DATE: 2001-12-17
PRIOR PLILING DATE: 2001-12-17
PRIOR PLILING DATE: 2001-12-17
PRIOR PLILING DATE: 2001-12-20
PRIOR PLILING DATE: 2001-12-30
PRIOR PLILING DATE: 2001-12-30
PRIOR PLILING DATE: 2001-12-31
PRIOR FILING DATE: 2001-12-31
PRIOR PLILING DATE: 2002-04-17
PRIOR PLILING DATE: 2002-04-17
PRIOR PLILING DATE: 2002-05-15
PRIOR PLILING DATE: 2002-05-15
PRIOR PLILING DATE: 2002-05-17
PRIOR PLILING DATE: 2002-05-17
PRIOR PLILING DATE: 2002-05-17
PRIOR PLILING DATE: 2002-05-17
PRIOR PLILING DATE: 2002-05-17
PRIOR PLILING DATE: 2002-05-17
PRIOR PLILING DATE: 2002-05-17
PRIOR PLILING DATE: 2002-05-17
PRIOR PLILING DATE: 2002-05-17
PRIOR PLILING DATE: 2002-05-17
PRIOR PLILING DATE: 2002-05-17
PRIOR PLILING DATE: 2002-05-17
PRIOR PLILING DATE: 2002-05-17
PRIOR PLILING DATE: 2002-05-17
PRIOR PLILING DATE: 2002-05-17
PRIOR PLILING DATE: 2002-05-18
PRIOR PLILING DATE: 2002-05-18
PRIOR PLILING DATE: 2002-05-19
PRIOR PLILING DATE: 2002-05-19
PRIOR PLILING DATE: 2002-05-19
PRIOR PLILING DATE: 2002-05-19
PRIOR PLILING DATE: 2002-05-19
PRIOR PLILING DATE: 2002-05-19
PRIOR PLILING DATE: 2002-05-19
PRIOR PLILING DATE: 2002-05-19
PRIOR PLILING DATE: 2002-05-19
PRIOR PLILING DATE: 2002-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 53 SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.2e+02;
es 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.1%; Score 7; DB 15; Best Local Similarity 100.0%; Pred. No. 3.2e+05 Matches 7; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 59712, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                     Guo, Xiaojia (Sasha)
Ji, Weizhen
Kekuda, Ramesh
                                                                                                                                                               Rieger, Daniel K.
Shenoy, Suresh G.
Spytek, Kimberly A.
Vernet, Cotine A.M.
Voss, Edward Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
                                                                                                         Li, Li
Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trawick, John
Gorman, Linda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Liangsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 NLAILEK 232
                                                                                                                                                                                                                                                                                                                  Zhong, Mei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 NLAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-282-122A-59712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-307-928A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
Sequence 859, Application US/10238075
Publication No. US20030148324A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: E.Coli, and biological uses of these polynucleotides and of their FILE REFERENCE: BLANDINE
CURRENT FILING DATE: 2002-09-10
FRIOR FERENCE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 221067, Application US/10424599; Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Terry, Roemer D.
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 8000
SOUTHWARE: ParentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.1%; Score 7; DB 14; Length 458; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.1%; Score 7; DB 14; Length 452; Best Local Similarity 100.0%; Pred. No. 3.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7310, Application US/10032585 Publication No. US20030180953A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 FADEKNY 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 FADEKNY 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 DIASDAF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 DIASDAF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-424-599-221067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 66
US-10-032-585-7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-032-585-7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-238-075-859
                                                                                                                                                          US-10-238-075-859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 7310
LENGTH: 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37583, Application US/10425114

Publication No. US2004003488A1

Publication No. US2004003488A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Xihua

APPLICANT: APPLICANT: Soreen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Boren E

APPLICANT: Boren E

APPLICANT: Boren E

APPLICANT: Boren E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen, Steven E

APPLICANT: Soreen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ö
GURENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-06
PRIOR PLING DATE: 2000-05-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-22
PRIOR PLING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 12; Length 448; 100.0%; Pred. No. 3.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Clone ID: LIB3960-022-A8_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
2.1%; Score 7; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 HNFAIMT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 LYSSGLL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 HNFAIMT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 LYSSGLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-282-122A-59712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-425-114-37583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-425-114-37583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 37583
LENGTH: 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

ô

us-10-025-730-1.oligo.rapb

```
ENGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence; No. US20030077587Ale = OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·
0
                                                                                                                                                                                                                                                                                                                                                               .<u>`</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stone, Budin M.
APPLICANT: Sheffield, Val C.
APPLICANT: Sheffield, Val C.
APPLICANT: Fingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
FILE REFRENCE: 21087.0017011
CURRENT APPLICATION NUMBER: US/09/952,464A
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 09/473,273
PRIOR APPLICATION NUMBER: 09/461,542
PRIOR APPLICATION NUMBER: 09/366,952
PRIOR APPLICATION NUMBER: 09/366,952
PRIOR PILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1999-08-04
PRIOR FILING DATE: 1997-03-21
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 490
                                                                                                                                                                                                                                                                                                       Query Match 2.1%; Score 7; DB 12; Length 488; Best Local Similarity 100.0%; Pred. No. 3.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.1%; Score 7; DB 10; Length 490; Best Local Similarity 100.0%; Pred. No. 3.6e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_41653C.1.pep
US-10-424-599-221067
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 221067
LENGTH: 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 38253, Application US/10425114
; Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 10, Application US/09952464A; Publication No. US20030077587A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 NLLRDKS 136
                                                                                                                                                                                 ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                151 RHEPLAK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   408 RHEPLAK 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-425-114-38253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 68
US-09-952-464A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-952-464A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT
                                                                                                                                                         TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

```
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 38253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09952464A
; Publication No. US20030077587A1
; GENERAL INFORMATION:
; APPLICANT: Stone, Edwin M.
; APPLICANT: Stone, Edwin M.
; APPLICANT: Sheffield, Val C.
; APPLICANT: Fingert, John
; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
; FILE REFERENCE: 21087-0017011
; FILE REFERENCE: 21087-0017011
; FILE REFERENCE: 21087-0017011
; FILE REFERENCE: 10017011
; PRIOR PELICATION NUMBER: 09/461,542
; PRIOR PILING DATE: 1999-12-18
; PRIOR PILING DATE: 1999-12-15
; PRIOR PILICATION NUMBER: 09/366,952
; PRIOR APPLICATION NUMBER: 09/366,952
; PRIOR PILICATION NUMBER: 09/366,952
; PRIOR PILICATION NUMBER: 09/366,952
; PRIOR PILICATION NUMBER: 09/366,952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.1%; Score 7; DB 10; Length 504 Best Local Similarity 100.0%; Pred. No. 3.7e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Richards, Julia
APPLICANT: Rozsa, Frank
TITLE OF INVENTION: Detecting and Treating Eye Disease
FILE REPERENCE: UM 06105
                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: LIB3106-102-C2_FLI.pep
US-10-425-114-38253
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
2.1%; Score 7; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/844,653
CURRENT FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin version 3.0
SEQ ID NO 173
LENGTH: 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 173, Application US/09844653 Publication No. US20030054347A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRGANISM: Homo sapiens US-09-844-653-173
                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 RHEPLAK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 RHEPLAK 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-844-653-173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-952-464A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
```

```
OTHER INFORMATION: Description of Artificial Sequence; No. US20030077587Ale = OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10086135

Publication No. US20020182677A1

Publication No. US20020182677A1

GAPPLICANT: Sheppard, Paul O.

APPLICANT: Chandrasekher, Yasmin A.

TITLE OF INVENTION: PANCREATIC AND COVARIAN POLYPEPTIDE

TITLE OF INVENTION: 2S1G58

FILE REFERENCE: 98-24

CURRENT FILING DATE: 2002-02-26

PRIOR PILING DATE: EARLIER FILING DATE: 1999-08-03

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/366,448

PRIOR PLING DATE: EARLIER FILING DATE: 1999-08-03

PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-03

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4

LENTHERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Pu
APPLICANT: Chen, Pu
APPLICANT: Chen, Pu
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
TITLE OF INVENTION: Disorders
FILE REFERENCE: 07425.0057.U801
CURRENT APPLICATION NUMBER: US/10/244,633
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: US/59/306,828
PRIOR FILING DATE: 1999-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
2.1%; Score 7; DB 10; Length 504;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.1%; Score 7; DB 13; Le Best Local Similarity 100.0%; Pred. No. 3.7e+02; Matches 7; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: 08/822,999
PRIOR FILING DATE: 1997-03-21
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-244-633-32
; Sequence 32, Application US/10244633
; Publication No. US20030068640A1
; GENERAL INFORMATION:
                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                              US-09-952-464A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-086-135-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
APPLICANT: Liu, Jingdong
APPLICANT: Zhou Xihua
APPLICANT: Shous Xihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Solation E
APPLICANT: Screen, Solation E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 18-21(3313)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 55451
LENGTH: 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.1%; Score 7; DB 14; Length 504 Best Local Similarity 100.0%; Pred. No. 3.7e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: UC-GMFLMINSOY077B08_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION AND APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATION APPLICATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 12; Le
100.0%; Pred. No. 3.7e+02;
tive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 09/227,881
PRIOR FILING DATE: 1999-01-11
NUMBER OF SEQ ID NOS: 38
SCFTWARE: Microsoft Word 97
SEQ ID NO 32
LENGTH: 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 55451, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 124, Application US/09800729; Patent No. US20020068319A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 RHEPLAK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      428 RHEPLAK 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-425-114-55451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 74
US-10-425-114-55451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-800-729-124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 124
LENGTH: 514
                                                                                                                                                                                                                                                                                                                                                                               US-10-244-633-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
```

425 RHEPLAK 431

ПЪ

```
Sequence 1163, Application US/10389566;
Sequence 1163, Application US/10389566;
Publication No. US20040025202A1;
GENERAL INFORMATION:
APPLICANT CARNOT Technology, LLC
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants;
FILE REFREENCE: 34-77(5290)D
CURRENT APPLICATION NUMBER: US/10/389,566
CURRENT FILING DATE: 2003-03-31
PRIOR FILING DATE: 2003-03-31
PRIOR PILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/385,301
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: PACENTIN VERSION 3.2
                                                                                                                                                                                      APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFRENCE: 38-77 ($2.900)
CIRRENT APPLICATION NUMBER: US/10/389,566
CURRENT APPLICATION NUMBER: US 60/365,301
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
PRIOR FLIING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR FLIING DATE: 2002-06-26
NUMBER: OS 50/392,018
PRIOR FLIING DATE: 2002-06-26
NUMBER: OS 50/392,018
STORF FLIING DATE: 2002-06-35
SOFTWARE: PATENTION DATE: 2002-06-26
NUMBER: OS 50/392,018
PRIOR PATENT SAFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 16; Length 534;
100.0%; Pred. No. 3.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 16; Length 534; 100.0%; Pred. No. 3.9e+02; vative 0; Mismatches 0; Indels
                                                                                                              Sequence 822, Application US/10389566 Publication No. US20040025202Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.13
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 EIVKILK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 EIVKILK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 EIVKILK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 EIVKILK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-389-566-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-389-566-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-389-566-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1163
LENGTH: 534
                                                                                           US-10-389-566-822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 822
LENGTH: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 79
                                                                   RESULT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Anou Yihua
APPLICANT: Cano Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21/3223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.1%; Score 7; DB 12; Length 524; Best Local Similarity 100.0%; Pred. No. 3.88+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
2.1%; Score 7; DB 11; Length 514;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                        2.1%; Score 7; DB 9; Length 514;
100.0%; Pred. No. 3.8e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; CTHER INFORMATION: Clone ID: PAT_MRT3847_41039C.1.pep
US-10-424-599-220386
                                                                                                                                                                                                                                                                                     US-09-033-245-2221
Sequence 2221, Application US/09833245
Publication No. US20040010134A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Abbumin Fusion Proteins
FILE REFERENCE: PF546FCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 2221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 220386, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                        Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRGANISM: Homo sapiens
US-09-833-245-2221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 RHEPLAK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              392 VAQLAQE 398
                                                                                                                                                                                                 392 VAQLAQE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 VAQLAQE 72
                                                                                                                                                   66 VAQLAQE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-220386
US-09-800-729-124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
```

δ d

ö

.. 0

ö

Gaps ö

US-10-369-493-14077

```
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 84
US-10-389-566-2425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-389-566-1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Squence 68937, Application US/10425114

Squence 68937, Application No. US2004003488A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: APPLICANT: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38 -21(53313)B
CURRENT APPLICATION NUSSER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128

LENGTH: 559
                                                                 APPLICANT: Go, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVEXTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF FILE REPRENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
FRICR APPLICATION NUMBER: US 60/360,039
FRICR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 14077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.1%; Score 7; DB 12; Length 559; Best Local Similarity 100.0%; Pred. No. 4.18+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.1%; Score 7; DB 15; Length 558; Best Local Similarity 100.0%; Pred. No. 4.1e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: UC-ZMFLMO17058D11_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)..(558)
CIHER INFORMATION: unsure at all Xaa locations
US-10-369-493-14077
Sequence 14077, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 93, Application US/10407866
; Publication No. US20040002593A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441 AVAQLAQ 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      543 AQLAQEL 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 AVAQLAQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 AQLAQEL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-425-114-68937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-425-114-68937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 82
US-10-407-866-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
Sequence 1261, Application US/10389566

Publication No. US20040025202A1

GENERAL INPORMATION:

APPLICANT: Monsanto Technology, LLC

APPLICANT: Laurie, Cathy C

TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants

FILE REFERENCE: 38-77(5290) 389,566

CURRENT APPLICATION NUMBER: US/10/389,566

CURRENT FILING DATE: 2003-03-15

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-25

PRIOR FILING DATE: 2002-06-26

NUMBER OF SEQ ID NOS: 2459

SOFTWARE: Patentin version 3.2

LENGTH: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2425, Application US/10389566
Publication No. US20040025202A1
GENERAL INFORMATION:
APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REFERENCE: 38-77 (52900) D
CURRENT APPLICATION NUMBER: US/10/389,566
CURRENT FILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/365,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
APPLICANT: Reed, John C.
APPLICANT: Reed, John C.
APPLICANT: Godzik, Adam
TITLE OF INVENTION: PAAD Domain-Containing Polypeptides,
TITLE OF INVENTION: Bacoding Nucleic Acids, and Methods of Use
FILE REFERENCE: 66654-10(LJ 5755)
CURRENT APPLICATION NUMBER: US/10/407,866
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 60/370,538
PRIOR FILING DATE: 2002-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 2.1%; Score 7; DB 15; Length 571; Local Similarity 100.0%; Pred. No. 4.2e+02; Pred 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 7; DB 16; Length 575; 100.0%; Pred. No. 4.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 93
LENGTH: 571
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-389-566-1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Mus musculus
US-10-407-866-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 LTRHKVL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 LTRHKVL 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 EILLKAN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 EILLKNQ 40
```

```
US-10-369-493-12179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 64320
LENGTH: 637
           SEQ ID NO 66875
                               LENGTH: 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Surveyer

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8

CURRENT APPLICATION WNDER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Monsanto Technology, LLC
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
FILE REPERENCE: 38-77 (5290) D
CURRENT APPLICATION NUMBER: US/10/389,566
CURRENT PILING DATE: 2003-03-31
PRIOR APPLICATION NUMBER: US 60/365,301
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
NUMBER OF SEQ ID NOS: 2459
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.1%; Score 7; DB 16; Length 576; Best Local Similarity 100.0%; Pred. No. 4.2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                              Query Match 2.1%; Score 7; DB 16; Length 575; Best Local Similarity 100.0%; Pred. No. 4.2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/392,018
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: PALENTIN VEYSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 66875, Application US/10425114
; Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1939, Application US/10389566; Publication No. US20040025202A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Arabidopsis thaliana
US-10-389-566-1939
                                                                                                                                                                                                                                                                             ORGANISM: Arabidopsis thaliana US-10-389-566-2425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 EILLKNQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 EILLKNQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 EILLKNO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 EILLKNO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-425-114-66875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-389-566-1939
                                                                                                                                                                                              SEQ ID NO 2425
LENGTH: 575
                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
Sequence 64320, Application US/10425114

Sequence 64320, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 30-21(53313) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQUENCE: 73128
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12179, Application US/10369493
; Sequence 12179, Application US/10369493
; Publication No. US20030233675A1
; Genbraal Information:
    APPLICANT: Gao, Yongwei
; APPLICANT: Gaiter, Steven C.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Goldman, Barry S.
; TITLE OF INVENTION: ELANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)8
; FILE REPERENCE: 2003-02-28
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICANION NUMBER: US 60/360,039
; PRIOR APPLICATION NUMBER: US 60/360,039
                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 15; Length 631;
100.0%; Pred. No. 4.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                         2.1%; Score 7; DB 12; Length 628; 100.0%; Pred. No. 4.5e+02; tive 0; Mismatches 0; Indel8
                                                FEATURE:
, OTHER INFORMATION: Clone ID: UC-ZMFLMO17161E07_FLI.pep
US-10-425-114-66875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: LIB3632-018-C12_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Mesorhizobium loti
                                                                                                                          Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12179
LENGTH: 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 DIASDAF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 DIASDAF 139
                                                                                                                                                                                                                                                                                           612 AQLAQEL 618
                                                                                                                                                                                                                                             67 AQLAQEL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays
TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                     RESULT 87
US-10-369-493-12179
```

g

ö

```
Sequence 2001, Application US/10369493
; Publication No. US2003023367541
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Galater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)8
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2071
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
       Indels
       ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
2.1%; Score 7; DB 15; Le
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 7; Conservative 0; Mismatches 0;
       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Agarwal, Pankaj
APPLICANT: Cogswell, John P.
APPLICANT: Kabnic, Kazen S.
APPLICANT: Kabnic, Kazen S.
APPLICANT: Lai, Ying-Ta
APPLICANT: Martensen, Shelby A.
APPLICANT: Martensen, Shelby A.
APPLICANT: Smith, Randall F.
APPLICANT: Smith, Randall F.
APPLICANT: Xiang, Zhaoying
APPLICANT: Xiang, Zhaoying
APPLICANT: Xia, Qing
APPLICANT: Xie, Qing
APPLICANT: Kizni, Safia K.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP50029
CURRENT APPLICATION NUMBER: US/10/312,088
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 60/213,161
PRIOR APPLICATION NUMBER: 60/213,161
PRIOR APPLICATION NUMBER: 60/213,161
PRIOR APPLICATION NUMBER: 60/213,161
PRIOR APPLICATION NUMBER: 60/213,161
PRIOR PILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 44
SEOTEMARE: PASSESEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Schizosaccharomyces pombe US-10-369-493-2071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34, Application US/10312088 Publication No. US20030219862A1 GENERAL INFORMATION:
     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-10-312-088-34
                                                    195 KVLVADF 201
                                                                                               519 KVLVADF 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 ADLQLID 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 ADLQLID 90
                                                                                                                                                                   RESULT 91
US-10-369-493-2071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-10-312-088-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 92
                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Sereen, Steven E
APPLICANT: Gereen, Steven E
APPLICANT: Gareen, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: APPLICANT: And E
APPLICANT: APPLICANT: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313)B
CURRENT PRPLICATION NUMBER: US/10/425,114
CURRENT FILING DAITS: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 72475
LENGTH: 637
                                                                                                    ö
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/10086464

Sequence 8, Application US/10086464

Publication No. US20020199218A1

GENERAL INFORMATION:

APPLICANT: GORING.
Daphne R. et al.

TILLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES

FILE REFERENCE: P 25,762-A USA

CURRENT APPLICATION NUMBER: US/10/086,464

CURRENT APPLICATION NUMBER: US 10/069,304

PRIOR PILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: PCT/CA00/00966

PRIOR FILING DATE: 1000-08-18

PRIOR FILING DATE: 1999-08-19

PRIOR FILING DATE: 1999-10-13

PRIOR FILING DATE: 1999-10-13

SEQ ID NOS: 27

SEQ ID NOS: 27

LENGTH. 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                               2.1%; Score 7; DB 12; Length 637; 100.0%; Pred. No. 4.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 12; Length 637;
100.0%; Pred. No. 4.6e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.1%; Score 7; DB 13; Length 731; Best Local Similarity 100.0%; Pred. No. 5.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Clone ID: UC-ZMFLB73106C12_FLI.pep
                                                                                                                                                                                                                                                                                       US-10-425-114-72475
Sequence 72475, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-086-464-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.v
                      Query Match
Best Local Similarity 100...
7; Conservative
                                                                                                                                                                                          284 LYSSGLL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 LYSSGLL 290
                                                                                                                                          73 LYSSGLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 LYSSGLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-10-425-114-72475
US-10-425-114-64320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-086-464-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                RESULT 89
```

ò

```
ö
                                                                                                                                                                                                                                                                  PERSILT 93

103-10-176-50

103-10-176-50-60

104-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50-60

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-50

105-10-176-70

105-10-176-70

105-10-176-70

105-10-176-70

105-10-176-70

105-10-176-70

105-10-176-70

105-10-176-70

105-10-176-70

105-10-176-70

105-10-176-70

105-10-176-70

105-10-176-70

105-10-176

105-10-176

105-10-176

105-10-176

105-10-176

105-10-176

105-10-176

105-10-176

105-10-176

105-10-176

105-10-176

105-10-176

105-10-176

105-10-176

105-10-176

105-10-176

105-10
                                                                          Gaps
                                                                          .
0
   Length 855;
                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
2.1%; Score 7; DB 14; Le
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 7; Conservative 0; Mismatches 0;
   DB 15; Le
Query Match 2.1%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 5.9
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                      75 SSGLLVT 81
                                                                                                                                                                                 77 SSGLLVT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-176-306-80
                                                                                                                                                                                                   q
```

```
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.1%; Score 7; DB 15; Length 888; 100.0%; Pred. No. 6.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/312,088
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: PCT/US01/19929
PRIOR FILING DATE: 2001-06-22
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PSECEN FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PSECEN FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PSECEN FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PSECEN FILING DATE: BELSEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 69966, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Hagelbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
                Sequence 38, Application US/10312088
Publication No. US20030219862A1
GENERAL INPORMATION:
APPLICANT: Agarwall, Pankaj
APPLICANT: Cogswell, John P.
APPLICANT: Kabnic, Karen S.
APPLICANT: Lai, Ying-Ta
APPLICANT: Martensen, Shelby A.
APPLICANT: Martensen, Shelby A.
APPLICANT: Mith, Randall F.
APPLICANT: Sinit, Yandall F.
APPLICANT: Strum, Jay C.
APPLICANT: Xiang, Zhaoying
APPLICANT: Xiang, Zhaoying
APPLICANT: Rizni, Safia K.
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GPS0029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 SSGLLVT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 SSGLLVT 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 95
US-10-282-122A-69986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu, H
US-10-312-088-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-312-088-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
```

Gaps

ö

0; Indels

g

Length 873;

ò

```
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-282-122A-69548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-369-493-3006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-369-493-3006
         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR PILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-23

PRIOR FILING DATE: 2000-11-23

PRIOR PAPLICATION NUMBER: 60/257,931

PRIOR PAPLICATION NUMBER: 60/257,931

PRIOR PAPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-02

PRIOR PILING DATE: 2001-02-03

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.1%; Score 7; DB 15; Length 893; Best Local Similarity 100.0%; Pred. No. 6.2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
2.1%; Score 7; DB 12; Length 891;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-282-122A-69548
; Sequence 69548, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          639 AQLAQEL 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                831 EEVSKSL 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 AQLAQEL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 EEVSKSL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-282-122A-69986
                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 69986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 96
US-10-334-143-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-334-143-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPERSSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TILLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 ($2052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION UNDERS: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-29
PRIOR PELING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
APPLICANT: Trawick, John
APPLICANT: Garr, Garnet
APPLICANT: Garr, Garnet
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: W.H.
APPLICANT: W.H.
FITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 15; Length 1170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 2.1%; Score 7; DB 12; Le Local Similarity 100.0%; Pred. No. 7.2e+02; Pred. 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 3006, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 69548
LENGTH: 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Thermotoga maritima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       647 TLIADLO 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 TLIADLO 87
```

```
Query Match
Best Local Similarity 100.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                     ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1101 VAÇLAÇE 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1105 VAQLAQE 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 VAQLAQE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 VAQLAQE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 102
US-09-764-853-554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-764-853-554
                                                                                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 1762
                                                                                                                                                                                                                                                                                                                                           US-10-044-807-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-399-385-5
                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 11; Length 1745; 100.0%; Pred. No. 1.1e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.1%; Score 7; DB 9; Length 1745; 100.0%; Pred. No. 1.1e+03; ive 0; Mismatches 0; Indels
                       0; Indels
                                                                                                                                                                                   Sequence 89, Application US/09800729
Fatent No. US2002068319A1
GENERAL INFORMATION:
FAPPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
FRIOR APPLICATION NUMBER: 60/155,709
FRIOR APPLICATION NUMBER: 60/155,709
FRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PATENTIN OF 220
Best Local Similarity 100.0%; Pred. No. 7.9e+02; Matches 7; Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT APPLICATION NUMBER: 06/229, 358
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2222, Application US/09833245; Publication No. US20040010134A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1084 VAQLAQE 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1084 VAQLAQE 1090
                                                            170 KYVELST 176
                                                                                               310 KYVELST 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 VAQLAQE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 VAOLAOE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-833-245-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-833-245-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1745
                                                                                                                                                      RESULT 99
US-09-800-729-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-800-729-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                            à
```

RESULT 101

```
US-10-044-807-2

Sequence 2, Application US/10044807

Sequence 2, Application No. US20020165187A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: YU, XUANCHUAN

TITLE OF INVENTION: NO. US20020165187A1e1 Human Protease and Polynucleotides Encodin:

TITLE OF INVENTION: NO. US20020165187A1e1 Human Protease and Polynucleotides Encodin:

TITLE OF INVENTION: NUMBER: USA

CURRENT FILING DATE: 2002-01-11

PRIOR FILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 2

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FREEEE/CONTAINED NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/10399385

Publication No. US20040033513A1

GENERAL INFORMATION:
APPLICANT: Camaschella, Clara
APPLICANT: Camaschella, Clara
APPLICANT: Oberkannis, Christian
TITLE OF INVENTION: METHOD AND PROBE FOR GENETIC DIAGNOSIS OF HEREDITARY HAEMOCHROMA
FILE REFERENCE: 37396/VIENNALAB
CURRENT APPLICATION NUMBER: US/10/399,385
CURRENT FILING DATE: 2003-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (533)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQUENCE 554, Application US/09764853
Facture No. US2002009672A1
GENERAL INFORMATION:
FAPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PUZO6
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 939
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 554
LENGTH 1766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .<u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.1%; Score 7; DB 13; Length 1762; Best Local Similarity 100.0%; Pred. No. 1.18+03; Matches 7; Conservative 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.1%; Score 7; DB 9; Length 1766; 100.0%; Pred. No. 1.1e+03; tive 0; Mismatches 0; Indels
```

```
Query Match 1.85
Best Local Similarity 100.(
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                          65 AVAQLA 70
                                                                                                                                                      6 AVAQLA 11
                                                                                                                                                                                                                                          US-09-864-761-46460
                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Camaschella, Clara
APPLICANT: Camaschella, Clara
APPLICANT: Kury, Friedrich
APPLICANT: Kury, Friedrich
APPLICANT: Willer School Canabar Christian
TITLE OF INVANTION: METHOD AND PROBE FOR GENETIC DIAGNOSIS OF HEREDITARY HAEMOCHROMAT
FILE REPERENCE: 37396/VIENNALAB
CURRENT APPLICATION NUMBER: US/10/399,385
CURRENT FILING DATE: 2003-04-16
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 15
LENGTH: 15
TYPE: PRT
CRGANISM: Homo sapiens
US-10-399-385-4
                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Spack, Edward
APPLICANT: Arimilli, Subhashini
APPLICANT: Arimilli, Subhashini
APPLICANT: Deshpande, Shrikant
APPLICANT: Wehner, Nancy
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Immunodominant Acetylcholine Receptor Alpha
TITLE OF INVENTION: Subunit Peptide:MHC Complexes
FILE REFERENCE: 014058-015810US
CURRENT PRILING DATE: 2002-09-30
PRIOR FILING DATE: 2002-09-30
PRIOR FILING DATE: 2001-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: acetylcholine receptor (AchR) alpha peptide OTHER INFORMATION: 330-343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.8%; Score 6; DB 14; Length 14; Best Local Similarity 100.0%; Pred. No. 1.6e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                          Length 11;
                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                        DB 12; Le
                                                                                                                                                                        1.8%; Score 6; DB 1
100.0%; Pred. No. 1.3
rative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 91
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 51
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                       US-10-261-798-51
; Sequence 51, Application US/10261798
; Publication No. US20030144477A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 4, Application US/10399385; Publication No. US20040033513A1; GENERAL INFORMATION:
                  SOFTWARE: Patentin version 3.0 SEQ ID NO 5 LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                 Query Match
Best Local Similarity 100...
6; Conservative
NUMBER OF SEQ ID NOS: 7
                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-399-385-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 EKQDKK 34
                                                                                                                                                                                                                                                            65 AVAOLA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 EKODKK 11
                                                                                                                                                                                                                                                                                          US-10-261-798-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 105
US-10-399-385-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                   d
```

```
ð
                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-774-639-312

Sequence 312, Application US/09774639

Publication No. US2003000355A1

GENERAL INFORMATION:

TITLE OF INVENTION: 90 Human Secreted Proteins

FILE REFERENCE: P201391

CURRENT APPLICATION NUMBER: US/09/774,639

CURRENT FILING DATE: 2001-07-09

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04

NUMBER OF SEQ ID NOS: 371

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.8%; Score 6; DB 10; Length 24; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                    Query Match
1.8%; Score 6; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
) OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.3 US-09-864-761-46460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVEMINION:

JAPPILIZANT: Ruben et al.

TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: PSO13P2

CURRENT APPLICATION NUMBER: US/09/969,730

CURRENT FILING DATE: 2001-00-04

PRIOR APPLICATION NUMBER: 09/774,639

PRIOR APPLICATION NUMBER: 09/244,112

PRIOR APPLICATION NUMBER: 09/244,112

PRIOR APPLICATION NUMBER: 00/244,112

PRIOR FILING DATE: 1999-02-04

PRIOR FILING DATE: 1999-02-04

PRIOR PRILING DATE: 1999-03-04

PRIOR APPLICATION NUMBER: 60/056,371

PRIOR APPLICATION NUMBER: 60/056,371

PRIOR PILING DATE: 1997-08-19

PRIOR FILING DATE: 1997-08-19

PRIOR PILING DATE: 1997-08-19

PRIOR PILING DATE: 1997-08-19

PRIOR APPLICATION NUMBER: 60/056,366

PRIOR PILING DATE: 1997-08-19

PRIOR APPLICATION NUMBER: 60/056,364

PRIOR FILING DATE: 1997-08-19

PRIOR PILING DATE: 1997-08-19

PRIOR FILING DATE: 1997-08-19

PRIOR FILING DATE: 1997-08-19

PRIOR PILING DATE: 1997-08-19

PRIOR PILING DATE: 1997-08-19

PRIOR APPLICATION NUMBER: 60/056,367

PRIOR PRILATION NUMBER: 60/056,367

PRIOR APPLICATION NUMBER: 60/056,367

PRIOR APPLICATION NUMBER: 60/056,367

PRIOR APPLICATION NUMBER: 60/056,367

PRIOR APPLICATION NUMBER: 60/056,367

PRIOR APPLICATION NUMBER: 60/056,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 239, Application US/09969730
; Publication No. US20030054443A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                 250 SKPENL 255
                                                                                                                                                                                                                                                                                                           11 SKPENL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 KKTDKA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKTDKA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-774-639-312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 108
US-09-969-730-239
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 107
                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                     à
```

```
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 TOPIVE 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 SGLLVT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 SGLĹVT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TOPÍVE 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-424-599-230826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-917-340-62
                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INCORANT: Pent, Sharron G.
APPLICANT: Pent, Sharron G.
APPLICANT: Pent, Sharron G.
APPLICANT: Pent, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: CHEM.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON OFFICE ACID FROME TITLE APPLICATION NUMBER: US/O1/05-23
FRIOR APPLICATION NUMBER: US/O1/05-23
FRIOR PILLING DATE: 2000-05-24
FRIOR PILLING DATE: 2000-05-24
FRIOR PILLING DATE: 2000-05-24
FRIOR PILLING DATE: 2000-09-27
FRIOR PILLING DATE: 2000-09-27
FRIOR PILLING DATE: 2000-09-27
FRIOR APPLICATION NUMBER: US/O1/05/06/06
FRIOR APPLICATION NUMBER: PCT/US/O1/06/06
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-30
FRIOR PELING DATE: 2001-01-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR APPLICATION NUMBER: 60/056,366
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR APPLICATION NUMBER: 60/056,344
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
PRIOR FILING DATE: 1997-08-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 373
SOFTWARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 16; Length 24;
100.0%; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.8%; Score 6; DB 16
Best Local Similarity 100.0%; Pred. No. 2.5s
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 45850, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 KKTDKA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 KKTDKA 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 110
US-09-864-761-45850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-621-363-239
                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
```

```
Sequence 230826, Application US/10424599
Sequence 230826, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
BAPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Show Yihua
APPLICANT: Can Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 230826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: MAP TO AC008998.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
US-09-864-761-45850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.8%; Score 6; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_50457C.1.pep
US-10-424-599-230826
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION WUMBER: US 09/774,203
PRIOR FILLNG DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 45850
LENGTH: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.8%; Score 6; DB 12; Lv
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TILLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 62, Application US/09917340; Patent No. US20020090369A1; GENERAL INFORMATION:
```

```
Sequence 33835, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: AppliCATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: MAP TO ACO04832.3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.7

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN PAGENTA, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2

OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 9; Length 42; 100.0%; Pred. No. 4.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRIOR FILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2001-01-30
PRIOR PILLING DATE: 2000-09-21
PRIOR PILLING DATE: 2000-06-21
PRIOR PILLING DATE: 2000-06-30
PRIOR PILLING DATE: 2000-06-30
PRIOR PILLING DATE: 2000-06-30
PRIOR PILLING DATE: 2000-06-30
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
PRIOR PILLING DATE: 2001-01-20
                                                                                               PRIOR AFFLIATION NUMBER: US 50/20/,456
PRIOR APPLICATION NUMBER: US 69/632,366
PRIOR PLIING DATE: 2000-08-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR PLIING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLIING DATE: 2000-10-30
PRIOR PLIING DATE: 2001-01-30
PRIOR PLIING DATE: 2001-01-30
PRIOR PLIING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PLIING DATE: 2001-01-30
PRIOR PLIING DATE: 2001-01-30
PRIOR PLIING DATE: 2001-01-30
PRIOR PLIING DATE: 2001-01-30
PRIOR PLIING DATE: 2001-01-30
PRIOR PLIING DATE: 2001-01-30
PRIOR PLIING DATE: 2001-01-30
PRIOR PLIING DATE: 2001-01-30
PRIOR PLIING DATE: 2001-01-30
PRIOR PLIING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 DKASEE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 DKASEE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 115
US-09-864-761-33835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-864-761-46961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Penn, Sharion US/09864761
; Sequence 46561, Application US/09864761
; Sequence 46561, Application US/09864761
; Sequence 46561, Application US/09864761
; Sequence 46561, Application: Sharion: Sharion: Sharion: Applicant: Penn, Sharion: Sharion: Applicant: Penn, Mensheng
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TILLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFFUL FOR TILLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE ERFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 4e+02;
-heq 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.8%; Score 6; DB 9;
Best Local Similarity 100.0%; Pred. No. 4e+02
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 9;
100.0%; Pred. No. 4e+(
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09917340
| Patent No. US2002093691,
| GENERAL INFORMATION: | APPLICANT: Murphy, Christopher J. APPLICANT: McAnulty, Jonathan F. APPLICANT: Reid, Ted W. TTILLE OF INVENTION: Transplant Media FILE REFERENCE: TPLANT-06468
| CURRENT APPLICATION NUMBER: US/09/917,340 | CURRENT PILING DATE: 2001-07-29 | PRIOR PILING DATE: 2000-07-28 | PRIOR PILING DATE: 2000-07-29 | PRIOR PILING DATE: 2000-07-29 | PRIOR PILING DATE: 2000-11-17 | PRIOR PILING DATE: 2001-07-29 | PRIOR PILING DATE: 2001-07-29 | PRIOR PILING DATE: 2001-07-29 | PRIOR PILING DATE: 2001-07-29 | PRIOR PILING DATE: 2001-05-15 | NUMBER OF SEQ ID NOS: 96 | SOFTWARE: Patentin Ver: 2.0 | SEQ ID NO 63 | LENGTH: 40
CURRENT FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR PRILING DATE: 2001-11-17
PRIOR FILING DATE: 2001-65-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Bos taurus
US-09-917-340-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 RROIGT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 RROIGT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-917-340-63
                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-917-340-62
                                                                                                                                                                                                                                                                                           SEQ ID NO 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

GENERAL INFORMATION:

```
OTHER INFORMATION: MAP TO ACO07846.1

CHERRINGORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1

CTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN UNG, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN HELLON, SIGNAL = 1.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 9; Length 43; 100.0%; Pred. No. 4.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR PLLING DATE: 2000-05-204
PRIOR PLLING DATE: 2000-05-26
PRIOR PLLING DATE: 2000-05-36
PRIOR PLLING DATE: 2000-09-03
PRIOR PLLING DATE: 2000-09-03
PRIOR PLLING DATE: 2000-10-04
PRIOR PLLING DATE: 2000-09-27
PRIOR PLLING DATE: 2000-09-27
PRIOR PLLING DATE: 2001-030
PRIOR PLLING DATE: 2001-03-30
PRIOR PLLING DATE: 2001-03-30
PRIOR PLLING DATE: 2001-03-30
PRIOR PLLING DATE: 2001-03-30
PRIOR PLLING DATE: 2001-03-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2001-01-30
PRIOR PLLING DATE: 2000-09-21
PRIOR PLLING DATE: 2000-09-21
PRIOR PLLING DATE: 2000-09-21
PRIOR PLLING DATE: 2000-09-21
PRIOR PLLING DATE: 2000-09-21
PRIOR PLLING DATE: 2000-09-21
PRIOR PLLING DATE: 2000-09-21
PRIOR PLLING DATE: 2000-09-21
PRIOR PLLING DATE: 2000-09-21
PRIOR PLLING DATE: 2000-09-21
PRIOR PLLING DATE: 2000-09-21
PRIOR PLLING DATE: 2000-09-21
PRIOR PLLING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 20
NAME/KEY: unsure
LOCATION: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 33835
LENGTH: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
```

ö

Gape

.

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-891-3628

TYPE: PRT ORGANISM: Homo sapiens FEATURE:

LENGTH: 43

NAME/KEY: SITE LOCATION: (9)

Query Match
1.8%; Score 6; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels

304 FLSSFQ 309

δ g

27 FLSSFQ 32

APPLICANT: Rosen et al.
TITLE OF INVENTION: Mucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3628

```
ö
                                                                                                             ; Sequence 372, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1e1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 15; Length 44;
100.0%; Pred. No. 4.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/491,404
PRIOR PILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-01-25
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-09-15
PRIOR PILING DATE: 2000-09-15
PRIOR PILING DATE: 2000-09-15
SEQID NO 372
SOFTWARE: PRECENT ON NOS: 944
SOFTWARE: PRECENT ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE ON STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STATE OF STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 157183, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Thea 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-291-265-372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 KIILFS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 KIILFS 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-424-599-157183
RESULT 117
US-10-291-265-372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

ö

Gaps

ö

0; Indels

; Sequence 3628, Application US/09764891 ; Publication No. US20030077808A1

RESULT 116 US-09-764-891-3628

```
Sequence 188181, Application US/10424599
| Publication No. US20040031072A1
| GENERAL INFORMATION |
| APPLICANT: La Rosa Thomas J |
| APPLICANT: APPLICANT: Cao Yongwei |
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement CURRENT FILING DATE: 2003-04-28 |
| CURRENT FILING DATE: 2003-04-28 |
| SEQ ID NO 188181 |
| LENGTH: 48 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 269667, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REPERRENCE: 38-21 (5323) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SSQ ID NO 269667
                                                                                                 NAME/KEY: SITE LOCATION: (43)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                           1.8%; Score 6; DB 10; Length 47; 100.0%; Pred. No. 4.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 6; DB 12; Length 48;
100.0%; Pred. No. 4.78+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_140941C.1.pep
US-10-424-599-188181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_85529C.1.pep
US-10-424-599-269667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                          6; Conservative
                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max
                                                                                                                                                                                                                                               Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                          102 NNILRR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 MLLKGY 133
                                                                                                                                                                                                                                                                                                                                                                    20 NNILRR 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 MLLKGY 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-424-599-269667
                                                                                                                                                                              US-09-764-872-445
                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
              LENGIH:
                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
File Reference: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement File REPRENCE: 38-21(53223) B CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 157183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·
0
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PALS2
CURRENT APPLICATION NUMBER: US/09/764,872
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 957
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 445
                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 12; Length 45; 100.0%; Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 46;
                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_112958C.1.pep
US-10-424-599-157183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: PAT MRT3847_114883C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.8%; Score 6; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(46)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                   100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 159316, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 445, Application US/09764872
; Publication No. US20030050231A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100...
6; Conservative
                                                                                                                                                                                                            ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                  126 LFMLLK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LFMLLK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 RRQIGT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-159316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-424-599-159316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 159316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 120
US-09-764-872-445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 119
```

ö

.; 0

```
Sequence 6116, Application US/10106698

Sequence 6116, Application US/10106698

Publication No. US20030109690A1

SEQUENCE INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptic

TITLE OF INVENTION: UNBER: US/10/106,698

CURRENT APPLICATION NUMBER: PZT/US00/26524

PRIOR PELLING DATE: 2000-09-28

PRIOR PELLING DATE: 1099-09-29

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR APPLICATION NUMBER: US 60/153,280

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR PELLING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: Patentin Ver. 3.0

LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 223344, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: La Rosa Thomas J
APPLICANT: APOLICANT: Cao yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 223554
LENGTH: 51
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 14; Length 50;
100.0%; Pred. No. 4.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 12; Length 51;
100.0%; Pred. No. 5e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_4371C.1.pep
US-10-424-599-223354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 249890, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION: APPLICANT: La Roba Thomas J. APPLICANT: Kovalic David K. APPLICANT: Zhou Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 IVEILL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 TEAVAQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 TEAVAQ 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 IVEIL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-424-599-223354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-424-599-249890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-106-698-6116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                              Sequence 174437, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La ROSA Thomas J
APPLICANT: APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICANT: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 174437
LENGTH: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: And Vihua
APPLICANT: And Vihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICANTON NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 186215
LENGTH: 49
                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
          1.8%; Score 6; DB 12; Length 48; 100.0%; Pred. No. 4.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.8%; Score 6; DB 12; Length 49;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
1.8%; Score 6; DB 12; Length 49;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT3847_128535C.1.pep US-10-424-599-174437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT3847_139165C.1.pep
US-10-424-599-186215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 186215, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                    6; Conservative
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 LKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 KYVELS 175
                                                                                                    80 VTLIAD 85
                                                                                                                                               33 VTLIAD 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 LKKTAP 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KYVELS 8
                                                                                                                                                                                                                                               US-10-424-599-174437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-424-599-186215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                         RESULT 123
                                                    Matches
                                                                                                                                               qq
                                                                                                       à
```

.. 0

```
APPLICANT: LE ROSA Thomas J
APPLICANT: LE ROSA Thomas J
APPLICANT: E ROSA Thomas J
APPLICANT: Show Yinua
APPLICANT: Show Yinua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38 22 (53223) B
FILE REFERENCE: 38 22 (53223) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ERQ ID NO 149472
LENGTH: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 247013
LENGTH: 53
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.8%; Score 6; DB 12; Length 53; Best Local Similarity 100.0%; Pred. No. 5.1e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  Length 53;
                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Clone ID: PAT_MRT3847_65082C.1.pep
                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_16029C.1.pep
US-10-424-599-192699
                                                                                                                                                                                                                                                               Query Match
1.8%; Score 6; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)..(53)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 149472, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-424-599-247013
; Sequence 247013, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 192699 LENGTH: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
                                                                                                                                  ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 ADFLEQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 ADFLEQ 48
                                                                                                                                                                                                                                                                                                                                                                                 25 LAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                    30 LAILEK 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-424-599-149472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-424-599-247013
                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 192699, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 39-21(53223)B
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement File Represence: 38-21(5)223) B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 249890 LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 12; Length 52; 100.0%; Pred. No. 5.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.8%; Score 6; DB 14; Length 52;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Clone ID: PAT MRT3847 6767C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15079, Application US/10156761
| Publication No. US20030119018A1
| GENERAL INFORMATION:
| APPLICANT: ISHIKAWA, HARUO
| APPLICANT: ISHIKAWA, JUN
| APPLICANT: ISHIKAWA, JUN
| APPLICANT: SHIRAWA, HOSSHI
| APPLICANT: SHIRAWA, HOSSHI
| APPLICANT: SHIRAWA, HOSSHI
| APPLICANT: SHIRAWA, HOSSHI
| APPLICANT: SHIRAWA, HOSSHI
| APPLICANT: SHIRAWA, HOSSHI
| APPLICANT: SHIRAWA, HOSSHI
| APPLICANT: SHIRAWA, HOSSHI
| APPLICANT: SHIRAWA, HOSSHI
| APPLICANT: SHIRAWA, HOSSHI
| APPLICANT: SHIRAWA, HOSSHI
| APPLICANT: SACKALI, YOSHIVUKI
| APPLICANT: LATTOR NOVEL POLYNUCLEOTIDES
| CURRENT FILING DATE: 2002-05-29
| PRIOR APPLICATION NUMBER: JP 2001-272697
| PRIOR APPLICATION NUMBER: JP 2001-272697
| PRIOR APPLICATION NUMBER: JP 2001-272697
| NUMBER OF SEQ ID NOS: 15109
| SEQ ID NO 15079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/424,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptomyces avermitilis US-10-156-761-15079
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100..
Lang 6; Conservative
                                                                                                                                                                                                                                                                        ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 NOPKLI 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 LYSSGL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 NOPKLI 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 LYSSGL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-424-599-192699
                                                                                                                                                                                                                                                                                                                                                             US-10-424-599-249890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 128
US-10-156-761-15079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

ਨੇ

```
; LOCATION: (12); CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-908-711-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.8%; Score 6; DB 9; Length 56;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/704,864
PRIOR PLILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01341
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01346
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
           PRIOR APPLICATION NUMBER: 09/764,891
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: En Rosa Thomas J
APPLICANT: En Rosa Thomas J
APPLICANT: About V thua
APPLICANT: The Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICANTON NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
LENGTH: 55
LENGTH: 55
                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 83, Application US/09908711

Sequence 83, Application US/09908711

Sequence 83, Application US/09908711

Sequence 83, Application US/09908711

SERENGAT: ROSAGE 41.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REPERENCE: PAL28

CURRENT APPLICATION NUMBER: US/09/908,711

CURRENT FILING DATE: 2001-07-20

PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2001-01-17

PRIOR PPLICATION NUMBER: US/09/764,867

PRIOR PPLING DATE: 2001-01-17

PRIOR PPLING DATE: 2001-01-17

PRIOR PPLING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: US/01/01345

PRIOR PPLING DATE: 2001-01-17

PRIOR PPLING DATE: 2001-01-17

PRIOR PLING DATE: 2001-01-17

PRIOR PLING DATE: 2001-01-17

PRIOR PLING DATE: 2001-01-17

PRIOR PLING DATE: 2001-01-17

PRIOR PLING DATE: 2001-01-17

PRIOR PLING DATE: 2001-01-17

PRIOR PLING DATE: 2001-01-17

PRIOR PLING DATE: 2001-01-17

PRIOR PLING DATE: 2001-01-17

PRIOR PLING DATE: 2001-01-17

PRIOR PLING DATE: 2001-01-17

PRIOR PLING DATE: 2001-01-17

PRIOR PLING DATE: 2001-01-17

PRIOR PLING DATE: 2001-01-17

PRIOR PLING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.8%; Score 6; DB 12; Length 55; Best Local Similarity 100.0%; Pred. No. 5.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                      Length 54;
                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_135980C.1.pep
US-10-424-599-182688
                               ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_105997C.1.pep
US-10-424-599-149472
                                                                                                                                                                              Query Match
1.8%; Score 6; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 132
US-10-424-599-182688
; Sequence 182688, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Glycine max
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 LKKTAP 337
                                                                                                                                                                                                                                                                                                                                     126 LFMLLK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 LKKTAP 44
                                                                                                                                                                                                                                                                                                                                                                                                                 46 LEMLLK 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 133
US-09-908-711-83
                                                                                                                                                                                                                                                                                                                                                                                                         QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
```

ô

Gaps ; 0

```
, OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-891-3081
                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: Mucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOO.6
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3081
LENGTH: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.8%; Score 6; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                  ; Sequence 3081, Application US/09764891; Publication No. US20030077808A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 VKILKD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 136
US-10-424-599-267396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: SITE
                                                                                         US-09-764-891-3081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                           Sequence 40021, Application Us/09864761
Sequence 40022, Application Us/09864761
Sequence 40022, Application Us/09864761
GERERAL NOTIONALINE STATEM G.
APPLICANT Raize, David R.
APPLICANT RAIZE, David R.
APPLICANT RAIZE, David R.
APPLICANT RAIZE, David R.
APPLICANT RAIZE, David R.
APPLICANT RAIZE, David R.
APPLICANT RAIZE, David R.
APPLICANT RAIZE, David R.
APPLICANT RAIZE RAIZE RAIZE STATESSION ANALYSIS BY MICRORRAM
FILLS APPLICANTED WINNERS: US 60/180,312
BRIOR PRICAPLICATION WINNERS: US 60/180,312
BRIOR PRICATION WINNERS: US 60/20,456
BRIOR PRICATION WINNERS: US 60/20,456
BRIOR PRICATION WINNERS: US 60/20,466
BRIOR PRICATION WINNERS: US 60/20,466
BRIOR PRICATION WINNERS: US 60/20,466
BRIOR PRICATION WINNERS: US 60/20,466
BRIOR PRICATION WINNERS: US 60/20,466
BRIOR PRICATION WINNERS: US 60/20,466
BRIOR PRICATION WINNERS: US 60/20,466
BRIOR PRICATION WINNERS: US 60/20,466
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BRIOR PRICATION WINNERS: PCT/0801/00666
BR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: MAP TO AC007358.2
OTHER INFORMATION: EXPERSEDED IN HBLLIO, SIGNAL = 1.1
OTHER INFORMATION: EST HUMAN HIT: A1276750.1, EVALUE 1.00e-25
OTHER INFORMATION: SMISSPROT HIT: P54660, EVALUE 7.70e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.8%; Score 6; DB 9; Ler
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
6 VKILKD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-864-761-49022
                                                                                                                                US-09-864-761-49022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 49022
셤
```

ò

Gaps

·,

```
Sequence 26(7396, Application US/10424599)
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: By Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
IERGENERAL SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.8%; Score 6; DB 12; Length 56;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_83480C.1.pep
US-10-424-599-267396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 178427, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , APPLICANT: La Rosa Thomas J
, APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 TKYISK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 TKYISK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-424-599-178427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 137
```

ö

Gaps ; 0

0; Indels

.. 0

```
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: En Rosa Thomas J
APPLICANT: About K
APPLICANT: About Subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subject to the subjec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 14; Length 58; 100.0%; Pred. No. 5.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 12; Length 60;
100.0%; Pred. No. 5.7e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_18409C.1.pep
US-10-424-599-195329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_76484C.1.pep
                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 5
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 5
LENGTH: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) TYPE: PRT
; ORGANISM: Eastern equine encephalitis virus
US-10-127-641-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 195329, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/285,601
PRIOR FILING DATE: 2001-04-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-424-599-259644
; Sequence 259644, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                               2002-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.(
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                               CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 LEQNYD 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 LEQNYD 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 PLFSKS 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 PLFSKS 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-424-599-195329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 259644
LENGTH: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOWE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annowmax Sequence Listing Engine vers. 1.1
## APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Mucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Soy Mucleic Acid Molecules and Other Molecules Associated With

FILE REFERENCE: 38-21(5323)8

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 178427

IRNGTH: 57

TYPE: pr.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hart, Mary Kate
TITLE OF INVENTION: Prophylactic and Therapeutic Monoclonal Antibodies
FILE REFERENCE: 003/251/SAP
CURRENT APPLICATION NUMBER: US/10/127,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: MAP TO AL137007.4

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.98

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.98

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.58

OTHER INFORMATION: EXPRESSED IN BOULT LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.62

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.58

OTHER INFORMATION: SYRESSED IN BRAIN, SIGNAL = 0.58

OTHER INFORMATION: SYRESSED IN BRAIN, SIGNAL = 0.58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 12; Length 57;
100.0%; Pred. No. 5.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14; Length 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_132137C.1.pep
US-10-424-599-178427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.8%; Score 6; DB 14; Le
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 138
US-10-029-386-27862
; Sequence 27862, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/10127641 Publication No. US20030099931A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 RHKVLV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 LKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 RHKVLV 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 LKLLGE 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATIC
US-10-029-386-27862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 27862
LENGTH: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-127-641-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          d
```

·,

```
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Exercite David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 202297
LENGTH: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-010-424-599-285560

US-010-424-599-285560

Sequence 285560, Application US/10424599

Publication No. US20040031072A1

Publication No. US20040031072A1

APPLICAMT: La Rosa Thomas J

APPLICAMT: La Rosa Thomas J

APPLICAMT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFREENCE: 38-21(5323)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

EMOUTH: 63

LENGTH: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 6; DB 12; Length 63; 100.0%; Pred. No. 6e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_31022C.1.pep
US-10-424-599-209297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT_MRT3847_99890C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.8%; Score 6; DB 12;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 6; Conservative 0; Mismatches 0
                                                                                            ; Sequence 209297, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 47397, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 PIVEIL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 PIVEIL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 QLIDFE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 QLIDFE 13
                                                                        US-10-424-599-209297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-424-599-285560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 146
US-09-864-761-47397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                             Sequence 191627, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: AROSA Thomas J
APPLICANT: APPLICANT: AND SON THE OF INVENTION:
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TILE REFERENCE: 38-21(5323)8
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 191627
LENGTH: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Shout I will a
APPLICANT: Shout I will a
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 18-21(5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 211257
LENGTH: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                 ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                           1.8%; Score 6; DB 12; Length 60; 100.0%; Pred. No. 5.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 62; . 5.9e+02; ches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.8%; Score 6; DB 12; Length 62; Best Local Similarity 100.0%; Pred. No. 5.9e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: PAT_MRT3847_32792C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_1505C.1.pep
US-10-424-599-191627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.8%; Score 6; DB 1;
Best Local Similarity 100.0%; Pred. No. 5.9
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 211257, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 AKIILF 161
                                                                                                                                                157 KIILFS 162
                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 AKIILF 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 SKSLQA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 SKSLQA 23
                                                                                                                                                                                            31 KILLES 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 143
US-10-424-599-211257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-211257
                                                                                                                                                                                                                                                                                           US-10-424-599-191627
US-10-424-599-259644
                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

ö

```
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_115339C.1.pep
US-10-424-599-159823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.8%; Score 6; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 QSLKLL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 QSLKLL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-335-977-5580
                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
APPLICANT: Hanzel, bavid K.
APPLICANT: Hanzel, bavid K.
APPLICANT: Chem. Wensheng
TITLE OF INVENTION: HAND GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL, FOR
TITLE OF INVENTION: HAND GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL, FOR
TITLE OF INVENTION: HAND GENOME AT 1.
CURRENT PELLICATION HOMBER: US 60/180,312
PRIOR PELLICATION NUMBER: US 60/180,312
PRIOR PELLICATION NUMBER: US 60/207,456
PRIOR PELLICATION NUMBER: US 60/207,456
PRIOR PELLICATION NUMBER: US 60/207,366
PRIOR PELLICATION NUMBER: US 60/205,366
PRIOR PELLICATION NUMBER: US 60/205,366
PRIOR PELLICATION NUMBER: US 60/205,359
PRIOR PELLICATION NUMBER: PCT/US01/0066
PRIOR PELLICATION NUMBER: PCT/US01/0066
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRIOR PELLICATION NUMBER: PCT/US01/00669
PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: MAP TO AC019083.5

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.56

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.54

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.53

OTHER INFORMATION: SWISSPROT HIT: F229775, EVALUE 2.00e-13

OTHER INFORMATION: EST_HUMAN HIT: A1991109.1, EVALUE 2.00e-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 9; Length 64; 100.0%; Pred. No. 6.1e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47397
LENGTH: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-864-761-47397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
```

. 0

Gaps

.; 0

Length 64; Indels

```
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELLCOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature LOCATION: (B) LOCATION 1...64
                                                                                                                                                                                                      & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Helicobacter pylori
; Sequence 5580, Application US/10335977; Publication No. US20040052799A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                    ADDRESSEE: LAHIVE & COCI
STREET: 28 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 5580:
                                                                                                                                                       10031
                                                                                                                                                                                                                                                                       STATE: Massachusetts
                                                                                                                                                          NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
```

ö

.. 0

6; Conservative

64 EAVAQL 69 EAVAQL 45

40

g

Sequence 159823, Application US/10424599; Publication No. US20040031072A1 GENERAL INFORMATION: APPLICANT: La Rosa Thomas J

RESULT 147 US-10-424-599-159823

```
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 211264, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 12; Length 67; 100.0%; Pred. No. 6.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 67;
                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_32799C.1.pep
US-10-424-599-211264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Clone ID: PAT_MRT3847_1510C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.8%; Score 6; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(67)
OTHER INFORMATION: unsure at all Xaa locations
                       Mismatches
                                                                                                                                                                                                                    US-10-424-599-191683
; Sequence 191683, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100.
nes 6; Conservative
                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 LKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 IENNIT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 LKLLGE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 IFWNIL 13
                                                                      18 VKILKD 23
                                                                                                                     14 VKILKD 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-424-599-211264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
LOCATION: (1)..(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-424-599-191683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 211264
LENGTH: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Abou Yihua
APPLICANT: Abou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICANTON NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
LENGTH: 66
LENGTH: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Acoultie David K
APPLICANT: Cao Yougwei
TITLE OF INVENTION: Soy Mucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
FURE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
UNDMBER OF SEQ ID NOS: 285684
                                                                                                                                             0;
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.8%; Score 6; DB 12; Length 65;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                              Length 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.8%; Score 6; DB 12; Length 66; Best Local Similarity 100.0%; Pred. No. 6.2e+02;
                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_120649C.1.pep US-10-424-599-165707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_3676C.1.pep
US-10-424-599-215660
                                                                                         1.8%; Score 6; DB 12; Le 100.0%; Pred. No. 6.1e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)..(66)
OTHER INFORMATION: unsure at all Xaa locations
;
US-10-335-977-5580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Sequence 165707, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 Sequence 215660, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                         Query Match 1.8
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 AKIILF 161
                                                                                                                                                                                         18 VKILKD 23
                                                                                                                                                                                                                                           35 VKILKD 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 AKIILF 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-424-599-165707
                                                                                                                                                                                                                                                                                                                                               US-10-424-599-215660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 215660
LENGTH: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                      a
G
```

ö

ô

```
Page 43

....rulCANT: Zhou Yihua

APPLICANT: Zhou Yihua

TILLE OF INVENTION: Soy Mucleic Acid Molecules and Other Molecules Associated With
TILLE OF INVENTION: Soy Mucleic Acid Molecules and Other Molecules Associated With
TILLE OF INVENTION: Soy Mucleic Acid Molecules and Other Molecules Associated With
TILLE OF INVENTION: 18-21(5223)B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILLING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 202460

LENGTH: 69

TYPE. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: En Rosa Thomas J
APPLICANT: En Rosalic David K
APPLICANT: And Tithus
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 242, Application US/10221278
Publication No. US20040034208A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TOTALE REFERENCE: 21272-045
CURRENT APPLICATION NUMBER: US/10/221,278
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 09/693,267
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR FILING DATE: 2000-09-19
PRIOR FILING DATE: 2000-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.8%; Score 6; DB 12; Length 69;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_24847C.1.pep
US-10-424-599-202460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT3847_79023C.1.pep
US-10-424-599-262460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 1.8%; Score 6; DB 12; Le
Local Similarity 100.0%; Pred. No. 6.5e+02;
les 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 262460, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 KSPNIQ 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 IEFLSS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 IEFLSS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KSPNIQ 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-262460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-221-278-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Abou Vibua
APPLICANT: Abou Vibua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38 4-21 (53223) B
CURRENT APPLICANION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
ESEQ ID NO 195946
                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Anou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38 – 21 (5223.3) B
CURRENT APPLICATION NUMBER: US/10/424, 599
CURRENT APPLICATION DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 2855684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.8%; Score 6; DB 12; Length 69; Best Local Similarity 100.0%; Pred. No. 6.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_101729C.1.pep
US-10-424-599-144751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_18966C.l.pep
US-10-424-599-195946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
1.8%; Score 6; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                            ; Sequence 144751, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 195946, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-424-599-202460
; Sequence 202460, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 IVEILL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 KDLLTR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 KDLLTR 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 IVEILL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-424-599-195946
                                                                                                                                                                                                             RESULT 153
US-10-424-599-144751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 144751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
```

```
Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 ILRRQI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 FLSSFQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 ILRROI 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-282-122A-76423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORCELL AND CONTRACTORY

JETLE OF INVENTION: No. US20030228584A1e1 Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-045

CURRENT APPLICATION NUMBER: US/10/291,172

CURRENT APPLICATION NUMBER: 09/693,267

PRIOR APPLICATION NUMBER: 09/665,363

PRIOR APPLICATION NUMBER: 09/665,363

PRIOR FILING DATE: 2000-00-19

PRIOR FILING DATE: 2000-00-19

PRIOR FILING DATE: 2000-00-19

PRIOR FILING DATE: 2000-07-14

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR PLING DATE: 2000-05-19

PRIOR PLING DATE: 2000-05-19

PRIOR PLING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , DB 15; Le.,,
No. 6.7e+02;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.8%; Score 6; DB 12; Length 71; Best Local Similarity 100.0%; Pred. No. 6.7e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 6; DB 1
100.0%; Pred. No. 6.7
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-01-0-282-122A-76423

Sequence 76423, Application US/10282122A

PUBLICATION NO. US20040029129A1

GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Ohlsen, Rari
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Tawick, John
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR PELLING DATE: 2000-05-19
PRIOR FILING DATE: 2000-07-10
NUMBER: 0F SEQ ID NOS: 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 242, Application US/10291172; Publication No. US20030228584A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100...
6; Conservative
                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-221-278-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-10-291-172-242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 SLKLLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 SLKLLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 SLKLLG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 SIKLIG 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-291-172-242
                                                                                                                                                                                                    SEQ ID NO 242
                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

```
APPLICANT: Yesaminor, Except. R.
APPLICANT: Assaminor, Except. R.
APPLICANT: Assaminor, Except. R.
APPLICANT: Assaminor, Except. R.
APPLICANT: Assaminor, Except. R.
CURRENT FILING DATE: 2003-20-20
FRIOR PRILICATION NUMBER: 60/10/10/8
FRIOR FILING DATE: 2003-20-20
FRIOR PRILICATION NUMBER: 60/10/10/8
FRIOR PRILICATION NUMBER: 60/10/10/8
FRIOR PRILICATION NUMBER: 60/10/10/8
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIOR FILING DATE: 2000-60-66
FRIEND FRIOR FILING DATE: 2000-60-67
FRIES FRIEND FRIENCE FILING DATE: 2000-60-67
FRIES FRIEND FRIENCE FILING DATE: 2000-60-67
FRIES FRIEND FRIENCE FILING DATE: 2000-60-67
FRIES FRIEND FRIENCE FILING DATE: 2000-60-67
FRIES FRIEND FRIENCE FILING DATE: 2000-60-67
FRIES FRIEND FRIENCE FILING DATE: 2000-60-67
FRIES FRIEND FRIENCE FILING DATE: 2000-60-67
FRIES FRIES FRIENCE FILING DATE: 2000-60-67
FRIES FRIES FRIENCE FILING DATE: 2000-60-67
FRIES FRIES FRIENCE FILING DATE: 2000-60-67
FRIES FRIES FRIES FRIENCE FILING DATE: 2000-60-67
FRIES FRIES FRIENCE FILING DATE: 2000-60-67
FRIES FRIES FRIENCE FILING DATE: 2000-60-67
FRIES FRIES FRIES FRIES FRIES FRIES FRIES FRIES FRIES FRIES FRIES FRIES FRIES FRIES FRIES
```

```
Sequence 56749, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Screen E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TILLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TILLE OF INVENTION Plants and Uses Thereof for Plant Improvement

CURRENT PAPLICANT: 2003-04-28

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128
                                                             APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Sovealic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 37263
LENGTH: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.8%; Score 6; DB 12; Length 74; Best Local Similarity 100.0%; Pred. No. 6.9e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 12; Length 74;
100.0%; Pred. No. 6.9e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: UC-ZMFLMO17036C08_FLI.pep US-10-425-114-56749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: LIB43-49-A12_FLI.pep US-10-425-114-37263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-864-408A-2574;
Sequence 2574, Application US/09864408A;
Publication No. US20040009474A1
GRUERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
Sequence 37263, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               293 ILLKNQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 FKVFVA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 ILLKNQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 FKVFVA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-425-114-56749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 56749
LENGTH: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 244014, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFRENCE: 38-21 (5323.8)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 74

LENGTH: 74
                                                                                                                                                                             APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: About Vibra
APPLICANT: About Vibra
APPLICANT: About Vibra
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
LENGTH: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.8%; Score 6; DB 12; Length 74;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_62372C.1.pep
US-10-424-599-244014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_25531C.1.pep
US-10-424-599-203219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 12; Le
100.0%; Pred. No. 6.8e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)..(73)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                               ; Sequence 203219, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Enc. Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 AVAQLA 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 DKASEE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 DKASEE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 AVAQLA 70
                                                                                      US-10-424-599-203219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: ungure LOCATION: (1)..(7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-424-599-244014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-425-114-37263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

ö

```
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                       Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Recipon, Herve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapien
                                       ORGANISM: Glycine max
                                                                                                                                                                                                                           158 IILFSN 163
                                                                                                                                                                                                                                                                  70 ILLESN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 LFSKSH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 LFSKSH 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-424-599-162228
                                                                                                                                                                                                                                                                                                                                                     US-10-002-344A-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-002-344A-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 200
LENGTH: 78
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INCORDATION:
APPLICANT: Leach, Martin D.
APPLICANT: Nehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
APPLICANT: Topper, James
APPLICANT: Topper, James
APPLICANT: Topper, James
APPLICANT: Topper, James
APPLICANT: Topper, James
APPLICANT: Topper, James
APPLICANT: TILLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: US/08/427
PRIOR FILING DATE: 2000-05-30
TITLE OF INVENTION: No. US20040009474Alel Human Polynucleotides and Polypeptides Encd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Shout K
APPLICANT: Shout Wilhua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plantes and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 253313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                        Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 9; Length 77; 100.0%; Pred. No. 7.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                      Score 6; DB 11; Le; Pred. No. 7.1e+02; 0; Mismatches 0;
               FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
FRIOR APPLICATION NUMBER: 60/206,690
FRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 76
LENGTH: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 574
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Sequence 253313, Application US/10424599 ; Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 574, Application US/09867550 Patent No. US20020082206A1
                                                                                                                                                                                                                                                                                                         100.08;
                                                                                                                                                                                                                                                                                        1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-867-550-574
                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 AVAQLA 70
                                                                                                                                                                                                                                                                                                                                                                        24 NLAILE 29
                                                                                                                                                                                                                                                                                                                                                                                                               16 NLAILE 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 AVAQLA 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-424-599-253313
                                                                                                                                                                                                                                               US-09-864-408A-2574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-867-550-574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                               qq
```

```
APPLICANT: Sun, Yongming
APPLICANT: Chen, Sei-Yu
APPLICANT: Chen, Sei-Yu
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prot
FILE REFERENCE: DEX-0241
CURRENT PELING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/242,998
PRIOR APPLICATION NUMBER: US 60/242,998
NUMBER OF SEQ ID NOS: 277
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILLS REPERENCE: 39-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 162228
LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                ò
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 13; Length 78; 100.0%; Pred. No. 7.2e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 6; DB 12; Length 80;
                                                                                     Length 78;
                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . OTHER INFORMATION: Clone ID: PAT_MRT3847_117509C.1.pep
US-10-424-599-162228
; OTHER INFORMATION: Clone ID: PAT_MRT3847_70767C.1.pep
US-10-424-599-253313
                                                                                     1.8%; Score 6; DB 12; Lv 100.0%; Pred. No. 7.2e+02; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 162228, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 200, Application US/10002344A Publication No. US20020172959A1 GENERAL INFORMATION:
```

```
US-09-738-626-4641
                                                                                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                     APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: About Shua
APPLICANT: Cao Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 198296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Excelled Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REPRESENCE: 38-21(53233)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 244639
LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                       ö
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 12; Length 80; 100.0%; Pred. No. 7.46+02; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 80;
100.0%; Pred. No. 7.4e+02; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_21086C.1.pep
US-10-424-599-198296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_62936C.1.pep
US-10-424-599-244639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.8%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No. 7.4
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                      ; Sequence 198296, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 244639, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 6; Conservative
                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 LIEFLS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 ROIGTR 112
Best Local Similarity
                                                               21 LKDNLA 26
                                                                                                       9 LKDNLA 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 LIEFLS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 ROIGTR 65
                                                                                                                                                                                                   US-10-424-599-198296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-424-599-244639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                     Matches
                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
```

```
US-09-858-664A-32

Sequence 32, Application US/09858664A

Patent No. US2002072491A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE REFERENCE: CL000927-CIP
CURRENT APPLICATION NUMBER: US/09/858,664A

CURRENT FILING DATE: 2001-05-17
PRIOR FILING DATE: 2000-11-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.8%; Score 6; DB 9; Length 82; Best Local Similarity 100.0%; Pred. No. 7.6e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 9; Lei
Local Similarity 100.0%; Pred. No. 7.5e+02;
nes 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/09/738,626

PRIOR APPLICATION NUMBER: 099/377484

PRIOR FILING DATE: 1999-12-16

PRIOR PLILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: 0P 00/159162

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059

SOFTWARE: PATENTIN VET: 3.0

SEQ ID NO 4641

LENGTH: 81
                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 82
                                                                                                                                                                                                                                                                                                                    APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; Sequence 4641, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Corynebacterium glutamicum
                                                                          APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                  TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                       HAYASHI, MIKIRO
                                                                                                                                                                                   OCHIAI, KEIKO
YOKOI, HARUHIKO
                                                                                                                                 ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
US-09-858-664A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 EILLKN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 BIVKIL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 EIVKIL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 EILLKN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-738-626-4641
```

ö

RESULT 174

RESULT 172

```
WESUL 1/3

US-10-697-263-33

Sequence 33, Application US/10697263

Sequence 33, Application US/10697263

Publication No. US20040063142A1

SERVERAL INFORMATION:

APPLICANT: WEI, Ming-Hui, et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: 10/210/697,263

CURRENT FILING DATE: 2003-10-31

PRIOR APPLICATION NUMBER: 09/859,664

PRIOR PILING DATE: 2001-022

PRIOR PILING DATE: 2001-02-17

PRIOR PILING DATE: 2001-11-14

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FEASESEQ for Windows Version 4.0

SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (69) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-877-1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                     GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION:
FILE REFERENCE: PC005
CURRENT APPLICANTION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1643
LIENGTH: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 12; Length 82; 100.0%; Pred. No. 7.6e+02; Ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 9; Length 82;
100.0%; Pred. No. 7.6e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1643, Application US/10242515; Publication No. US20040009488A1
                   Sequence 1643, Application US/09764877
Patent No. US20020147140A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.8
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 EILLKN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 SSGLLV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 SSGLLV 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 EILLKN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 176
US-10-242-515-1643
                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
US-09-764-877-1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (81)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-697-263-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) LOCATION: (81) ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-242-515-1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
LOCATION: (51)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (69) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                  CURRENT APPLICATION NUMBER: US/10/242,515
CURRENT FILING DATE: 2002-09-13
FRIOR PAPLICATION NUMBER: 09/764,877
FRIOR PELING DATE: 2001-01-71
FRIOR PELING DATE: 2001-01-31
FRIOR APPLICATION NUMBER: 06/199,065
FRIOR APPLICATION NUMBER: 60/190,628
FRIOR APPLICATION NUMBER: 60/214,886
FRIOR APPLICATION NUMBER: 60/214,886
FRIOR APPLICATION NUMBER: 60/217,487
FRIOR APPLICATION NUMBER: 60/217,487
FRIOR APPLICATION NUMBER: 60/225,758
FRIOR APPLICATION NUMBER: 60/225,758
FRIOR APPLICATION NUMBER: 60/225,758
FRIOR APPLICATION NUMBER: 60/225,758
FRIOR APPLICATION NUMBER: 60/225,478
FRIOR APPLICATION NUMBER: 60/225,447
FRIOR APPLICATION NUMBER: 60/225,447
FRIOR APPLICATION NUMBER: 60/213,496
FRIOR FILING DATE: 2000-07-11
FRIOR PELING DATE: 2000-07-11
FRIOR PELING DATE: 2000-07-14
FRIOR FILING DATE: 2000-07-14
FRIOR FILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-07-14
FRIOR FILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-08-14
FRIOR FILING DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3412, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEC ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
                                TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC005C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.8%; Score 6; DB 15; Le
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
APPLICANT: Rosen et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 SSGLLV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 SSGLLV 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 177
US-09-764-891-3412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1643
LENGTH: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3412
LENGTH: 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

g

```
Sequence 245645, Application US/10424599

Sequence 245645, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 245645

LENGTH: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: MAP TO ACO11456.2

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN PELACENTA, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN PELY, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN PELY, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN PERY, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN PERY, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN PERY, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN PERY, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN PERY, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN PERY, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN PERY, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN PERY, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN PERY, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN PERY, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN PERY, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN PERY, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN PERY, SIGNAL = 2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB.9; Length 84; 100.0%; Pred. No. 7.7e+02; tive 0; Mismatches 0; Indels
                         PRIOR AFFLIANTION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELLOR ON NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2010-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_6384C.1.pep US-10-424-599-245645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 VELSTF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 VELSTF 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-864-761-37566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37566, Application US/09864761
Patent No. US20020048763A1
APPLICANT: Name Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Harzel, David K.
APPLICANT: Harzel, David K.
APPLICANT: Chen, Wenhaheng
ITITE OF INVENTION: USONOWEDERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: UNMER EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-00-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
PRIOR FILING DATE: 2000-09-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 231338, Application US/10424599
Sequence 231338, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Tou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 1010/4223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 231338
                                                                                                                                                                o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                                    Gaps
                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 6; DB 12; Length 83; 100.0%; Pred. No. 7.7e+02; tive 0; Mismatches 0; Indels
                                                                                    Length 83;
                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_5091C.1.pep
US-10-424-599-231338
                                                                                DB 10; Le
                                                                            1.8%; Score 6; DB 1
100.0%; Pred. No. 7.7
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
                                                                            Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 SSFQKE 311
                                                                                                                                                                                                                                        75 SSGLLV 80
                                                                                                                                                                                                                                                                                                                    21 SSGLLV 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 SSFOKE 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-424-599-231338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-864-761-37566
US-09-764-891-3412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
```

ð

ò

```
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US20040009474Alel Human Polynucleotides and Polypeptides Ence
FILE REPERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOPTWARE: FASKSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-301-1603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (45)
OTHER INFORMATION: Kaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (73)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                     1.8%; Score 6; DB 9; Length 86;
100.0%; Pred. No. 7.9e+02;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 8152, Application US/09864408A; Publication No. US20040009474A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Lac 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LFSKSH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 LFSKSH 18
                                      12 KMPLFS 17
3 KMPLFS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-864-408A-8152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
LOCATION: (30)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
LOCATION: (81)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                               a
  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 211413, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICANT: 0003-04-28
UNUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                 Sequence 186473, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION.
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 186473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                               .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 12; Length 85; 100.0%; Pred. No. 7.8e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.8%; Score 6; DB 12; Length 85; Best Local Similarity 100.0%; Pred. No. 7.8e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                      Length 84;
                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) OTHER INFORMATION: Clone ID: PAT_MRT3847_139399C.1.pep
US-10-424-599-186473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Clone ID: PAT_MRT3847_32932C.1.pep
                  1.8%; Score 6; DB 12; Le
100.0%; Pred. No. 7.7e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)..(85)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 6; Conservative
                  Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Glycine max
                                                                                                       228 SLKLLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 EIVKIL 57
                                                                                                                                              34 SLKLLG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 EIVKIL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-424-599-211413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-424-599-211413
                                                                                                                                                                                                                                   US-10-424-599-186473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 211413
LENGTH: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
```

ð

SEQ ID NO 8152

```
US-10-424-599-165968

Sequence 165968, Application US/10424599

Sequence 165968, Application US/10424599

Publication No. US20040031072A1

SEQUENCE INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: APPLICANT: Avoid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 2003-04-28

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 165968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 251249, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: APPLICANT: And Withua

APPLICANT: APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILLE REFERENCE: 39-21 (5323) B

CURRENT FILING DATE: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

LENGTH: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 12; Length 88; 100.0%; Pred. No. 8.1e+02; tive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12; Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_120885C.1.pep
US-10-424-599-165968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: PAT_MRT3847_68906C.1.pep
US-10-424-599-251249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 12; L. 100.0%; Pred. No. 8.1e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 8935, Application US/10335977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 VEILLK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 QSLKLL 232
                                             75 VKILKD 80
      VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 VEILLK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-424-599-251249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 OSLKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-335-977-8935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 189
                                  Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
      à
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: La Covale Thomas J
APPLICANT: La Covalic David K
APPLICANT: And Vibua
APPLICANT: Zhou Vibua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE PERENERAL APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 153190
                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                         Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 257, Application US/09764887
Fatent No. US202020042096A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPRENCE: PALIS
CURRENT APPLICATION NUMBER: US/09/764,887
CURRENT APPLICATION ADATE: 2001-01-17
FILE REPRENCE: PALIS
SEQ ID NOS: 2010-01-17
NUMBER OF SEQ ID NOS: 658
SOFTWARE PATENTION OF SEQ ID NOS: 2.0
SEQ ID NO 257
LENGTH: 88
                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 87;
                                                                                                      Query Match 1.8%; Score 6; DB 11; Length 87; Best Local Similarity 100.0%; Pred. No. 8e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 12; Length 87;
100.0%; Pred. No. 8e+02;
vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 9; Length 88;
100.0%; Pred. No. 8.1e+02;
vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_109355C.1.pep
US-10-424-599-153190
                                                                                                                                                                                                                                                                                                                                                ; Sequence 153190, Application US/10424599
; Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                             63 TEAVAQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                             63 TEAVAQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 KEPPTE 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 KEPPTE 20
                                                                                                                                                                                                                                                                                                    RESULT 185
US-10-424-599-153190
                                                             US-09-864-408A-8152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (87)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-764-887-257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-764-887-257
LENGIH: 87
                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db
```

·;

.. 0

```
2000-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                    PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                         ADPLICATION.

ADPLICANT: DOUGLAS SMITH et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES

RELATING TO HELICOBACTER PYLORI FOR

DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.

TILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PA113C1
CURRENT APPLICATION NUMBER: US/10/073,961
CURRENT FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: 09/764,887
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR RILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 6; DB 12; Length 88; 100.0%; Pred. No. 8.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...88
SEQUENCE DESCRIPTION: SEQ ID NO: 8935:
                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mandragouras, Amy E. REGISTRATION VUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
                                                                                                                                 ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Helicobacter pylori
                                                                                                                                                                                                             ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/10073961
o. US20030077602A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 8935:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 88 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
                                                                                                                                                                  CITY: Boston
STATE: Massachusetts
Publication No. US20040052799A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 IRDLKK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 IRDLKK 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-073-961-257; Sequence 257, Applica; Publication No. US200; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-335-977-8935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
RELIGIORATION NUMBER: 60/220,964

RAPPLICATION NUMBER: 60/220,964

RELING DATE: 2000-07-28

RELING DATE: 2000-10-20

REPLING DATE: 2000-11-20

REPLING DATE: 2000-11-17

REPLING DATE: 2000-11-17

RAPPLICATION NUMBER: 60/249,299

RELING DATE: 2000-11-17

RAPPLICATION NUMBER: 60/241,785

RELING DATE: 2000-10-20

REPLING DATE: 2000-10-20

REPLING DATE: 2000-10-20

REPLING DATE: 2000-11-01

REPLING DATE: 2000-11-01

REPLING DATE: 2000-11-01

REPLING DATE: 2000-11-01
                                                                                                                             FILING DATE: 2000-07-26
APPLICATION NUMBER: 60/217,496
FILING DATE: 2000-07-11
                                                                                                                                                                                                                                FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/218,290
FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-08-22
APPLICATION NUMBER: 60/216,647
FILING DATE: 2000-07-07
APPLICATION NUMBER: 60/225,267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-12-08
APPLICATION NUMBER: 60/235,834
FILING DATE: 2000-09-27
APPLICATION NUMBER: 60/234,274
FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-08-14

FILING DATE: 2000-08-14

FILING DATE: 2000-09-29

APPLICATION NUMBER: 60/224,519
APPLICATION NUMBER: 60/217,487
FILING DATE: 2000-07-11
                        FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/225,758
                                                                         FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/220,963
FILING DATE: 2000-07-26
                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/226,868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/216,880
FILING DATE: 2000-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/225,270 FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/251,869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-09-21
APPLICATION NUMBER: 60/234,223
FILING DATE: 2000-09-21
APPLICATION NUMBER: 60/228,924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-08-30
APPLICATION NUMBER: 60/224,518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/236,368 FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/251,856
FILING DATE: 2000-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-09-25
APPLICATION NUMBER: 60/229,343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/229,287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/229,513
FILING DATE: 2000-09-05
                                                                                                                                                                                                          APPLICATION NUMBER: 60/225,447
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/225,757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/251,868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/229,344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/234,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-09-01
APPLICATION NUMBER: 60/229,345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILING DATE: 2000-12-08
```

```
OR FILING DATE: 2000-08-14

OR APPLICATION NUMBER: 60/249,218

OR APPLICATION NUMBER: 60/249,218

OR APPLICATION NUMBER: 60/249,208

OR FILING DATE: 2000-11-17

OR APPLICATION NUMBER: 60/249,213

OR FILING DATE: 2000-11-17

OR APPLICATION NUMBER: 60/249,212

OR APPLICATION NUMBER: 60/249,207

OR APPLICATION NUMBER: 60/249,207

OR APPLICATION NUMBER: 60/249,207

OR APPLICATION NUMBER: 60/249,207

OR APPLICATION NUMBER: 60/249,207

OR APPLICATION NUMBER: 60/249,207

OR APPLICATION NUMBER: 60/249,207

OR APPLICATION NUMBER: 60/249,207

OR PILING DATE: 2000-11-17
                                                                                                                  R FILING DATE: 2000-09-05

R APPLICATION NUMBER: 60/236,367

R PILING DATE: 2000-09-29

R APPLICATION NUMBER: 60/237,039

R FILING DATE: 2000-10-02

R APPLICATION NUMBER: 60/237,038

R APPLICATION NUMBER: 60/237,038

R APPLICATION NUMBER: 60/237,038

R APPLICATION NUMBER: 60/235,700

R FILING DATE: 2000-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R FILING DATE: 2000-10-02

R APPLICATION NUMBER: 60/240,960

R APPLICATION NUMBER: 60/239,935

R FILING DATE: 2000-10-13

R FILING DATE: 2000-10-13

R FILING DATE: 2000-10-13

R FILING DATE: 2000-10-13

R APPLICATION NUMBER: 60/239,937

R FILING DATE: 2000-10-13

R APPLICATION NUMBER: 60/241,787

R FILING DATE: 2000-10-20

R APPLICATION NUMBER: 60/241,787

R FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/236,802
FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/237,037
FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/237,040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/215,135
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/225,266
PRIOR FILING DATE: 7000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIOR FILING DATE: 2000-11-17
RIOR APPLICATION NUMBER: 60/249,210
RIOR FILING DATE: 2000-11-17
RIOR PELICAL NUMBER: 60/226,681
PRIOR FILING DATE: 2000-08-22
RIOR APPLICATION NUMBER: 60/225,759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/225,213
PRIOR FILING DATE: 2000-08-14
PRIOR PELING DATE: 2000-08-12
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/227,182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RICR APPLICATION 2000-08-14
PRIOR PELICATION NUMBER: 60/235,836
PRIOR APPLICATION NUMBER: 2000-09-27
                                          FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/229,509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/246,532
FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/249,216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION DATE: 2000-09-2,

RILING DATE: 2000-09-2,

APPLICATION NUMBER: 60/230,438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,211
PRIOR FILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/249,215
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/231,413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/249,244
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/249,217
FILING DATE: 2000-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/249,264
                                      2000-09-08
                                                                                                                            PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR
```

```
US-10-424-599-268688, Application US/10424599

Sequence 268688, Application US/10424599

Publication No. US20040031072A1

SEQUENCE LA ROBARTION:

APPLICANT: La Roba Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwai

TITLE OF INVENTION: Blants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION NUMBER: US/10/424,599

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

SEQ ID NO 268688

LENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 14; Length 88; 100.0%; Pred. No. 8.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT3847_84648C.1.pep
US-10-424-599-268688
PRIOR APPLICATION NUMBER: 60/249,214
PRIOR PILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,297
PRIOR PELING DATE: 2000-11-17
PRIOR PELING DATE: 2000-19-14
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-19
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 VKILKD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
```

1.8%; Score 6; DB 12; Length 89;

Query Match

```
APPLICANT: Ocomen, Raymond P. TITLE OF INVENTION: Identification of Polymucleotides INTLE OF INVENTION: Encoding No. US20030158396Alel Helicobacter Polypeptides in the IITLE OF INVENTION: Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16350, Application US/10424599
| Sequence 16350, Application US/10424599
| Sequence 16350, Application No. US20040031072A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Kovalic David K
| APPLICANT: Cao Yongwei
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
| TITLE OF INVENTION: Soy Nucleic Acid Molecules Associated With
| TITLE OF I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.8%; Score 6; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 12; Length 90;
100.0%; Pred. No. 8.2e+02;
rative 0; Mismatches. 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_118713C.1.pep US-10-424-599-163560
                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/882,227
CURRENT APPLICATION NUMBER: US/09/882,227
CURRENT FILING DATE: 2001-06-15
PRIOR FILING DATE: 1997-07-29
NUMBER OF SEQ ID NOS: 638
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 186702, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                     Miller, Charles
Tomb, Jean-Francois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
             Al-Garawi, Amal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 IRDLKK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 IASDAF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 IRDLKK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 IASDAF 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 194
US-10-424-599-163560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-186702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-882-227-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 114
                                     APPLICANT:
APPLICANT:
APPLICANT:
          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                            Gaps
                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۰,
                                                                                                                                                                                                                                                                                                                 Sequence 8936, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
    APPLICANT: DOUGLAS SMITH et al
    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
    RELATING TO HELICOBACTER PYLORI FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 12; Length 89; 100.0%; Pred. No. 8.1e+02; tive 0; Mismatches 0; Indels
                                 Indels
      Pred. No. 8.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 02109-1875
COMPUTER FREADBLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COATION: (B) LOCATION 1...89

SEQUENCE DESCRIPTION: SEQ ID NO: 8936:
US-10-335-977-8936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEB: LAHIVE & COCKFIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 114, Application US/09882227; Publication No. US20030158396A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 8936:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 89 amino acide
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; APPLICANT: Kleanthous, Harold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                               111 TRSPTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329 IRDLKK 334
   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 IRDLKK 41
                                                                                                                                                            28 TRSPTV 33
                                                                                                                                                                                                                                                                                      US-10-335-977-8936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-882-227-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 193
                              Matches
```

ó

ö

```
TITLE OF INVENTION: SOLVE Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFREENCE: 38-21 (53223) B CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 206794
                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.8%; Score 6; DB 12; Length 91; Best Local Similarity 100.0%; Pred. No. 8.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 92;
                                                                                                                                                  Length 90;
                                                                                                                                                                                           0; Indels
                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT3847_95379C.1.pep
US-10-424-599-280571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_28762C.1.pep
US-10-424-599-206794
                                                                                                                                             Query Match
1.8%; Score 6; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
1.8%; Score 6; DB 11; Le
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 6; Conservative 0; Mismatches 0;
       LOCATION: (1)..(90)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 206794, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Chou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 LGELIL 237
                                                                                                                                                                                                                                                                                      61 KILKDN 66
                                                                                                                                                                                                                                           19 KILKDN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 LGELIL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 PAEIVK 19
                                                                                                                                                                                                                                                                                                                                                                                 US-10-424-599-206794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-864-408A-8758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-864-408A-8758
                                                       FEATURE:
                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Anou Yihua
APPLICANT: Cano Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(35223)
EURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                         Query Match
1.8%; Score 6; DB 12; Length 90;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.8%; Score 6; DB 12; Length 90; Best Local Similarity 100.0%; Pred. No. 8.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_139604C.1.pep
US-10-424-599-186702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_141013C.1.pep
US-10-424-599-188262
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 186702
LENGTH: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 188262, Application US/10424599 ; Publication No. US20040031072A1 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 280571, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                   TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                    289 PIVEIL 294
                                                                                                                                                                                                                                                                                                                                                                                               39 PIVEIL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 NLAILE 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 NLAILE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-424..599-188262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-424-599-280571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 280571
LENGTH: 90
                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ਨੇ
```

```
Sequence 256649, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
APPLICANT: APPLICANT: Noraled With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5322)B
CURRENT FILING DATE: 2003-04-28
UNUMBER OF SEQ ID NOS: 285684
US-10-424-599-161289
; Sequence 161289, Application US/10424599
; Sequence 161289, Application WS/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Zhou Yihua
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JADICATION NO. 00--
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.8%; Score 6; DB 12; Length 93; Best Local Similarity 100.0%; Pred. No. 8.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.8%; Score 6; DB 12; Length 93; Best Local Similarity 100.0%; Pred. No. 8.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Clone ID: PAT_MRT3847_116662C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: Clone ID: PAT_MRT3847_73778C.1.pep
US-10-424-599-256649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 8937, Application US/10335977 ; Publication No. US20040052799A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 ILLKON 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 SLKLLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 ILLKNO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 SLKLLG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-424-599-256649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-424-599-161289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 256649
LENGTH: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 161289
LENGTH: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-335-977-8937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                             Sequence 157299, Application US/10424599
| Publication No. US20040031072A1
| GENERAL INFORMATION |
| APPLICANT: La Rosa Thomas J
| APPLICANT: La Rosa Thomas J
| APPLICANT: Anounce of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the property of the pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23814, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Low Youngwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLE REFERENCE: 38-21 (5223.8)
CURRENT APPLICANT: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 92
LENGTH: 92
LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 12; Length 92; 100.0%; Pred. No. 8.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.8%; Score 6; DB 12; Length 92; Best Local Similarity 100.0%; Pred. No. 8.4e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Clone ID: PAT_MRT3847_113060C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: PAT_MRT3847_53159C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)..(92)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 LKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 LKLLGE 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 IVKILK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 IVKILK 59
                                   PAEIVK 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-424-599-233814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-157298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

ö

```
Sequence 282678, Application US/10424599; Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILER REFERENCE: 38-21(5323)B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OP SEQ ID NOS: 285684
LENGTH: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 284907, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(3523)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó:
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 1.8%; Score 6; DB 12; Length 97; Best Local Similarity 100.0%; Pred. No. 8.8e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 97;
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:

CHER INFORMATION: Clone ID: PAT_MRT3847_99299C.1.pep

US-10-424-599-284907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_9727C.1.pep
US-10-424-599-282678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Le
                 100.0%; Pred. No. 8.8e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)..(97)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 1
100.0%; Pred. No. 8.8
tive 0; Mismatches
              Best Local Similarity 100. Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279 VFVASP 284
                                                                                                                  81 TLIADL 86
                                                                                                                                                             ||||||
48 TLIADL 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 VFVASP 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 LLVTLI 83
                                                                                                                                                                                                                                                                                                                        US-10-424-599-282678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-424-599-284907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 284907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                  Matches
                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 234125, Application US/10424599
Sequence 234125, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: DIABER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/202-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 234125
LENGTH: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 12; Length 96; 100.0%; Pred. No. 8.7e+02; Ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_53439C.l.pep
US-10-424-599-234125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALECTRICAL AND STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE STREET OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/993,002
FILING DATE: 17:DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (B) LŌCATION 1...96.
SEQUENCE DESCRIPTION: SEQ ID NO: 8937;
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
                                   ADDRESSEE: LAHIVE & COCKFIELD STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Helicobacter pylori
                                                                                                                                        STATE: Massachusetts
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                 COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: UNIX
                                                                                                        CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 IRDLKK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 IRDLKK 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-424-599-234125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-335-977-8937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
```

1.8%; Score 6; DB 12; Length 97;

Query Match

```
Sequence 170968, Application US/10424599

Fublication No. UG20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 170968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                              APPLICANT: Cao Yongwei TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Improvement FITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53223)B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.8%; Score 6; DB 12; Length 99; Best Local Similarity 100.0%; Pred. No. 9e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.8%; Score 6; DB 12; Length 99; Best Local Similarity 100.0%; Pred. No. 9e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_111761C.1.pep
US-10-424-599-155860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: PAT_MRT3847_12539C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(99)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 194060, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 FNNILR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 FNNILR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 GLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-424-599-170968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-424-599-170968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-424-599-194060
                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 155860
LENGTH: 99
                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                              Sequence 3935, Application US/10369493
; Sequence 3935, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
    APPLICANT: Cao, Yongwei
    APPLICANT: Hinkle, Gregory J.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLICANT: Goldman, Barry S.
    APPLRON NUMBER: Goldman, Barry S.
    APPLRON NUMBER: Goldman, Barry S.
    APPLRON NUMBER: Goldman, Barry S.
    APPLRON NUMBER: Goldman, Barry S.
    APPLRON NUMBER: Goldman, Barry S.
    APPLRON NUMBER: Goldman, Barry S.
    APPLRON NUMBER: Goldman, Barry S.
    APPLRON NUMBER: Goldman, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Solu Yihua
APPLICANT: Solu Yihua
APPLICANT: Can Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 147796
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 15; Length 97; 100.0%; Pred. No. 8.8e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.8%; Score 6; DB 12; Length 99; Best Local Similarity 100.0%; Pred. No. 9e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , OTHER INFORMATION: Clone ID: PAT_MRT3847_104481C.1.pep
US-10-424-599-147796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 155860, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-424-599-147796
; Sequence 147796, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Neurospora crassa
US-10-369-493-3935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 RDLKKT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 EIVKIL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 RDLKKT 11
12 LLVTLI 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 EIVKIL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 210
US-10-424-599-155860
                                                                                                              RESULT 208
US-10-369-493-3935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
```

ð

. 0

Indels

290 IVEILL 295

Length 101;

```
; OTHER INFORMATION: Clone ID: PAT_MRT3847_103066C.1.pep
US-10-424-599-146233
                                                                                                                                                                   Query Match
1.8%; Score 6; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 6; Conservative 0; Mismatches 0;
                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 164813, Application US/10424599
Publication No. US20040031072A1
Publication No. US20040031072A1
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53.23.) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: About Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Solution Sol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERNCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 194060
LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 12; Length 100; 100.0%; Pred. No. 9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 6; DB 12; Length 99; 100.0%; Pred. No. 9e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_119844C.1.pep
US-10-424-599-164813
                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Clone ID: PAT_MRT3847_17262C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 146233, Application US/10424599; Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 KPENLK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 KPENLK 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 PTEAVA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 PTEAVA 83
                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-424-599-194060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-424-599-164813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-424-599-146233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 164813
LENGTH: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
```

```
..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.8%; Score 6; DB 15; De Best Local Similarity 100.0%; Pred. No. 9.1e+02; Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEE FULL-LENGTH CONA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2002-09-14
                                                                           US-10-094-749-1868; Sequence 1868, Application US/10094749; Publication No. US20030219741A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 852, Application US/09925302; Patent No. US20020044941A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
                                                                                                                                                          APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
                                                                                                                                                                                                                                                           ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1868
                                                                                                                                                                                                                                                                                                                                                             NAGAI, KEIICHI
IRIE, RYOTARO
                                                                                                                                                                                                                       WAKAMATSU, AI
SATO, HIROYUKI
                                                                                                                                                                                                                                                                                                                                             OTSUKA, KAORU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-094-749-1868
                                                                                                                                                                                                                                                                                        ISONO, 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 SLKLLG 233
16 İVBİLL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 SLKLLG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-925-302-852
                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                  APPLICANT
APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT
                                                                                                                                                                                                                                                                                                                          APPLICANT
                                                                                                                                                                                                                                                                                                                                                               APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT
                                                            RESULT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 216
```

```
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE PEPERENCE: 38-21(5323.9)B CURRENT APPLICATION NUBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: MAP TO AL121778.4

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 20

OTHER INFORMATION: EXPRESSED IN BLALOO, SIGNAL = 75

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN HEAR, SIGNAL = 7.9

OTHER INFORMATION: EXPRESSED IN FEAL, SIGNAL = 3.4

OTHER INFORMATION: SWISSPROT HIT: P25444, EVALUE 1.00e-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.8%; Score 6; DB 9; Length 102;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
         PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PELING DATE: 2000-09-21

PRIOR PELING DATE: 2000-09-21

PRIOR PELING DATE: 2000-09-21

PRIOR PELING DATE: 2000-09-30

PRIOR PELING DATE: 2000-06-30

PRIOR PELING DATE: 2000-06-30

PRIOR PELING DATE: 2010-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers: 1.1

**COLID NO 36927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_67090C.1.pep US-10-424-599-249236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: (1)..(103)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 249236, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 FKVFVA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 FKVFVA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-424-599-249236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-864-761-36927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 249236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE APPLICATION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERBUCE: Aeomica.x-1
CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-302-852
                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (91)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.8%; Score 6; DB 9; Length 102; Best Local Similarity 100.0%; Pred. No. 9.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PRILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR PELICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUARGENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36927, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 VADFLE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 VADFLE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-864-761-36927
                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                     LOCATION: (74)
                                                                                                                      SEQ ID NO 852
LENGTH: 102
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
```

Gaps

```
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
TITLE DE TOUGHT: Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Severit Sever
                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.8%; Score 6; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                           1.8%; Score 6; DB 9; Length 104;
100.0%; Pred. No. 9.4e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.8%; Score 6; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THILE OF INVENTION: variants of PROTEIN KINASES THILE OF INVENTION: variants of PROTEIN KINASES FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
FRIOR PILING DATE: 2000-11-28
FRIOR PELING DATE: 2000-11-28
FRIOR PELING DATE: 2000-01-5
FRIOR PILING DATE: 2000-04-15
FRIOR PILING DATE: 2000-04-12
FRIOR PILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 273
FRIOR FILING DATE: 2000-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 177, Application US/09771161A Patent No. US20020110811A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 478, Application US/09876997
Publication No. US20030152921A1
GENERAL INFORMATION:
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-876-997-478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                  189 DLLTRH 194
                                                                                                                                                     Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 DLLTRH 194
                                                                                                                                                                                                                                                                                                                                       54 DLLTRH 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 DLLTRH 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-771-161A-177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER SOFTWARE: Paten
SEQ ID NO 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-771-161A-177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-876-997-478
                                                  US-09-731-872-478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 177
                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 222
                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-US-131-872-478

Sequence 478, Application US/09731872

Sequence 478, Application US/09731872

Sequence 478, Application US/09731872

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

APPLICANT: Bober, Severin

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

FURRENT APPLICATION NUMBER: US/09/731,872

CURRENT PILING DATE: 2000-12-07

PRIOR FILING DATE: 1999-12-08

PRIOR FILING DATE: 2000-03-06

NUMBER OF SEQ ID NOS: 482

SOFTWARE: Patent.pm

SEQ ID NO 478

LENGTH: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Conley, Pamela
APPLICANT: Conley, Pamela
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Taw, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
TITLE OF INVENTION: Thereby
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICANTION NUMBER: US/09/867,550
CURRENT FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)

OTHER INFORMATION: Wherein Xaa may be any one of Leu or Ser or Trp or Pro or Gln or OTHER INFORMATION: Met or Thr or Lys or Val or Ala or Glu or Gly

NAME/KEY: VARIANT

LOCATION: (104)

OTHER INFORMATION: Wherein Xaa may be any one of Ala or Pro or Ser or Thr

US-09-867-550-76
                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                       .;
                                       1.8%; Score 6; DB 12; Length 103; 100.0%; Pred. No. 9.3e+02; Ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.8%; Score 6; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 76, Application US/09867550 ; Patent No. US20020082206A1
Query Match
Best Local Similarity 100.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 IVEILL 295
                                                                                                                                                                              81 TLIADL 86
                                                                                                                                                                                                                                                   73 TLIADL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 IVELL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-731-872-478
                                                                                                                                                                                                                                                                                                                                                                                             US-09-867-550-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 76
LENGTH: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                               g
```

```
US-10-424-599-200671
US-10-424-599-200671
Sequence 200671, Application US/10424599
Publication No. US20040031072A1
Sequence 200671.
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 200671
LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 267540, Application US/10424599
| Publication No. US20040031072A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Zhou Yihua
| APPLICANT: Zhou Yihua
| APPLICANT: Zhou Yihua
| APPLICANT: Zhou Yihua
| APPLICANT: APPLICANT: Son Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Son Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| FILE REFERENCE: 38-21(5323) B
| CURRENT APPLICATION NUMBER: US/10/424,599
| CURRENT FILING DATE: 2003-04-28
| NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.8%; Score 6; DB 12; Length 107; Best Local Similarity 100.0%; Pred. No. 9.6e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.8%; Score 6; DB 12; Length 107; Best Local Similarity 100.0%; Pred. No. 9.6e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: PAT_MRT3847_23231C.1.pep
US-10-424-599-200671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_83619C.1.pep
US-10-424-599-267548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 70895, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 KLLGEL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 HKTQPI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 KLLGEL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 HKTOPI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-424-599-267548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 227
US-10-425-114-70895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 267548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                  Sequence 216376, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 216376
LENGTH: Los
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Glenn, Matthew APPLICANT: Grigor, Marray R. APPLICANT: Grigor, Marray R. APPLICANT: Grigor, Marray R. APPLICANT: Molenaar, Adrian J. Grigor in Molenaar, Adrian J. TITLE OF INVENTION: Compositions isolated from bovine TITLE OF INVENTION: Compositions gland and methods for their use. FILE REFERENCE: 11000.1044U1.con
CURRENT APPLICATION: WUMBER: US/10/263,828
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 136
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8: BastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 14; Length 106;
100.0%; Pred. No. 9.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 12; Length 105; 100.0%; Pred. No. 9.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: PAT_MRT3847_37416C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)..(105)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 83, Application US/10263828
Publication No. US20030138905A1
GENERAL INFORMATION:
APPLICANT: Havukkala, Ilkka J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.(
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Glycine max
                            192 TRHKVL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 HEPLAK 157
                                                                            27 TRHKVL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 HEPLAK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 KKTDKA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 KKTDKA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Bovine
US-10-263-828-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: unsure
                                                                                                                                                                                    US-10-424-599-216376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-424-599-216376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-263-828-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                         d
                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

Gaps

.. 0

Gaps

0;

```
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 191237
LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
us-10-025-

APPLICANT: Tabaeka, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313) B

CURRENT APPLICATION NUMBER: US/10/425,114

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 70895

TYPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAPE: TAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 178787, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53223)
GURRENT APPLICATION NUMBER: US/10/424,599
GURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 178787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19137, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.8%; Score 6; DB 12; Length 107;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_132461C.1.pep US-10-424-599-178787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: LIB3959-004-D11_FLI.pep
US-10-425-114-70895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.8%; Score 6; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)..(108)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 KLLGEL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 KLLGEL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 KKTDKA 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 KKTDKA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-424-599-178787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 229
US-10-424-599-191237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
```

```
APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US20040009474Alel Human Polynucleotides and Polypeptides Enco
FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.8%; Score 6; DB 11; Length 109; Best Local Similarity 100.0%; Pred. No. 9.8e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                       1.8%; Score 6; DB 12; Length 108; 100.0%; Pred. No. 9.7e+02; tive 0; Mismatches 0; Indels
) OTHER INFORMATION: Clone ID: PAT_MRT3847_14706C.1.pep
US-10-424-599-191237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FLING DATE: 2000-055-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 43428, Application US/10282122A; Publication No. US20040029129A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               Sequence 6796, Application US/09864408A Publication No. US20040009474A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                      Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                  227 QSLKLL 232
                                                                                                                                                                                                              44 OSLKLL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 GLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 GLLVTL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 231
US-10-282-122A-43428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-864-408A-6796
                                                                                                                                                                                                                                                                                                            US-09-864-408A-6796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 6796
LENGTH: 109
                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
```

```
ö
                      PRIOR FILING DATE: 2000-05-20, PRIOR FILING DATE: 2000-05-20, PRIOR PILING DATE: 2000-05-26, PRIOR PILING DATE: 2000-05-26, PRIOR PILING DATE: 2000-05-26, PRIOR PILING DATE: 2000-09-06, PRIOR PILING DATE: 2000-09-06, PRIOR PILING DATE: 2000-09-06, PRIOR PELING DATE: 2000-09-06, PRIOR PILING DATE: 2000-09-06, PRIOR PELING DATE: 2000-10-23, PRIOR PILING DATE: 2000-10-23, PRIOR PILING DATE: 2000-10-23, PRIOR PILING DATE: 2000-11-27, PRIOR PAPLICATION NUMBER: 60/257, 931, PRIOR PAPLICATION NUMBER: 60/257, 931, PRIOR PILING DATE: 2001-12-27, PRIOR PILING DATE: 2001-12-27, PRIOR PILING DATE: 2001-12-27, PRIOR PILING DATE: 2010-12-26, PRIOR PILING DATE: 2010-12-26, PRIOR PILING DATE: 2010-12-26, PRIOR PILING DATE: 2010-12-26, PRIOR PILING DATE: 2010-12-16, PRIOR APPLICATION NUMBER: 60/269, 308, PRIOR PILING DATE: 2010-102-16, PRIOR PILING DATE: 2010-102-16, PRIOR PILING DATE: 2010-102-16, PRIOR PILING DATE: 2010-102-16, PRIOR PILING DATE: 2010-102-16, PRIOR PILING DATE: 2010-102-16, PRIOR PILING DATE: 2010-102-16, PRIOR PILING DATE: 2010-102-16, PRIOR PILING DATE: 2010-102-16, PRIOR PILING DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PRIOR DATE: 2010-102-16, PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: U5/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 12; Length 109;
100.0%; Pred. No. 9.8e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 71923, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2003-02-20
PRIOR PAPPLICATION WUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-07
PRIOR PELING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PELING DATE: 2000-02-3
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 EKLLQS 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 EKLLOS 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-282-122A-43428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-282-122A-71923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 43428
LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

```
TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
FULE REFERENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cao, Yongwei TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53113)B CURRENT APPLICATION NUMBER: US/10/425,114
                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                           Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SEQ ID NO 71923
LENGTH: 109
                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                    Query Match
1.8%; Score 6; DB 12; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 12; Length 109;
100.0%; Pred. No. 9.8e+02;
rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_75368C.1.pep
US-10-424-599-258409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)..(109)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 258409, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Staphylococcus haemolyticus
US-10-282-122A-71923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 46701, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhou, Yihua
Kovalic, David K.
Screen, Steven E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.(
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                199 ADFLEQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 ADFLEQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 ILKDNL 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 ILKDNL 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-424-599-258409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 234
US-10-425-114-46701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 258409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 233
                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

```
FEATURE:
// OTHER INFORMATION: Clone ID: PAT_MRT3847_88632C.1.pep.US-10-424-599-273101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
                      ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                          27 ILEKQD 32
                                                                                                                                                                                                                                                    83 ILEKOD 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 LIDFEG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 LIDFEG 62
                                                                                                                                                                                                                                                                                                             RESULT 237
US-10-424-599-181030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-424-599-181030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-424-599-188662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unBure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 238
                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ଚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-424-599-266911

Sequence 266911, Application US/10424599

Publication No. US20040031072A1

Sequence 266911, Application US/10424599

Publication No. US20040031072A1

APPLICANT: La Rosa Thomas J

APPLICANT: APPLICANT: Acou Yihua

APPLICANT: APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 266911

LENGTH: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 273101, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Covalic David K
APPLICANT: Covalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
SEQ ID NO 273101
LENGTH: 111
TYPE: PRT
                                                                                                                                                                                                                                                                      ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                            Query Match
1.8%; Score 6; DB 12; Length 110;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 12; Length 111;
100.0%; Pred. No. 9.9e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Clone ID: PAT_MRT3847_83040C.1.pep
                                                                                                                                                 ; OTHER INFORMATION: Clone ID: 700570435_FLI.pep
US-10-425-114-46701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(111)
OTHER INFORMATION: unsure at all Xaa locations
CURRENT FILING DATE: 2003-04-28 WINDERS OF SEQ ID NOS: 73128 SEQ ID NO 46701 LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                              79 LVTLIA 84
                                                                                                                                                                                                                                                                                                                                      71 LVTLIA 76
                                                                                                     ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 VKILKD 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-424-599-266911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-424-599-273101
                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                à
```

```
Sequence 181330, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO. 181030
LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 188662, Application US/10424599
Publication No. US20040031072A1
Publication No. US20040031072A1
Publication No. US20040031072A1
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 18-21(5.322)B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 285684
                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
Query Match
1.8%; Score 6; DB 12; Length 111;
Best Local Similarity 100.0%; Pred. No. 9.98+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 12; Length 113;
100.0%; Pred. No. 1e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: PAT_MRT3847_134484C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_141376C.1.pep
US-10-424-599-188662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)..(113)
OTHER INFORMATION: unsure at all Xaa locations
```

```
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE AUDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BLA74, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BLA74, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BRA74, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.8%; Score 6; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING OPERATING MSDOS version 6.2 SOFTWARE: ASCII Text
      PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-01-30
PRIOR FILING DATE: 2000-01-30
PRIOR FILING DATE: 2000-01-30
PRIOR FILING DATE: 2000-01-30
PRIOR FILING DATE: 2000-05-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 68, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 QSLKLL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 OSLKLL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION:
US-09-864-761-37175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 37175
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-765-272-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                       Sequence 235299, Application US/10424599

Publication No. US2004003107241

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: APPLICANT: Along

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: NUMBER: US/10/424,599

CURRENT APPLICANTON NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28
                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
1.8%; Score 6; DB 12; Length 113;
100.0%; Pred. No. 1e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 12; Length 116;
100.0%; Pred. No. 1e+03;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: PAT_MRT3847_54502C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT PILING DATE: 2001-05-23
PRIOR PILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-06-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRELICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR PRELICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37175, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                               Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 YEKLIQ 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 YEKLLO 105
                                                                                                                     23 DNLAIL 28
                                                                                                                                                                                  10 DNLAIL 15
                                                                                                                                                                                                                                                                                                        US-10-424-599-235299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-424-599-235299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-864-761-37175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 235299
LENGTH: 116
      Query Match
                                                                                                                        à
                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

; 0

Gaps

; 0

```
US-09-939-980-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-278-087A-50
                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: No. US20020082234Alel Prokaryotic Polynucleotides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 9; Length 117;
100.0%; Pred. No. 1e+03;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: VSA

COMPUTER: VSA
ZIP: 19406-0939
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFFWARE: FastSEQ for Windows Version 2.0
SOFFWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/939,980
FILING DATE: 27-Aug-2001
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/936,165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: amino acid

STRANDEDRESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-765-272-68
                                                                              NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REPERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50549
TELECOMMINICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 347, Application US/09939980; Patent No. US20020082234A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lonetto, Michael
Nicholas, Richard
Pratt, Julie
Reichard, Richard
Rosenberg, Martin
Ward, Judith
                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burnham, Martin
Hodgson, John
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Knowles, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Black, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 FEGKKD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 FEGKKD 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-939-980-347
```

```
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: School, Yihua
APPLICANT: School, Vihua
APPLICANT: School, Jack E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Tabaska, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)8
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ryo Rujii
TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 12; Length 119;
100.0%; Pred. No. 1.1e+03;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                         / Match 1.8%; Score 6; DB 9; Length 117; Local Similarity 100.0%; Pred. No. 1e+03; les 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: 700380835_FLI.pep US-10-425-114-42612
                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 347:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edwards & Angell, LLP
STREET: 101 Federal Street
CITY: BOSTON
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 42612, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50, Application US/10278087A
Publication No. US20030138817A1
GENERAL INFORMATION:
APPLICANT: Shuji Hinuma
Yasuaki Ito
IRLEX: «Unknown»
INFORMATION FOR SEQ ID NO: 347:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02209
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 KILKDN 107
                                                                                                                                                                                                                                                                                                                                                  18 VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                1 VKILKD 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 KILKDN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-425-114-42612
```

```
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                   FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 272118, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/09893737 Patent No. US20020110855A1 GENERAL INFORMATION:
                                                                                                                                                                                                        ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 RCGIML 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 KPENLK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 KPENLK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 RCGIML 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-424-599-272118
                                                                                                                                                                                                                                                       NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                        US-10-424-599-240972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-893-737-26
                                                                                                                                                                                    PRT
                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 240972, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
            COMPUTER: ITAL. KINDER ALLE COMPATIONE
COMPUTER: ITAL PC COMPATIONE
SOSTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/278,087A
FILING DATE: 31-Jan-2003
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION NUMBER: 09/461,436
FILING DATE: 11-MAR-1998
APPLICATION NUMBER: 09/461,436
FILING DATE: 11-MAR-1998
APPLICATION NUMBER: 08/513,974
FILING DATE: 11-MAR-1998
APPLICATION NUMBER: 08/513,974
FILING DATE: 10-AUG-1995
APPLICATION NUMBER: PCT/VP95/01599
FILING DATE: 10-AUG-1995
APPLICATION NUMBER: 7-093989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 14; Length 119;
100.0%; Pred. No. 1.1e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 45753 DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-439-4444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189273
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: 4.0known>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-278-087A-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 6-270017
FILING DATE: 02-NOV-1994
APPLICATION NUMBER: 6-236357
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-236356
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-189274
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 7-057186
FILING DATE: 16-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 7-007177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 20-JAN-1995
APPLICATION NUMBER: 6-326611
FILING DATE: 28-DEC-1994
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-439-4170
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 KDVTQI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 KDVTQI 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-424-599-240972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
```

```
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Applicant: Acid Molecules and Other Molecules Associated With
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 285684
                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                             DB 12; Length 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.8%; Score 6; DB 12; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                   OTHER INFORMATION: Clone ID: PAT_MRT3847_59624C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_87741C.1.pep
US-10-424-599-272118
                                                                                                                                                                          Query Match
1.8%; Score 6; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
ITLE OF INVENTION MANMALIAN SECRETED PROTEINS
FILE REFERENCE: 00-41
CURRENT APPLICATION NUMBER: US/09/893,737
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,446
PRIOR APPLICATION NUMBER: US 60/215,446
PRIOR PILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 329
SOFTWARE: FastSEQ for Mindows Version 3.0
LOCATION: (1)...(121)
OTHER INFORMATION: unsure at all Xaa locations
```

```
Query Match
                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Shou Yihua
APPLICANT: Cano Vongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 175359
LENGTH: 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 186519, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 186519
SEQ ID NO 186519
LENGTH: 125
                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.8%; Score 6; DB 12; Length 125;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                Length 123;
                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_129368C.1.pep
US-10-424-599-175359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_13943C.1.pep
US-10-424-599-186519
                                                                                                                        1.8%; Score 6; DB 9; Ler
100.0%; Pred. No. 1.1e+03;
trive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: (1)..(125)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                ; Sequence 175359, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                6; Conservative
                                                         ; ORGANISM: Homo sapiens
US-09-893-737-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Glycine max
                                                                                                                                                                                                                                         101 VAÇLAÇ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Glycine max
                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                       66 VAQLAQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 AQLAQE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 AQLAQE 84
                                                                                                                                                                                                                                                                                                                             US-10-424-599-175359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-424-599-186519
                   LENGTH: 123
TYPE: PRT
; SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
                                                                                                                                                              Matches
                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
```

```
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Show Yihua
APPLICANT: Can Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 241645
LENGTH: 125
                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                             ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
            Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 12; Length 125; 100.0%; Pred. No. 1.1e+03; tive 0; Mismatches 0; Indels
                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_62038C.1.pep
US-10-424-599-243645
Ouery Match
1.8%; Score 6; DB 12; Le
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                    ; Sequence 243645, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: April 12, 2004, 10:42:31 Job time : 49 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Glycine max
                                                                                                   155 LAKIIL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 QIRDLK 333
                                                                                                                                              89 LAKIIL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 QIRDLK 47
                                                                                                                                                                                                                                             US-10-424-599-243645
```

```
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 15, Appli
Sequence 1553, Ap
Sequence 1575, A
Sequence 5, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 9612, Ap
Sequence 10987, A
Sequence 11246, A
Sequence 11246, A
Sequence 11246, A
Sequence 11246, A
Sequence 11246, A
Sequence 11316, A
Sequence 11316, A
Sequence 11316, A
Sequence 11316, A
Sequence 11316, A
Sequence 11316, A
Sequence 11316, A
Sequence 11316, A
Sequence 11316, A
Sequence 11316, A
Sequence 11316, A
Sequence 11316, A
Sequence 6452, Ap
                                                                 April 12, 2004, 10:33:58 ; Search time 22 Seconds (without alignments) 790:816 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                         1 MKKMPLFSKSHKNPAEIVKI......FADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                          389414
                                                                                                                                                                                                                                                                                                                                    Issued_Patents_Ah:*
!: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
!: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
!: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
!: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
!: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
!: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
!: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                     389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                         Post-processing: Listing first 300 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                         OM protein - protein search, using sw model
                                                                                                                                                                            Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                  US-10-025-730-1
337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLIGO
                                                                                                                                                                                                                           0
                                                                                                                            Perfect score:
                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                          Word size :
                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                         Sequence:
                                                                                                                                                                                                    Searched:
                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 2 3 4 5 4 5 5 6 7 8 8 9 7 8 8 9 7 8 8 9 7 8 8 9 7 8 8 9 7 8 8 9 7 8 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7 8 9 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.
```

28 7 2.1 449 4 US-09-741-243C-8 31	ednence ednence ednence ednence ednence ednence ednence ednence ednence ednence	ence 1, ence 1	000000000000000000000000000000000000000	iequence 21, iequence 64, iequence 64, iequence 63, iequence 54, iequence 55, equence 55, equence 32, equence 688 equence 443 equence 443 equence 443 equence 443 equence 443 equence 688 equence 443 equence 584	Sequence 18411, A Sequence 68, Appl Sequence 68, Appl Sequence 50, Appl Sequence 354, Appl Sequence 355, App Sequence 5393, App Sequence 4824, Appl Sequence 472, Appl Sequence 372, Appl Sequence 372, Appl Sequence 634, Appl Sequence 634, Appl Sequence 634, Appl Sequence 634, Appl Sequence 634, Appl Sequence 634, Appl Sequence 634, Appl Sequence 1265, Appl Sequence 1265, Appl Sequence 1265, Appl Sequence 1265, Appl
C C C C C C C C C C C C C C C C C C C	US-09-741-243C-8 US-09-489-039A-877 US-09-489-039A-978 US-09-056-285A-10 US-08-724-466B-2 US-08-882-164D-2 US-08-649-432-1 US-08-649-432-1 US-08-649-432-1 US-08-649-33C-1 US-08-688-33R-1 US-08-68-33R-1	US-09-220-459-1 US-08-938-669A-32 US-08-946-56BB-1 US-08-822-999-3 US-09-056-285A-8 US-09-039A-1295 US-09-800-729-124 US-09-489-039A-12034 US-08-026-138B-3 US-08-026-138B-3 US-08-026-138B-3 US-09-800-729-124 US-09-800-729-124 US-09-800-729-12034 US-09-800-729-13		US-08-326-119A-21 US-09-621-976-6437 US-09-621-976-6438 US-09-543-681A-6553 US-09-573-681A-6553 US-09-673-395A-510 US-09-673-395A-510 US-09-673-395A-510 US-09-134-001C-4534 US-09-134-001C-6127 US-09-134-000C-6127 US-09-134-000C-6127 US-09-134-000C-6127 US-09-134-000C-6127 US-09-134-000C-6127 US-09-134-000C-6127 US-09-621-976-4368	US-08-25-291A-1941 US-08-961-083-68 US-08-91-165A-347 US-08-513-974B-50 US-08-513-974B-354 US-08-513-974B-354 US-09-134-000C-3508 US-09-134-000C-3508 US-09-328-35-4824 US-09-328-35-4824 US-09-328-35-372 US-09-312-38-372 US-09-732-210-804 US-09-732-210-804
	44444444000000	www.u.u.a.a.a.a.a.a.	4 2 2 4 4 4 1 1 2 2 2 2 1 1 1 1 1 1 1 1	M 性 存 存 存 存 存 存 存 存 存 存 存 存 存 存	***************
	W 4 4 4 4 4 4 4 4 W W W W	504 504 504 504 504 510 620 316 65 65	ы 4 М Ц Ц Ц Ц Ц В В В В Ф Ф Ф Ф Ф Ф Ф В В В В В В В В В	46 61 61 63 64 64 64 64 64 64 64 64 64 64 64 64 64	1117 1117 1119 1119 1119 1128 1129 1131 1133 1134
			, ч ч ч ч ч ч ч ч ч ч ч ч ч ч ч ч ч ч ч		
1 1 1 1 1 1 1 1 1 1		rrrrrrrrrrr	, , , , , , , , , , , , , , , , , , , ,	୬ ୬ ୬ ୬ ୬ ୬ ୬ ୬ ୬ ୬ ୬ ୬ ୬ ୬ ୬ ୬	<u>୰୰୰୰୰୰୰୰୰୰୰୰୰୰୰</u>
	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 4 4 4 4 4 4 4 4 0 10 10 11 0 ሀ ሀ ሠ 4 10 10 10 10 10 10 10 10 10 10 10 10 10	u w w w w w w w w w w w w w w w w w w w	88 88 88 88 88 88 88 88 88 88 88 88 88	1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 12, Appli Sequence 12, Appli Sequence 2, Appli Sequence 12, Appli Sequence 12, Appli Sequence 2, Appli Sequence 2, Appli Sequence 12, Appli Sequence 12, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 2, Appli Seq	zec aniianha
3 US-09-374-493-13 3 US-09-374-493-13 3 US-09-374-824-13 4 US-09-134-824-13 5 US-09-134-902-13 5 US-09-134-000C-3737 5 US-09-134-000C-3737 6 US-09-134-000C-3737 7 US-09-107-532A-4050 1 US-09-107-532A-4050 1 US-09-107-532A-4050 1 US-09-107-532A-2943 1 US-09-107-532A-2943 1 US-09-252-991A-27921 1 US-09-252-991A-27921 1 US-09-252-991A-27921 1 US-09-252-991A-27921 1 US-09-252-991A-27921 1 US-09-252-991A-27921 1 US-09-252-991A-27921 1 US-09-252-991A-27921 1 US-09-252-991A-27921 1 US-09-252-991A-27921 1 US-09-252-991A-27921 1 US-09-252-991A-27921 1 US-09-252-991A-27921 1 US-09-252-991A-27921 1 US-09-333-39-12 1 US-09-333-39-12 1 US-09-333-39-12 1 US-09-333-39-12 1 US-09-333-39-12 1 US-09-333-39-12 1 US-09-333-39-12 1 US-09-333-39-12 1 US-09-333-39-12 1 US-09-333-39-12 1 US-09-333-30-12 1 US-09-333-30-12 1 US-09-333-30-12 1 US-09-333-30-12 1 US-09-333-30-12 1 US-09-333-30-12 1 US-09-333-31-59-12 1 US-09-333-32-139-32-330 1 US-09-333-32-330 1 US-09-252-991A-31854 1 US-09-252-991A-31854 1 US-09-134-000C-4914 1 US-09-252-991A-31854 1 US-09-333-32-330 1 US-09-333-32-332-330 1 US-09-333-32-332-330 1 US-09-333-32-332-332-330 1 US-09-333-32-332-332-332-332-332-332-332-332	
######################################	
11111111111111111111111111111111111111	
Sequence 5, Appli Sequence 54, App Sequence 11504, A Sequence 113120, A Sequence 731, Appli Sequence 731, Appli Sequence 731, Appli Sequence 3120, Appli Sequence 3120, Appli Sequence 3131, Appli Sequence 5210, Appli Sequence 5210, Appli Sequence 5210, Appli Sequence 5210, Appli Sequence 5211, Appli Sequence 5211, Appli Sequence 5211, Appli Sequence 5211, Appli Sequence 5211, Appli Sequence 5211, Appli Sequence 5211, Appli Sequence 5211, Appli Sequence 5211, Appli Sequence 5211, Appli Sequence 5211, Appli Sequence 5211, Appli Sequence 6211, Appli Sequence 6211, Appli Sequence 6211, Appli Sequence 6211, Appli Sequence 1121, Appli Sequence 1121, Appli Sequence 1121, Appli Sequence 1121, Appli Sequence 1121, Appli Sequence 2121, Appli Sequence 2121, Appli Sequence 2131, Appli Sequence 2131, Appli Sequence 2131, Appli Sequence 2131, Appli Sequence 2131, Appli Sequence 2131, Appli Sequence 2131, Appli Sequence 2131, Appli Sequence 2131, Appli Sequence 2131, Appli Sequence 2131, Appli Sequence 2131, Appli Sequence 221, Appli Sequence 221, Appli Sequence 22111, Appli Sequence 22111, Appli Sequence 22111, Appli Sequence 22111, Appli S	
US-08-381-621-5 US-08-459-906-5 US-08-459-906-5 US-08-459-906-5 US-08-459-906-5 US-09-489-039A-13120 US-09-489-039A-13120 US-09-372-3731 US-08-372-381 US-08-372-381 US-08-372-381 US-08-372-381 US-09-322-391A-30905 US-09-134-001C-4854 US-09-134-476-554 US-09-134-476-554 US-09-134-476-554 US-09-134-476-554 US-09-138-452-4965 US-09-138-452-4965 US-09-138-452-4965 US-09-138-452-4965 US-09-138-452-4965 US-09-138-452-4965 US-09-138-452-4965 US-09-138-4965 US-09-138-496-039A-12490 US-09-138-496-039A-12490 US-09-138-496-039A-12490 US-09-138-496-039A-12490 US-09-138-496-039A-10973 US-09-391-741A-2 US-09-391-741A-2 US-09-391-741A-34 US-09-391-7	
2 US-08-383-621-5 3 US-08-459-906-5 4 US-09-459-906-5 4 US-09-459-906-5 4 US-09-489-033A-1120 5 US-08-489-033A-1120 5 US-09-489-033A-1120 6 US-09-489-033A-1120 6 US-09-489-033A-1320 6 US-09-134-001C-4894 6 US-09-134-001C-4895 6 US-09-134-001C-4895 6 US-09-134-001C-4895 6 US-09-134-001C-4895 6 US-09-134-001C-4895 6 US-09-134-001C-4895 6 US-09-134-001C-308 6 US-09-1	
135 2 US-08-383-621-5 Sequence 5, 136 4 US-08-389-135 Sequence 5, 136 4 US-09-349-0394-1120 Sequence 5, 136 4 US-09-349-0394-1130 Sequence 15, 136 4 US-09-349-0394-1130 Sequence 15, 136 4 US-09-340-0394-1130 Sequence 15, 136 4 US-09-340-0394-1329 Sequence 15, 136 4 US-09-340-0394-1329 Sequence 15, 136 4 US-09-340-0394-1329 Sequence 15, 136 4 US-09-340-0394-1399 Sequence 15, 136 4 US-09-340-0394-1399 Sequence 15, 136 4 US-09-340-0394-1399 Sequence 15, 136 4 US-09-340-0394-1399 Sequence 15, 136 4 US-09-340-0394-1399 Sequence 16, 136 4 US-09-340-0394-1399 Sequence 16, 136 4 US-09-340-0394-1399 Sequence 16, 136 4 US-09-340-0394-1399 Sequence 16, 136 4 US-09-340-0394-1399 Sequence 16, 136 4 US-09-340-0394-1399 Sequence 16, 136 4 US-09-340-0394-1399 Sequence 16, 136 4 US-09-340-0394-1399 Sequence 16, 136 4 US-09-340-0394-1399 Sequence 16, 136 4 US-09-340-0394-1399 Sequence 16, 136 4 US-09-340-0394-1399 Sequence 16, 136 4 US-09-340-0394-1399 Sequence 16, 136 4 US-09-340-0394-1399 Sequence 16, 136 4 US-09-340-0394-1399 Sequence 17, 136 4 US-09-340-0394-1399 Sequence 17, 136 4 US-09-340-0394-1399 Sequence 17, 136 4 US-09-340-0394-1399 Sequence 17, 136 4 US-09-340-0394-1399 Sequence 17, 136 4 US-09-340-0394-1399 Sequence 17, 136 4 US-09-340-0394-1399 Sequence 17, 136 4 US-09-340-0394-1399 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-0394-1394 Sequence 17, 136 4 US-09-340-1394 Sequence 17, 136 4 US-09-340-1394 Sequence 17, 13	
135 2 US-08-383-621-5 Sequence 5, 136 4 US-09-489-039A-11504 Sequence 5, 136 4 US-09-489-039A-1320 Sequence 1, 136 4 US-09-370-288-3-33 Sequence 1, 131 4 US-09-370-388-3-33 Sequence 1, 151 2 US-08-328-327A-423 Sequence 1, 151 2 US-08-328-325-579 Sequence 1, 152 4 US-09-328-352-579 Sequence 2, 152 4 US-09-328-352-579 Sequence 2, 152 4 US-09-189-476-526 Sequence 2, 152 4 US-09-189-476-526 Sequence 2, 152 4 US-09-189-476-526 Sequence 2, 152 4 US-09-189-476-526 Sequence 2, 152 4 US-09-189-476-526 Sequence 2, 152 4 US-09-189-476-526 Sequence 2, 152 4 US-09-189-476-526 Sequence 2, 153 4 US-09-189-476-526 Sequence 2, 154 4 US-09-189-476-526 Sequence 2, 154 4 US-09-189-476-526 Sequence 2, 154 4 US-09-189-476-526 Sequence 2, 154 4 US-09-189-476-526 Sequence 2, 154 4 US-09-189-476-526 Sequence 2, 154 4 US-09-189-476-526 Sequence 2, 154 4 US-09-189-476-530 Sequence 2, 154 4 US-09-191-474-3 Sequence 2, 154 4 US-09-191-474-3 Sequence 2, 154 4 US-09-191-474-3 Sequence 2, 154 4 US-09-191-474-3 Sequence 2, 154 4 US-09-191-474-3 Sequence 2, 154 4 US-09-191-489-039A-1910 Sequence 2, 154 4 US-09-191-489-039A-1910 Sequence 2, 154 4 US-09-191-489-039A-1910 Sequence 2, 154 4 US-09-191-489-039A-1910 Sequence 2, 154 4 US-09-191-491-252 Sequence 2, 154 4 US-09-191-491-253 Sequence 2, 154 4 US-09-191-491-253 Sequence 2, 154 4 US-09-191-491-253 Sequence 2, 154 4 US-09-191-491-253 Sequence 2, 154 4 US-09-191-491-253 Sequence 2, 154 4 US-09-191-491-253 Sequence 2, 154 4 US-09-191-491-253 Sequence 2, 154 4 US-09-191-491-253 Sequence 2, 154 4 US-09-191-491-253 Sequence 2, 154 4 US-09-191-491-253 Sequence 2, 155 4 US-09-191-491-253 Sequence 2, 155 4 US-09-191-491-253 Sequence 2, 155 4 US-09-191-491-253 Sequence 2, 155 4 US-09-191-491-253 Sequence 2, 155 4 US-09-191-491-253 Sequence 2, 155 4 US-09-191-491-253 Sequence 2, 155 4 US-09-191-253-31, 154 Sequence 2, 155 4 US-09-191-253-31, 154 Sequence 2, 155 4 US-09-191-253-31, 154 Sequence 2, 155 4 US-09-191-253-31, 154 Sequence 2, 155 4 US-09-191-253-31, 154 Sequence 2, 155 4 US-09-191-253-31, 15	

; SOFTWARE: PERL Program ; SEQ ID NO 1 ; LENGTH: 337 ; TYPE: PRT	; ORGANISM: Homo sapiens ; FEATURE: -	; OTHER INFORMATION: 3734805 US-09-190-965-1		g 23	37; Conservative 0; Mismatch		1	Db 1 MKKMPLFSKSHKNPAEIVKILKDNLAILEKONKKTDKASEVSKSLOAMKSILCGTNRKE 60		;	DD 61 PPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYIS 120	Qy 121 AHPHILFMLLKGYEAPOIALRCGIMLRECTBHEBIARTIT.BENABBBERNAB CHERT 100		LZI AHPHILFMLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNQFRDFFKYVELSTFDIA 180	Qy 181 SDAFATFKDLLTRHKVLVADFLEONXDTTFRDVERTIAGENXVERGOGIVITGETT CONTINUES OF THE CONTINUES			OY 241 NFAIMTKYISKPENLKLMMNILIRDKSPNIOFBAFHVFKUFVASPHFFFODTUBETTLENNDE 200		DD 241 NFAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPK 300	Qy 301 LIEFLSSFOKERTDDEOFADEKNYLIKOTRDIKKTAD 327		JD 301 LIEFLESSFOKERIDDEQFADEKNYLIKQIRDLKKTAP 337		TESTUT 2	1-507-0/1-50-00-00-00-00-00-00-00-00-00-00-00-00-	; Patent No. 6365371			Guegler,	APEDITONITY COTTEN CITE .	NVENTION:	REFERENCE: PF-0635 US	APPLICATION NUMBER: U	CORKENT FILLING DATE: 1999-112-22	FIGURE FILING DATE: 1998-11-13	: NUMBER OF SEQ ID NOS: 5	SOFIWAKE: PEKL Program
0 0 0 0	Sequence 28, Appl Sequence 7860, Ap	n 00 i	Sequence 4, Appli Sequence 4, Appli	15,	Segmence 15, Appl Segmence 7457 an	. 10	~ ~	Sequence 5380, Ap Sequence 2, Appli	12,	Sequence 12, Appl	· œ	o, .	sequence 10, Appl Sequence 2, Appli	5	21182	Sequence 11/17, A Sequence 5006, An			Segmence 6633, Ap	1 4	CI (Sequence 2, Appli Semience 2, Appli	498	N 5	Sequence 4593, Ap			ຜ່າ	Sequence 8, Appli	Sequence 6, Applia	-	1, A		Seguence 11654, A	14,	3001	sequence 2, Appli	
1 US-08-746-789A-2 4 US-09-570-593-5 4 US-09-543-681A-6429 4 US-09-543-68189 7 US-09-747-6-75	02-SU 08-09	US-09	US-10	1 US-08-769-309A-15		US-09-328-352-525	4 US-09-252-991A-17911 4 US-09-107-532A-5360	1 US-08-696-139-2	4 US-09-594-669-12 4 US-10-112-432-12		4 US-09-564-559B-8								US-09-489-039A-11613	US-09-328-352-4643	US-US-U07-484-2 US-09-309-682-2	US-09-594-669-2	US-09-134-000C-4980	US-10-112-432-2 US-09-328-352-4593	US-09-489-039A-9016	US-09-594-669-10	US-10-112-432-10	US-08-080-255-8 US-08-465-713-8	PCT-US93-05857-8	-09-328-352-6	US-09-107-532A-4173	US-09-414-189-1	US-US-IVI-8/9-2 US-09-489-0308-11664	US-08-769-309A-14	US-08-994-570-14	US-09-252-991A-30013 US-09-416-212-2	7-717	
371 371 371 873											409				414 4			427 4	-	429 4			430 4		432 4		434 4				441 4	4 H	212	53	53	454 4		
2000000 000000	أجأجأ	44	i	н н	7		4 ~1	Н,		7	e e	lt	r-i -	-i -	ا جا	.i.	-i -	i	<u>ب</u>	.i -	; ;;	i.	. a	i ~i	٠i ,	.i.		i	H	1.8	۲۰ 00 0	0 a	. 6	1.8	ы. 6.	о е • н		
ω φ φ φ φ 																															o u					ο ω		
247 248 249 250 251	252 253	254 255	256	258	259	260	262	263	265	266	267	269	270	272	273	274	276	277	278	27.9	281	282	283 284	285	286	787	289	290	291	292	2 2 C	295	296	297	B 6 7	0		

```
Sequence 1, Application US/09190965
Patent No. 6071721
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgene, Gina A.
ITLE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REFERENCE: PF-0635 US
CURRENT APPLICATION NUMBER: US/09/190,965
CURRENT FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 5
ALIGNMENTS
                                                    RESULT 1
US-09-190-965-1
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PPTEAVAQLAQELYSSGLLVTLIADLQLIDFBGKKDVTQIFNNILRRQIGTRSPTVEXIS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKMPLFSKSHKNPAEIVKILKDNLAILEKQDKKTDKASEEVSKSLQAMKEILCGTNEKE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 337; DB 4; Length 337;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 337; Conservative 0; Mismatches 0; Indels
VI: Tang, Y. Tom

VI: Guegler, Karl J.

VI: Gorley, Neil C.

VI: Gorgone, Gina A.

F INVENTION: CALCIUM BINDING PROTEIN

FERENCE: PF-0635 US

APPLICATION NUMBER: US/09/470,253
                                                                                                                                                                                                                                                               LLING DATE: 1999-12-22
LICATION NUMBER: 09/190,965
ING DATE: 1998-11-13
                                                                                              Application US/09470253
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: 3734805
US-09-470-253-1
                                                                                                                                                                                                                                                                                                              SEQ ID NOS: 5
PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                             FORMATION:
                                                                                                                                                                                                                                                                                                                                                               337
                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

ò

Gaps

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                6.8%; Score 23; DB 4; Length 341;
100.0%; Pred. No. 1.3e-14;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15; DB 3; Le
Pred. No. 1.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

4.5%; Score 15; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorley, Neil C.
APPLICANT: Gragone, Gina A.
TITLE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REFERENCE: PF-0635 US
CURRENT APPLICATION NUMBER: US/09/190,965
CURRENT FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Mail C.
APPLICANT: Gorgone, Gina A.
TITLE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REPERBENCE: PF-0635 US
CURRENT APPLICATION NUMBER: US/09/470,253
CURRENT FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: 09/190,965
PRIOR FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
4.5%; Score 15; DB.
Best Local Similarity 100.0%; Pred. No. 1.1.
                                                                                                                                                                   244 IMTKYISKPENLKLMMNLLRDKS 266
                                                                                                                                                                                                               245 IMTKYISKPENLKLMMNLLRDKS 267
                                                                                                                                                                                                                                                                                               US-09-190-965-4

Sequence 4, Application US/09190965

; Patent No. 6071721

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09470253; Patent No. 6365371; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 LRRQIGTRSPTVEYI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 LRRQIGTRSPTVEYI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: 91794137
US-09-190-965-4
                                                                              Query Match
Best Local Similarity 100.0
Matches 23; Conservative
             ; OTHER INFORMATION: g262934
US-09-470-253-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: 91794137
US-09-470-253-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-470-253-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                     à
                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                               61 PPTEAVAQLAQELYSSGLLVTLIADLQLIDFEGKKDVTQIFNNILRRQIGTRSPTVEYIS 120
                                         121 AHPHILFMLLKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDIA 180
                                                                                121 AHPHILFMILKGYEAPQIALRCGIMLRECIRHEPLAKIILFSNOFRDFFKYVELSTFDIA 180
                                                                                                                              181 SDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRH 240
                                                                                                                                                            181 SDAFATFKDLLTRHKVLVADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRH 240
                                                                                                                                                                                                                   241 NFAIMTKYISKPENLKIMMNILRDKSPNIQFEAFHVFKVFVASPHKTQPIVEILLKNQPK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%; Score 23; DB 3; Length 341; 100.0%; Pred. No. 1.3e-14; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                      301 LIEFLSSFOKERTDDEOFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                    301 LIEFLSSFOKERTDDEGFADEKNYLIKQIRDLKKTAP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-190-965-3
Sequence 3, Application US/09190965
Patent No. 6707721
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
TILLE REPERENCE: PF-0635 US
CURRENT APPLICATION: CALCIUM BINDING PROTEIN
FILE REFERENCE: PF-0635 US
CURRENT APPLICATION NUMBER: US/09/190,965
CURRENT FILING DATE: 1998-11-13
NUMBER OF SEQ ID NGS: 5
SOFTWARE: PERL PROGram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorgone, Gina A.
TITLE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REFERENCE: PP-0655 US
CURRENT APPLICATION NUMBER: US/09/470,253
FRIOR APPLICATION NUMBER: 1999-12-22
PRIOR PEPLICATION NUMBER: 09/190,965
PRIOR FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 IMTKYISKPENLKLMMNLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 IMTKYISKPENLKLMMNLLRDKS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 3, Application US/09470253; Patent No. 6365371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.C
Matches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: -
OTHER INFORMATION: 9262934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PERL Program
SEQ ID NO 3
LENGTH: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Mus sp.
FEATURE: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-470-253-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-190-965-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                  qq
                                                                                                                                                                 g
                                         ò
                                                                                                                              ò
                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                          d
                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

ö

Gaps

ö

Gaps

```
Sequence 23, Application US/09345473E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5196333-9
;Patent No. 5196333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-621-976-5453
                                                                                                                                                                                                                                                                     US-09-345-473E-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 5453
LENGTH: 99
                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO:9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5196333-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THEREOF
                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                   Ωp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
4.2%; Score 14; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.2%; Score 14; DB 4; Length 377; 100.0%; Pred. No. 1.2e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                         APPLICANT: Tang, Y. Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Clina A.
TITLE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REFERRINGE: PF-0635 US
CURRENT APPLICATION NUMBER: US/09/190,965
CURRENT FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorgone, Gina A.
TITLE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REFERENCE: PF-0635 US
CURRENT APPLICATION NUMBER: US/09/470,253
CURRENT FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: 09/190,965
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL PROGram
SEQ ID NO 5
LENGTH: 377
                                                                                                                         Sequence 5, Application US/09190965; Patent No. 6071721; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-470-253-5
Sequence 5, Application US/09470253
Patent No. 6365371
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Caenorhabditis elegans
                     105 LRRQIGTRSPTVEYI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 LRRQIGTRSPIVEY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 LRRQIGTRSPTVEY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 LRRQIGTRSPTVEY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FEATURE: -
; OTHER INFORMATION: 91255838
US-09-190-965-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 LRRQİGTRSPTVEY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: 91255838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 5
LENGTH: 377
                                                                                                     US-09-190-965-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-470-253-5
                                                                                                                                                                                                                                                                                                                                                                                                        PRT
                                                                                        RESULT 7
                              ДQ
à
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CHALFIE, MAKIN, WOLINSKY, EVE; DRISCOLL, MONICA; TITLE OF INVENTION: DNA SEQUENCES INVOLVED IN NEURONAL; DEGENERATION, MULTICELLULAR ORGANISMS CONTAINING SAME AND USES
Parent No. 558901

GNERAL INFORMATION:

GNERAL INFORMATION:

TITLE OF INVENTION: No. 65880381 Kinases and Uses Thereof
FILE REFERENCE: 35800/183781

CURRENT APPLICATION NUMBER: US/09/345,473E

CURRENT FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 62

SOFTWARE PASTERO for Windows Version 4.0

LENGTH: 923
                                                                                                                                                                                                                                                                                                                                                        2.4%; Score 8; DB 4; Length 923; 100.0%; Pred. No. 24; Cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 545. Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Unmes Minhe Edwards, J.B.
APPLICANT: Glochano, J.Y.
ITILE OF INVENTION: SENSET.054PR2
GURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
2.1%; Score 7; DB 6
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/530,968
FILING DATE: 30-MAY-1990
                                                                                                                                                                                                                                                                                ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.(
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      449 SSGLLVTL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                           75 SSGLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 LVTLIAD 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 LVTLIAD 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: -73..-1
US-09-621-976-5453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
```

DB 4; Length 99;

2.1%; Score 7;

RESULT 9 US-09-345-473E-23

; 0

φ

```
CORRESPONDENCE ADDRESS:
                                                                                        Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US96-07709-5
                                                                                        CITY: Der
STATE: CC
COUNTRY:
ZIP: 802(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TILE OF INVENTION: MYGUSIN-LIKE GENE EXPRESSED IN NORMY REAL ROLLS.

FILE REPERENCE: ABCMICA-7

CURRENT PILING DATE: 2001-05-25

PRIOR PILING DATE: 2001-05-26

PRIOR PLICATION NUMBER: US 60/207,456

PRIOR PLICATION NUMBER: GB 24263.6

PRIOR PLICATION NUMBER: GB 24263.6

PRIOR PLING DATE: 2000-10-04

PRIOR PLING DATE: 2000-10-09-27

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SHANNON, MARK
TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 99;
                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/08450944

Patent No. 5789194

GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
APPLICANT: Wisnewski, Nancy
ITILE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
ITILE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
             Pred. No. 31;
                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1%; Score 7; E
100.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                                                                                                                                                                                                  Sequence 15755, Application US/09866108A Patent No. 6686189 GENERAL INFORMATION:
APPLICANT: GU, Yizhong APPLICANT: JI, Yonggang APPLICANT: PENN, Sharron G. APPLICANT: HANZEL, David K.
                100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RANK, David R. CHEN, Wensheng
             Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 NLLRDKS 69
                                                                                                        59 KEPPTEA 65
                                                                                                                                                               87 KEPPTEA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-866-108A-15755
                                                                                                                                                                                                                                                                 RESULT 12
US-09-866-108A-15755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-08-450-944-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                      a
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7; DB 1; Length 205;
Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application PC/TUS9607709
(GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
APPLICANT: WISHOWSKI, Nancy, TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS NUMBER OF SEQUENCES: 43
CORRESPONDENCES: 43
CORRESPONDENCES: ABDRESS:
ADDRESSEB: Sheridan Ross & McIntosh SIREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.25
                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC comparible
OPERATING SYSTEM: F-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 23-MAY-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.1%; Score 7; DB 1
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 25.020
RECORNICATION NUMBER: 2618-30-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07709
FILING DATE: 23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-9700
TELEPAX: (303) 863-023
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (303) 863-97C
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 205 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-450-944-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 RDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1700 Linc CITY: Denver STATE: Colorado COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 RDLKKTA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                        Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
```

٥;

```
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%; Score 7; DB 5;
100.0%; Pred. No. 65;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.

REGISTRATION NUMBER: 32,020
REFERENCE/COCKET NUMBER: 2618-30-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-9700
TELEFAX: (303) 863-9700

TELEFAX: (303) 863-9700

TELEFAX: (303) 863-9703

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
             FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                       ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 221 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US96-07709-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 RDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 RDLKKTA 115
                                                                                                                                                                                                                                                                                                                                                                                                 117 AEIVKIL 123
                                                                                                                                                                                                                                                                                                                                                       15 AEIVKIL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Colorado COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 18
US-09-252-991A-30691
                                                                                                                                                                                                                               US-09-489-039A-9612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US96-07709-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
CITY: De
                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 17
                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9612, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                       Gaps
                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 1; Length 221; 100.0%; Pred. No. 65; 0; Indels tive 0; Mismatches 0; Indels
                                                                                                                                            DB 5; Length 205; . 61;
                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
APPLICANT: Wisherwski, Nancy
TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentle PC-DOS/MS-DOS
SOFTWARE: Patentle Release #1.0, Version #1.25
CURSIT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,944
FILING DATE: 23-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGBWT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 37,459
TELECOMMUNICATION INFORMATION:
                                                                                                                                         Query Match 2.1%; Score 7; DB 5
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2, Application US/08450944
; Patent No. 5789194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (303) 863-9700
                 LENGTH: 205 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (303) 863-970
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 221 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 100.
Matches 7; Conservative
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                              MOLECULE TYPE: protein PCT-US96-07709-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 RDLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 RDLKKTA 115
                                                                                                                                                                                                                               330 RDLKKTA 336
                                                                                                                                                                                                                                                                         93 RDLKKTA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1700 Lin
CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 16
US-09-489-039A-9612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-450-944-2
                                                                                                                                                                                                                                                                                                                                                            US-08-450-944-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
Query Match 2.1%; Score 7; DB 4; Length 221; Best Local Similarity 100.0%; Pred. No. 65; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                             Sequence 2, Application PC/TUS9607709
GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
APPLICANT: Tripp, Cynthia A.
TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/07709 FILING DATE: 23-MAY-1996 CLASSIFICATION:
```

```
APPLICANT: Gary Brecon et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: PINEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT ELILNG DATE: 2000-01-27
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10987
LENGTH: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION:
TITLE OF INVENTION: NUCLEBELE ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11246
LENGTH: 341
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 7; DB 4; Length 341;
100.0%; Pred. No. 96;
tive 0; Mismatches 0; Indels
                                                                                                           Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 4;
100.0%; Pred. No. 96;
tive 0; Mismatches
                                                                                                           Query Match 2.1%; Score 7; DB 4; Best Local Similarity 100.0%; Pred. No. 96; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    Sequence 10987, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11246, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Klebsiella pneumoniae
                                         ORGANISM: Klebsiella pneumoniae US-09-489-039A-9238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 PKLIEFL 305
                                                                                                                                                                                                        299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKLIEFL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 PKLIEFL 49
                                                                                                                                                                                                                                                      43 PKLIEFL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-489-039A-11246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-489-039A-10987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-489-039A-11246
                                                                                                                                                                                                                                                                                                                                                 US-09-489-039A-10987
LENGTH: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: GAYR RELTON

TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: UNMARR: US/09/543,681A

CURRENT APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344
                                                             APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AREQUENCE: 107196.136
CURRENT PRILING DATE: 107196.136
CURRENT PILING DATE: 1999-02-18
PRIOR PPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9238. Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ALD AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA;
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: 2709.204001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.1%; Score 7; DB 4; Length 276; Best Local Similarity 100.0%; Pred. No. 79; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.1%; Score 7; DB 4;
100.0%; Pred. No. 85;
vative 0; Mismatches
Sequence 30691, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 4229, Application US/09543681A; Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Proteus mirabilis US-09-543-681A-4229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||||
55 QLIDFEG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 QLIDFEG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 AVAQLAQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 AVAQLAQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-30691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 19
US-09-543-681A-4229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-489-039A-9238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 4229
LENGTH: 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          엄
```

ö

.; 0

Gaps

.. 0

```
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERENCE: 107196_136 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 RIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 RIOR APPLICATION NUMBER: US 60/094,190 RIOR APPLICATION NUMBER: US 60/094,190 RIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                           Sequence 6452, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1997-08-15
PRIOR PILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 345;
                                                       Length 343;
                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                  2.1%; Score 7; DB 4;
100.0%; Pred. No. 97;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 2.1%; Score 7; DB 4;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.1%; Score 7; DB 4;
100.0%; Pred. No. 98;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22992, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION: Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
----- 7; Conservative
                                                                            Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                      299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 AILEKOD 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 AILEKOD 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 VSKSLOA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 VSKSLOA 10
                                                                                                                                                                                                  45 PKLIEFL 51
     US-09-489-039A-11316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-252-991A-22992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-252-991A-22992
                                                                                                                                                                                                                                                                                                      US-09-134-000C-6452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-134-000C-6452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 6452
LENGTH: 345
                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4130, Application US/09128352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                 GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT PILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11316, Application US/09489039A
Fatent No. 6610836
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILLE REFERENCE: 2009.2004001
FILLE REFERENCE: 2.009.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
FRICK APPLICATION NUMBER: US 60/117,747
FRICK RILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.1%; Score 7; DB 4; Length 343; Best Local Similarity 100.0%; Pred. No. 97; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
2.1%; Score 7; DB 4; Length 341;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels
                  Sequence 11507, Application US/09489033A
Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Acinetobacter baumannii
US-09-328-352-4130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Klebsiella pneumoniae US-09-489-039A-11507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299 PKLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 PKLIEFL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 PKLIEFL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-489-039A-11316
US-09-489-039A-11507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-328-352-4130
                                                                                                                                                                                                                                                                                                                           SEQ ID NO 11507
LENGTH: 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4130
LENGTH: 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
```

ö

0; Gaps

ô

0; Gaps

```
Fingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.1%; Score 7; DB 4; Length 490; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                2.1%; Score 7; DB 4; Length 449;
100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: RC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: UIA-010.28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-Apr-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-056-285A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Arnold, Beth E. REGISTRATION NUMBER: 35,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 10, Application US/09056285A
; Patent No. 6403307
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Stone, Edwin M.
Sheffield, Val C.
Alward, Wallace L.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08724466B; Patent No. 6063606; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 490 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617-832-7000
                                                                                              TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02109-2170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                    174 LSTFDIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 NLLRDKS 136
PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 9088
                                                                                                                                                                                                                                                                                                                                                    171 LSTFDIA 177
                                                                                                                                                   US-09-489-039A-9088
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-056-285A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 32
US-08-724-466B-2
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ઠે
                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                          ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gary Breton et. al TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUWONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.1%; Score 7; DB 4; Length 384; 100.0%; Pred. No. 1.1e+02; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.1%; Score 7; DB 4; Length 449; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                      APPLICANT: Rice, John
APPLICANT: Sevala, Veeresh
APPLICANT: Stewart, Sandy
TITLE OF INVENTION: NOVEL PLANT PORPHOBILINOGEN AND FUSION
FILLE OF INVENTION: PROTEIN THEREOF
FILE REFERENCE: 2022US
                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/741,243C
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/171,785
PRIOR FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER FO SEQ ID NOS: 14342
SEQ ID NO 9778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9088, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8778, Application US/09489039A Patent No. 6610836
                                                                    GENERAL INFORMATION: APPLICANT: Crawford Jr., John Milton
                       Sequence 8, Application US/09741243C Patent No. 6399352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-09-741-243C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 HNFAIMT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 HNFAIMT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 LLRDKSP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 LLRDKSP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Gary Bro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-489-039A-908B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 29
US-09-489-039A-8778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-489-039A-8778
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D
D
```

ö

Gaps

```
282 SLQAMKE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1299 PENT
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 SLQAMKE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
CLONE: TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D.C.
                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                              US-08-882-164D-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-336-235A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-336-235A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.1%; Score 7; DB 3; Length 492; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                         STREET: Box 25, Commerce Court West
CITY: Toronto
ZIP: M5L 1A9
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage
COMPUTER: COMPA, 1BM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
CURRENT APPLICATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.4 Mb storage
APPLICANT: Petkovich, P. Martin, White, Jay A., PAPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Cassels & Graydon STREET: Box 25, Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Petkovich, P. Martin, White, Jay A.,
APPLICANT: Beckett, Barbara R., Jones, Glenville
TITLE OF INVENTION: Retinoid Metabolizing Protein
UNDMER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSE: Blake, Cassels & Graydon
STREET: Box 25, Commerce Court West
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4
COMPUTER: COMPAO, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
SOFTWARE: WORD PERFECT
CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/08/682,164D
FILING DATE: June 25, 1997
PRIOR APPLICATION DATA:
APPLICATION WIMBER: 08/667,546
FILING DATE: June 21, 1996
FILING DATE: June 21, 1996
                                                                                                                                                                                                                                                                                                                                   CURRENT AFPLICATION DAIA:

APPLICATION NUMBER: US/08/724,466B
FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/67,546
FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REJESTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50767/00004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRARATERSTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50767/00004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08882164D Patent No. 6306624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/724,466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: June 2 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 SLOAMKE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Ontario
FRY: Canada
M5L 1A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 SLOAMKE 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY:
US-08-724-466B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-882-164D-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
```

```
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION:
TELEPHONE: (202) 383-7451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MARSH, DAVID
REGISTRATION NUMBER: 41,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
                                                                                                                                                                                                                                                                                                                               TELEFAX: (202) 383-6610 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 497 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 504 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match .
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 NLLRDKS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
CLONE: TIGR
                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20004
                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US95-14024-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-645-900A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D
COUNTRY:
        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                              US-08-649-432-1

Sequence 1, Application US/08649432

Sequence 1, Application US/08649432

Patent No. 5789169

GENERAL INFORMATION:
APPLICANT: NGUYEN, THAI D.
APPLICANT: POLANSKY, JON R.
APPLICANT: HUANG, WEIDONG

TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS OF GLAUCOMA NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application PC/TUS9514024
GENERAL INFORMATION:
APPLICANT: NGUYEN, THAI D.
APPLICANT: POLANSKY, JON R.
APPLICANT: HUANG, WEIDONG
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS OF GLAUCOMA NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWERY & SIMON
STREET: 1299 PENNSYLVANIA AVE., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 2.1%; Score 7; DB 1; Length 497; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,432
FILING DATE: 1.7-MAY-1996
CLASSIFICATION: 17-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/336,235
                                                                                                                                                                                                                                                                                                         SEE: HOWREY & SIMON: 1299 PENNSYLVANIA AVE., N.W. WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: AUGRAGET, JEFFEZ I
REGISTRATION NUMBER: 32,680
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 497 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
||||||||
134 NLLRDKS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 NLLRDKS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
CLONE: TIGR
                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C.
                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US95-14024-1
                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-649-432-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 36
```

```
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 5; Length 497;
100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1. Application US/08645900A; Patent No. 5849879; GENERAL INFORMATION: APPLICANT: NGUYEN, THAI D. APPLICANT: POLANSKY, JON R. APPLICANT: POLANSKY, JON R. TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS OF TITLE OF INVENTION: GLAUCOMA NUMBER OF SEQUENCES: 3 CORRESPONDINCE ADDRESS: ADDRESSEE: HOWREY E. SIMON STREET: 1299 PENNSYLVANIA AVE., N.W. CHENTY. MASHINGTON
ZIP: 20004

ZIP: 20004

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 14 MAY 1996
CLASSIFICATION: 530
```

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
0
                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 504;
                                                                                                      DB 2; Length 504;
                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                          APPLICANT: NGUYEN, THAI D.
APPLICANT: POLANSKY, JON R.
APPLICANT: PULANG, WEIDONG FOR THE DIAGNOSIS OF
TITLE OF INVENTION: GLAUCOMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,238A
FILING DATE: 25 JUNE 1997
CLASSIFICATION: 435
                                                                                                Query Match
2.1%; Score 7; DB 2; Ler
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.1%; Score 7; DB 2
100.0%; Pred. No. 1.4
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVE., N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-667-790A-1; Sequence 1, Application US/08667790A; Patent No. 5861497 General INFORMATION: APPLICANT: POLANSKY, JON R.
                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08882238A Patent No. 5854415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MARKH DAVID
REGISTRATION NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                               TOPOLOGY: linear
MOLECULE TYPE: No. 5849879e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: No. 5854415e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 504 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
            STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                     144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 NLLRDKS 150
                                                                                                                                                                      260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 NLLRDKS 266
amino acid
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20004
                                                                                                                                                                                                                                                          RESULT 38
US-08-882-238A-1
                                                                US-08-645-900A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-882-238A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                        à
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09220459

Patent No. 6150161

GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D

APPLICANT: Polansky, Jon R

APPLICANT: Polansky, Jon R

APPLICANT: Polansky, Jon R

APPLICANT: Polansky, Jon R

TITLE OF INVENTION: Methods for the Diagnosis of Glaucoma

FILE REFERENCE: 07425.0056

CURRENT FILING DATE: 1994-12-24

CURRENT FILING DATE: 1994-12-24

EARLIER FILING DATE: 1996-05-17

EARLIER FILING DATE: 1996-05-17

EARLIER FILING DATE: 1996-05-17

EARLIER FILING DATE: 1995-10-20

EARLIER FILING DATE: 1995-11-03

NUMBER OF SEQ ID NOS: 3

SOFTHARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.1%; Score 7; DB 2; Length 504; 100.0%; Pred. No. 1.4e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 504;
                                                                                                                                                                                                                    CIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,790A
FILING DATE: 21 JUNE 1996
CLASSIFICATION:
                  TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS OF TITLE OF INVENTION: GLAUCOMA
                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVE., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MARSH, DAVID
REGISTRATION NUMBER: 41,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: No. 5861497e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 504 amino acids
TYPE: amino acid
STRANDEDNESS: single
APPLICANT: HUANG, WEIDONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 NLLRDKS 266
                                                                                                                                                    WASHINGTON
                                                                                                                                                                            : D.C.
RY: US
20004
                                                                                                                                                    CITY: WAS
STATE: D.
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-667-790A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-220-459-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-220-459-1
```

.. 0

```
METHODS FOR THE DIAGNOSIS OF GLAUCOMA
   TITLE OF INVENTION: METHODS FOR THE DI
TITLE OF INVENTION: GLAUCOMA
NUMBER OF SECUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVE., N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-822-999-3; Sequence 3, Application US/08822999; Patent No. 6271026
                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEPAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: No. 6248867e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 504 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02109-2170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDAL
STREET: CAL
TWY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-546-568B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                 RESULT 41
US-08-938-669A-32
; Sequence 32, Application US/08938669A
; Patent No. 6117188
; GENERAL INFORMATION:
    APPLICANT: Nguyen, Thai D.
    APPLICANT: Polansky, Jon R.
    TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
    TITLE OF INVENTION: RELATED DISEASES
    NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
    ADDRESSE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.1%; Score 7; DB 3; Length 504; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                       Indels
Pred. No. 1.4e+02;
: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20004-2402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 07425-0034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DARN:
APPLICATION NUMBER: 08/791,154
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mendelson, Elliot
REGISTRATION NUMBER: P-42,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08546568B; Patent No. 6248867; GENEAL INFORMATION: APPLICANT: NGUYEN, THAI D. APPLICANT: HUANG, WEIDONG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS: LENGTH: 504 amino acids
   100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein FRAGMENT TYPE: N-terminal
                     7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202 383-6610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                 144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 NLLRDKS 266
                                                        260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-938-669A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-546-568B-1
                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                        ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Stone, Edwin M.
APPLICANT: Sheffield, Val C.
APPLICANT: Alward, Wallace L.M.
TITLE OF INVENTION: GLAUCOMA COMPOSITIONS AND THERAPEUTIC
TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
NUMBER OF EGURNCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 504;
STATE: D.C.
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: THE PC COMPATIBLE
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/546,568B
FILING DATE: 20 October 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MARRSH DAVID
REGISTRATION NUMBER: 41,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION NOMBER: US/08/82,999
FILING DATE: 21-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/82,1999
FILING DATE: 30-JAN-1997
FILING DATE: 30-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 7; DB 3
100.0%; Pred. No. 1.4
tive 0; Mismatches
```

Gaps

```
.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stone, Edwin M.

Sheffield, Val C.
Alward, Wallece L.M.
Fingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
CORRESPONDENCE: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCTURES PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-Apr-1998
ATTORNEY/AGRYT INFORMATION:
NAME: Arnold, Beth B.
RECISTRATION NUMBER: 35,430
FEFERENCE/DOCKET NUMBER: UIA-010.28
TELECOMMUNICATION INFORMATION:
TELEPAX: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.1%; Score 7; DB 3; Length 504; 100.0%; Pred. No. 1.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: FOLEY, HOAG & ELIOT LLP STREET: One Post Office Square
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
08-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
ATTORNAY AGENT INFORMATION:
NAME:
NAME:
REGISTRATION NUMBER:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09056285A Patent No. 6403307 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 504 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                          : 504 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
Les 7; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 44
US-09-056-285A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-056-285A-8
                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-822-999-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

2.1%; Score 7; DB 4; Length 504;

Query Match

```
Sequence 32, Application US/09106828
Patent No. 6475724
GENERAL INFORMATION:
APPLICANT: NGUYGEN, Thai D.
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Pu
APPLICANT: Chen, Pu
APPLICANT: Chen, Pu
APPLICANT: Chen, Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis An
CURRENT APPLICATION NUMBER: US/09/306,828
CURRENT FILING DATE: 1999-06-07
EARLIER APPLICATION NUMBER: US 09/227,881
EARLIER FILING DATE: 1999-01-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12958, Application US/09489039A

Sequence 12958, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT GATY Breton et. al
APPLICANTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
CURRENT APPLICATION UNDER: 2709,2004001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
RUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12958
LENGTH: 510
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.1%; Score 7; DB 4; Length 504; 100.0%; Pred. No. 1.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.1%; Score 7; DB 4; Length 510; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
Best Local Similarity 100.0%; Fred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 47
US-09-800-729-124
Sequence 124, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Word 97
SEQ ID NO 32
LENGTH: 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                           260 NLLRDKS 266
                                                                                                                            144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 NLLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 NLLRDKS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 APQIALR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 APQIALR 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-489-039A-12958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-489-039A-12958
                                                                                                                                                                                                                                US-09-306-828-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-306-828-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                           ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ઠ
```

us-10-025-730-1.oligo.rai

```
227 QSLKLLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                  71 ÖSLKLIG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JAPAN
                                                                                                                                                           US-09-489-039A-12036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Ni:
STATE: Ni:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-026-138E-3
                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-026-138E-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                 TYPE: PRT
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 50
                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709, 22044001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò.
                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.1%; Score 7; DB 4; Length 514; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 551; . 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1. Application US/09741243C
Patent No. 6399352
GENERAL INFORMATION:
APPLICANT: Crawford Jr., John Milton
APPLICANT: Sevala, Veeresh
APPLICANT: Sevala, Veeresh
APPLICANT: Sevala, Veeresh
TITLE OF INVENTION: NOVEL PLANT PORPHOBILINOGEN AND FUSION
TITLE OF INVENTION: PROTEIN THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTHER INFORMATION: A plant thioredoxin-porphobilinogen CTHER INFORMATION: synthase fusion protein US-09-741-243C-2
APPLICANT: Ni et al.
TILE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.1%; Score 7; DB 4
Best Local Similarity 100.0%; Pred. No. 1.5
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 2022US
CURRENT APPLICATION NUMBER: US/09/741,243C
CURRENT FILING DATE: 2000-12-19
PRIOR FILING DATE: 1999-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12036, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                          TYPE: PRT
COGANISM: Homo sapiens
US-09-800-729-124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 LLRDKSP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483 LLRDKSP 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  392 VAÇLAÇE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 VAQLAQE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 49
US-09-489-039A-12036
                                                                                                                                                                                                                     SOFTWARE: Pat
SEQ ID NO 124
LENGTH: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 48
US-09-741-243C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

```
Gaps
                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Sequence 3, Application US/08026138E
Patent No. 5502166
GENERAL INPORMATION:
APPLICANT: MASSACOSIM MISHINA
TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nishiohata Residence 1-107
                                                                                                                                                                                                                 Length 620;
                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUBLICATION INFORMATION:
AUTHORS: Masayoshi MISHINA
TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 to 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS v.5 SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                            2.1%; Score 7; DB 4; Len
100.0%; Pred. No. 1.7e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 39563/1992
FILING DATE: 26-FEB-1992
APPLICATION NUMBER: JP 173155/1992
FILING DATE: 30-JUN-1992
APPLICATION NUMBER: JP 215017/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: JP 303878/1992
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12036
LENGTH: 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION ATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F-4551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 5214, Nishlohata-machi
CITY: Nijgata-shi
STATE: Nijgata-ken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hamburg, C.Bruce
REGISTRATION NUMBER: 22,389
REFERENCE, DOCKET NUMBER: F-4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single strand
                                                                                                                                         ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 986-2340
TELEPAX: (212) 953-773
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1239 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                       Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 951
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE TYPE: brain
```

```
LENGTH: 3433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AGID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT PEPELICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 14067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
2.1%; Score 7; DB 4; Length 3168;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.1%; Score 7; DB 4; Length 1745; Best Local Similarity 100.0%; Pred. No. 4.2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
Query Match 2.1%; Score 7; DB 1; Length 1239; Best Local Similarity 100.0%; Pred. No. 3.18+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ni et al.
ITILE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044p1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR PILING DATE: 2000-09-22
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14067, Application US/09489039A; Patent No. 6610836; GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 10, Application US/09091501B
; Patent No. 6518413
                                                                                                                                                                                                                                                                     Sequence 89, Application US/09800729
Patent No. 6605592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: Homo sapiens
US-09-800-729-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1084 VAQLAQE 1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1959 NLAILEK 1965
                                                                                                                                           101 TEAVAOL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 VAQLAQE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 NLAILEK 30
                                                                                                  63 TEAVAQL 69
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-489-039A-14067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-489-039A-14067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 53
US-09-091-501B-10
                                                                                                                                                                                                                    RESULT 51
US-09-800-729-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
```

```
; LOUGATION: (239) ... (250)
; OTHER INFORMATION: Description of Artificial Sequence: Full length
; OTHER INFORMATION: utrophin construct; Xaa = unknown
US-09-091-501B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.1%; Score 7; DB 4; Length 3433; Best Local Similarity 100.0%; Pred. No. 7.8e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 75, Application US/08432871C
Patent No. 5877010
GENERAL INFORMATION:
APPLICANT: Locb, Lawrence A.
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
           APPLICANT: Tineley, Jonathon M
APPLICANT: Tineley, Sonathon M
APPLICANT: Davies, Kay E
TITLE OF INVENTION: Utrophin gene expression
FILE REFERENCE: 620-42
CURRENT APPLICATION UNMERS: US/09/091,501B
CURRENT FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: PCT/GB96/03156
PRIOR FILING DATE: 1996-12-19
PRIOR PLING DATE: 1996-12-19
PRIOR FILING DATE: 1996-12-19
PRIOR FILING DATE: 1996-07-26
PRIOR APPLICATION NUMBER: GB 961579.9
PRIOR FILING DATE: 1996-07-26
PRIOR APPLICATION NUMBER: GB 962174.2
PRIOR FILING DATE: 1996-10-24
NUMBER OF SEQ ID NOS: 15
SOUTHWARE: PATCHIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MCMASTERS, DAVID D.
REGISTRATION NUMBER: 33,963
REFERENCE TOOKET NUMBER: 240052.409C1
TELECOMMUNICATION INFORMATION:
TELEFRAX: (206) 622-4900
TELEFRAX: 3723836
INFORMATION FOR SEQ ID NO: 75:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/432,871C
FILING DATE: 02-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 02-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1182 VKILKDN 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 VKILKDN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X: US
98104-7092
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-432-871C-75
```

us-10-025-730-1.oligo.rai

```
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 3723836
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 LILDRH 240
                                                                                                                                                     98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 17 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LILDRH 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-270-956-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-270-956-82
                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 2; Length 15; 100.0%; Pred. No. 56; tive 0; Mismatches 0; Indels
                                                                                                                                                     Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,871C
FILING DATE: 02-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 82, Application US/08432871C

Patent No. 5877010

GENERAL INFORMATION:
APPLICANT: Loeb, Lawrence A.
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 75, Application US/09270956
Patent No. 6451571
GENERAL INFORMATION:
APPLICANT: Loeb, Lawrence A.
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                 Query Match 1.8%; Score 6; DB 2;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:

NAME: McMesters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 240052.409C1

TELECOMMUNICATION INFORMATION:

TELEFROME: (206) 622-4900

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (206) 622-631

TELEFROE: (20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 LILDRH 240
// TYPE: amino acid
// TOPOLOGY: linear
US-08-432-871C-75
                                                                                                                                                                                                                                                                                                          235 LILDRH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LILDRH 6
                                                                                                                                                                                                                                                                                                                                                                                       1 LILDRH 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-432-871C-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 56
US-09-270-956-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 15;
                                                                                                                                                                  OFFWALLS SYSTEM: YC-LUCY MALE SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,956
FILING DATE: 17-MAR-1999
CLASSIFICATION: 435
ATTOMENYAGENT INFORMATION:
NAME: MCMASTER: David D.
REGISTRATION NUMBER: 33,963
REPRENCE/DOCKET NUMBER: 240052.409C3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 682-6931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Washington
COUNTRY: US
ZIP: 98104-7092
ZOMPUTER READABLE FORM:
MEDIUM TYPE: FLOPBY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 82, Application US/09270956
Patent No. 6431571
GENERAL INFORMATION:
APPLICANT: Black, Margaret E.
TITLE OF INVENTION: THYMIDINE KINASE MUTANTS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 4;
100.0%; Pred. No. 56;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFREENCE/DOCKET NUMBER: 240052.409C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US/09/270,956
17-MAR-1999
N.
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELER: 3723836
TINFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abus.
STREET: 6500
CITY: Seattle
Seattle
Washington
```

```
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                              Sequence 4. Application US/07965663A
Patent No. 5424290
GENERAL INFORMATION:
APPLICANT: Lee, Maloy W.
APPLICANT: Prasad, Kari U.
TITLE OF INVENTION: No. 5424290el Biologically Active Peptides and
TITLE OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /note= "May be a C-terminal amide, and/or may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                               0; Indels
                                                                                                            Query Match
1.8%; Score 6; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.8%; Score 6; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER REALDLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/965,663A
FILING DATE: 26-0CT-1992
CLASSITCATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FORTIS: J6-0CT-1992
TELECOMMUNICATION NUMBER: 05387.0039-00000
TELEPHONE: 202-408-4400
TELEPHONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C. COUNTRY: United States of America ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 59
US-08-033-873-8
, Sequence B, Application US/08033873
, Patent No. 5459235
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1300 I Street, N.W. CITY: Washington
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 22 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                          235 LILDRH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 IVKILK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 İVKİLK 21
                                                                                                                                                                                                                                                   1 LILDRH 6
                                                                                                                                                                                                                                                                                                                                               US-07-965-663A-4
                                                              US-09-270-956-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-965-663A-4
                                                                                                                                                                                                          à
```

```
.
0
               APPLICANT: CULLOR, JAMES S.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
TITLE OF INVENTION: NEUTROPHILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE NEUTROPHILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 1; Length 38; 100.0%; Pred. No. 1.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                            SCFWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/033,873
FILING DATE: 19930319
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHREN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 91.0552
TELECOMMULICATION INFORMATION:
TELEPHONE: (519) 535-9001
TELEPHONE: (519) 535-901
TELEPAT: (619) 535-9049
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                    NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
CORRESSEE: CAMPBEL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: CAMPBELL AND FLORES
STRET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALLFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/356,832
FILING DATE: 12-DEC-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,873
                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 8, Application US/08356832; Patent No. 5821224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: SELSTED, MICHAEL E.
APPLICANT: CULLOR, JAMES S.
TITLE OF INVENTION: NOUTROPHILE
TITLE OF INVENTION:
APPLICANT: SELSTED, MICHAEL E.
                                                                                                                                                                                                                                                       ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-033-873-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
KY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 RRQIGT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-356-832-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
```

```
RESULT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                 ઠે
                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 61
US-08-988-705-8
Sequence 8, Application US/08988705
Patent No. 6211148
GENERAL INFORMATION:
APPLICANT: Selsted Michael E.
APPLICANT: Cullor, James S.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
MUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                            DB 2; Length 38; 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: CAMPBELL & FLORES, LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                          Query Match
1.8%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRICKATION DATA:
PRICKATION NUMBER: US 08/033,873
PRICKATION NUMBER: US 08/033,873
PRICKATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/356,832
PILING DATE: 13.DEC.1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 3-0C 2918
TELECOMMUNICATION INFORMATION:
                                                                                   P-UC 9552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                      NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUTHERS: 31,815
REFERENCE/DOCKET NUMBER: P-UC
TELECOMMUNICATION INFORMATION:
TELEFAN: (619) 535-9001
TELEFAX: (619) 535-8049
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                               : MOLECULE TYPE: peptide US-08-356-832-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          San Diego
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                  106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 RRQIGT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

1.8%; Score 6; DB 3; Length 38;

Query Match

```
ö
                        Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/08033873
; Patent No. 5459235
; GENERAL INFORMATION:
    APPLICANT: SELSTED, MICHAEL E.
    APPLICANT: SELSTED, MICHAEL E.
    APPLICANT: CULLOR, JAMES S.
    TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
    TITLE OF INVENTION: NEUTROPHILS
    NUMBER OF SEQUENCES: 22
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: CAMPBELL AND FLORES
                                                                                                                                                                                                                          Sequence 7, Application US/08033873
Patent No. 5459235
CENERAL INFORMATION:
APPLICANT: SELSTED, MICHAEL B.
APPLICANT: CULLOR, JAMES S.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE TITLE OF INVENTION: NUTROPHILS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 1; Length 40;
100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0; Indels
100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
VURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/033,873
FILING DATE: 19930319
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: CAMPBELL AND FLORES
STREET: SAN DIEGO
CITY: SAN DIEGO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                         SSEE: CAMPBELL AND FLORES
1: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
SAN DIEGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN A.
REGISTRATION UNDRER: 31, 815
REFERENCE/DOCKET UNDRER: P-UC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-9001
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 amino acids
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: SAN DALLY
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
3Y: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 RRQIGT 111
                                                                   106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 RRQIGT 30
                                                                                                                23 RRQIGT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-033-873-9
                                                                                                                                                                                                         US-08-033-873-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 63
```

```
TYPE: amino acid
TOPOLOGY: linear
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 RROIGT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 RRQIGT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 66
US-08-988-705-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08356832
Patent No. 5821224
GENERAL INFORMATION:
APPLICANT: SELSTED MICHAEL E.
APPLICANT: CULLOR, JAMES S.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE TITLE OF INVENTION: NUTROPHILS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,832
FILING DATE: 12-DEC-1994
CLASSIFICATION: B14
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,873
FILING DATE: 19-DMR-1993
ATTORNEY AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN A.
RECISTRATION NUMBER: 3-14
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION NUMBER: 3-15
RECISTRATION 
                                                                                   MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/033,873

FILING DATE: 19310319

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: CAMPBELL, CATHRIN A.

REGISTRATION NUMBER: B-UC 9552

FELECOMMUNICATION INFORMATION:

TELEPONE: (619) 535-8949

INFORMATION FOR SEC ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: ATTORNEY INFORMATION:

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID

TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (619) 535-900
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CALIFORNIA
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 RROIGT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-356-832-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                      Gaps
                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: SELSTED, MICHAEL E.

APPLICANT: CULLOR, JAMES S.

TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
TITLE OF INVENTION: A22
CORRESPONDENCE ADDRESS:
ADDRESSE: CAMPBELL AND FLORES
STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
CITY: SAN DIEGO
STATE: CALLFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.8%; Score 6; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                         Query Match
1.8%; Score 6; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSINION DATA:
APPLICATION NUMBER: US/08/356,832
FILING DATE: 12-DEC-1994
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,873
FILING DATE: 19-MR-1993
ATTORNEY AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN A.
REGISTRATION NUMBER: 31,915
REFERENCE/DOCKET NUMBER: 31-00
TIBECOMMUNICATION INDERS: 31-00
TIBECOMMUNICATION INDERS: 31-00
TIBECOMMUNICATION INDERS: 31-00
TIBECOMMUNICATION INDERS: 31-00
                                                                                                                                                                                                                                                                                                                                                                        US-08-356-832-9; Sequence 9, Application US/08356832; Patent No. 5821224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 7, Application US/08988705
; Patent No. 6211148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-08-356-832-9
, MOLECULE TYPE: peptide US-08-356-832-7
```

```
LENGTH: 46 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 RROIGT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Wash:
STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-057-762-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
APPLICANT: Selsted, Michael E.
APPLICANT: Cullor, James S.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE ITILE OF INVENTION: NEUTROPHILS
TITLE OF INVENTION: NEUTROPHILS
CORRESPONDENCE: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-988-705-9

US-08-988-705-9

Sequence 9, Application US/08988705

Patent No. 6211148

GENERAL INFORMATION:

APPLICANT: Selated, Michael E.

APPLICANT: Cullor, James S.

TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE

TITLE OF INVENTION: NEUTROPHILS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 3; Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: CAMPBELL & FLORES, LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                              ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033,873
FILING DATE: 19-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/356,832
FILING DATE: 13-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 2918
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 7:
SEGUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States
                                                                                                                                                                                             California
: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               San Diego
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 RRQIGT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 RROIGT 30
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92122
                                                                                                                                                                                                                                          92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-988-705-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY:
STATE:
                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 67
```

```
GENERAL INFORMATION:
APPLICANT: GARY BREION
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,1002-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.8%; Score 6; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 6; DB 4; Length 52;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jobert, S. APPLICANT: Jobert, S. APPLICANT: Glordano, J.Y. TITLE OF INVENTION: ESTS and Encoded Human Proteins. FILE REPERRICE: GENSET. 054 PR2. CURRENT APPLICATION NUMBER: US/09/621,976 CURRENT FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 19335 SOFTWARE: Patent.pm SSQ ID NO 6438 LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Scc...
100.0%; Pred. No. 1...
0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/543,681A
                 CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 6437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Sequence 6353, Application US/09543681A ; Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6438, Application US/09621976
Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; GENERAL INFORMATION:
; APPLICANT: Dummas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Xaa = Gly, Val
US-09-621-976-6438
                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa = Ala, Gly
                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa = Phe, Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 30
OTHER INFORMATION: Xaa = Ala,Gly
FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 10v..
                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 SLKLLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 SLKLLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 SLKLLG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 SLKLIG 20
                                                                                                                                                                                                        NAME/KEY: UNSURE
LOCATION: 30
                                                                                                                                                                                                                                                                    NAME/KEY: UNSURE LOCATION: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-543-681A-6353
                                                                                                                                                                                                                                                                                                                                 US-09-621-976-6437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-621-976-6438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 51
                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: PERL, ANDRAS
TITLE OF INVENTION: HUMAN TRANSALDOLASE: AN AUTOANTIGEN WITH
TITLE OF INVENTION: A FUNCTION IN METABOLISM
NUMBER OF SEQUENCES: 24
                                                                                                     Query Match 1.8%; Score 6; DB 2; Length 46; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 3; Length 46; 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 70
US-09-621-976-6437
Sequence 6437, Application US/09621976
Retent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Miline Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,119A
FILING DATE: 19-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33,949
SR: 280932000100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000 Pennsylvania Avenue N.W
                                                                                                                                                                                                                                                                                                                              ; Sequence 21, Application US/08326119A; Patent No. 6018021; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: LIVNATE, SHUTEL
REGISTRATION NUMBER: 2809
TELECOMMUTICATION INFORMATION:
TELECHONE: (202) 887-1500
TELEPHONE: (202) 822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 822-0168
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: Z0006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 46 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2.
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,
US-08-326-119A-21
        TYFE: SINSTRANDEDNESS: SIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 2000 rem
                                                                                                                                                                                     230 KLLGEL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 KLLGEL 235
    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 KLLGEL 20
                                                                                                                                                                                                                             15 KLLGEL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                               US-08-326-119A-21
                                                              US-09-057-762-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GCN4 no Cys
US-09-091-814-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 3; Length 64; 100.0%; Pred. No. 2.1e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anthony-cahill, Spencer J.
APPLICANT: Bpp. Janet K
APPLICANT: Bpp. Janet K
APPLICANT: Bpp. Janet K
APPLICANT: Mathews J.
APPLICANT: Mathews J., Antony
TILLE OF INVENTION GLOBINS CONTAINING BINDING DOMAINS
FILE REFERENCE: BXTP22005
CURRENT APPLICATION NUMBER: US/09/091,814
CURRENT APPLICATION NUMBER: 1998-06-22
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 4; L
100.0%; Pred. No. 2e+02;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 25, Application US/09091814 ; Patent No. 6218513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 LKLLGE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 SLKLLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 LKLLGE 46
                                                             16 LEKODK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SLKLLG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 76
US-09-134-001C-4534
                                                                                                                                             US-09-673-395A-510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-673-395A-510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-091-814-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                    g
                          ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.8%; Score 6; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                           Query Match 1.8%; Score 6; DB 4; Length 60; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
COMPUTER: PC
CORPWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: misc_feature
) LOCATION: (B) LOCATION 1...61
) SEQUENCE DESCRIPTION: SEQ ID NO: 5451:
US-09-107-532A-5451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Enterococcus faecium
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6353
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 5451, Application US/09107532A; Patent No. 6583275; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5451:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 61 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                ; ORGANISM: Proteus mirabilis US-09-543-681A-6353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                             158 IILFSN 163
                                                                                                                                                                                                                                                                                                                                     17 IILFSN 22
                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-107-532A-5451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
                                                                                                                              TYPE: PRT
                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 73
                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                   dd
```

٠<u>;</u>

Gaps

; 0

ö

Gaps

0;

```
Sequence 6127, Application US/09134000C
Sequence 6127, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WIMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US 60/055,778
FRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENT IN VERSION 3.1
SOFTWARE: PATENT IN VERSION 3.1
SEQ ID NO 6127
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 4; Length 82; 100.0%; Pred. No. 2.6e+02; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 4; Length 82; 100.0%; Pred. No. 2.6e+02; tive 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: 09/711,134
PRIOR FILING DATE: 2000-11-11
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Control of the control of the court of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 EILLKN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 EILLKN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 EILLKN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 EILLKN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 80
US-09-134-000C-6127
                                                                                                                                                                                                                                                                                                        US-09-858-664A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-274-978-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
Sequence 4534, Application US/0913400LC
Patent No. 6380370
APENEAL INPORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/054,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR APPLICATION UNMBER: US 60/065,779
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR APPLICATION NUMBER: US 60/065,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-858-664A-32

Sequence 32, Application US/09858664A

Sequence 32, Application US/09858664A

Sequence 32, Application US/09858664A

GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF PREPRENCE: CLOO9927-CLT

CURRENT PELICATION NUMBER: US/09/858,664A

CURRENT FILING DATE: 2001-05-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 4; Length 73;
100.0%; Pred. No. 2.3e+02;
7ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 6; DB 4; Length 66;
100.0%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: JOSET, S.
APPLICANT: Gooder, S.
APPLICANT: Gooder, S.
TITLE COF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5578
LENGTH: 73
TYPE: PAT
TYPE: PAT
CREAMISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0%; Pred. No. 2.1
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5578, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIEAVA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 PTEAVA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 GLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 GLLVTL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: -14..-1
US-09-621-976-5578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-134-001C-4534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 77
US-09-621-976-5578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 4534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
```

ö

Gaps

à 셤

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 4; Length 93; 100.0%; Pred. No. 2.9e+02; tive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Undert, S.

APPLICANT: Johert, S.

APPLICANT: Johert, S.

TITLE APPLICANT: GENERAL, S.Y.

TITLE OF INVENTION: ESTE and Encoded Human Proteins.

FILE REFERENCE: GENERT. 054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SEQ ID NO 4269

LENGTH: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION UNDERS: US/09/621,976
CURRENT FILNG DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...93
SEQUENCE DESCRIPTION: SEQ ID NO: 4435:
                                          REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
  NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-621-976-4269
; Sequence 4269, Application US/09621976
; Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 5842, Application US/09621976
; Patent No. 6639063
                                                                                                     INFORMATION FOR SEQ ID NO: 4435:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Homo sapiens
US-09-621-976-4269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 KNYLIK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 PLFSKS 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 KNYLIK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 PLFSKS 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-107-532A-4435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-621-976-5842
                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
                                                 ö
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                            APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Way, Yonnie S.
APPLICANT: Wu, Yonnie S.
TITE OF INVENTION: ALLI-fungal Proteins and Methods for Their Use
FILE REFERRNCE: 38-21(15.04)
CURRENT FILING DATE: 2000-12-07
PRIOR PILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                 .;
0
Query Match
1.8%; Score 6; DB 4; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 87; . 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/05171
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 4
100.0%; Pred. No. 2.7
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 82
US-09-107-532A-4435
; Sequence 4435, Application US/09107532A
; Patent No. 6893275
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                            US-09-732-210-888
Sequence 888, Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Methanococcus jannaschii
US-09-732-210-888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                              154 PLAKII 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 AEIVKI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 AEIVKI 50
                                                                                                                                       58 PLAKII 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
```

à g

ö

```
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REPRENCE/COCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPRAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 347, Application US/08936165A
; Patent No. 6348582
GENERAL INFORMATION:
APPLICANT: Black, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lonetto, Michael
Nicholas, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pratt, Julie
Reichard, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burnham, Martin
Hodgson, John
                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Knowles, David
                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                    single
      PRIOR APPLICATION DATA:
                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: PA
STATE: PA
COUNTRY: USA
TP: 19406-0939
                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 FEGKKD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 FEGKKD 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-936-165A-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                              US-08-961-083-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <del>Q</del>
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18411, Application US/09252991A

Sequence 18411, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILLE REFERENCE: 107196, 136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-18

SEQ ID NO 18411

LENGTH: 114

LENGTH: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 68, Application US/08961083
| Patent No. 6159469
| GENERAL INFORMATION: APPLICANT: Choi et. al. TITLE OP INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
| CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: STREET: 9410 Key West Avenue STREET: 9410 Key West Avenue STREET: MACKVILLE Avenue STREET: MACKVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 4; Length 114;
100.0%; Pred. No. 3.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                               1.8%; Score 6; DB 4; Length 104;
100.0%; Pred. No. 3.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-18411
                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 EKLLQS 219
                                                                                                                                                                                                                                                               189 DLLTRH 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 EKLLOS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Maryland
                                                                                                                                                                                                                                                                                                    54 DLLTRH 59
                                                                                              ; NAME/KEY: SIGNAL
; LOCATION: -51...1
US-09-621-976-5842
                                                                                                                                                                                                                                                                                                                                                                                  US-09-252-991A-18411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-961-083-68
SEQ ID NO 5842
LENGTH: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                             FEATURE:
                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

```
Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides, TITLE OF INVENTION: Polypeptides and Their Uses NUMBER OF SECUENCES: 534 CORRESPONDENCE ADDRESS:
Query Match
1.8%; Score 6; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPREATING SYSTEM: DOS
OSTWARE: FattSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTOMNEY AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRENCE/DOCKET NUMBER: 950549
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAX: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSEE: SmithKline Beecham Corporation
T: 709 Swedeland Road
King of Prussia
```

```
| Sequence 68, Application US/09536784
| Patent No. 6573082
| GENERAL INFORMATION:
| APPLICANT: Choi et. al.
| TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
| NUMBER OF SEQUENCES: 452
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.8%; Score 6; DB 4; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                              Query Match 1.8%; Score 6; DB 4; Length 117; Best Local Similarity 100.0%; Pred. No. 3.6e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/91,083
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/91,083
ATTORNEY/AGENT INFORMATION:
NAME: MICHAEL S. WATKE
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 68: US-09-536-784-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 117 amino acids
; INFORMATION FOR SEQ ID NO: 347:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 68: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                   SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Maryland COUNTRY: USA
                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 FEGKKD 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 FEGKKD 24
                                                                                                                                                                                                                                                                                                                                     18 VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                    1 VKILKD 6
                                                                                                                                                             ; MOLECULE TYPE:
US-08-936-165A-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 88
US-09-536-784-68
```

RESULT 89 US-08-513-974B-50

```
APPLICANT: FUKUSUMİ, Shoji
APPLICANT: Obgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/513,974B FILING DATE: 14-SEP-1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION 1979

PRIOR APPLICATION DATA

APPLICATION NUMBER: PCT/JP95/01599

FILING DATE: 10-AUG-1995

PILING DATE: 10-AUG-1995

FILING DATE: 19-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: UP 7-057186

FILING DATE: 16-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: UP 7-007177

FILING DATE: 20-JAN-1995

PRIOR APPLICATION NUMBER: UP 7-007177

FILING DATE: 20-JAN-1995

PRIOR APPLICATION NUMBER: UP 7-007177

FILING DATE: 20-JAN-1995

PRIOR APPLICATION NUMBER: UP 6-326611

FILING DATE: 28-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:

FILING DATE:

PILING DATE:

PLONOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

PILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

PRIOR APPLICATION NUMBER:

PRIOR APPLICATION NUMBER:

PRIOR APPLICATION NUMBER:

PRIOR APPLICATION NUMBER:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-189274

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-189274

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 50, Application US/08513974B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Resnick, David S. REGISTRATION NUMBER: 34,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                  Fujii, Ryo
Ohtaki, Tetsuya
     Sequence ... 6114139
Patent No. 6114139
GENERAL INFORMATION:
GENERAL HINUMA, Shuji
APPLICANT: Hinuma, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 119 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                       Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02109
                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
```

```
CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                        ;
                                                                                                                                          Query Match 1.8%; Score 6; DB 3; Length 119; Best Local Similarity 100.0%; Pred. No. 3.6e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Hosoya, Masaki
APPLICANT: Obtaki, Tetsuya
APPLICANT: Pukusumi, Shoji
APPLICANT: Obji, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUNITATION OF A COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-5EP-1995
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 7-057186
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 6-126611
FILING DATE: 20-JAN 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 6-226357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-513-974B-354
; Sequence 354, Application US/08513974B
; Patent No. 6114139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-513-974B-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    95 KDVTQI 100
                                                                                                                                                                                                                                                                                                                                                               45 KDVTQI 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 90
                                                                                                                                                                                                                                                                                                                                                        Dp
```

```
..
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.8%; Score 6; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Orlaki, Tetsuya
APPLICANT: Orlaki, Shoji
APPLICANT: Orlaki, Shoji
APPLICANT: Orlaki, Shoji
APPLICANT: Orlaki, Razuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: 9RODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE PATENTIN STATEM SOFTWARE WITH SOFTWARE PATENTIN BATA:

APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMER: US/08/513,974B
FILING DATE: US/08/513,974B
FILING DATE: US/08/513,974B
FILING PATE: US/08/513,974B
FILING APPLICATION DATA:
APPLICATION NUMBER: US/08/599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 355, Application US/08513974B Patent No. 6114139
                  APPLICATION NUMBER: UP 6-189272
FILING DATE: ILL-AUG-1994
ATTORNEY AGENT INFORMATION:
NAME: Resnick, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                          NAME: Resnick, David S.
REGISTRATION NUMBER: 34,255
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPAX: 617-523-3400
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                   in LENGTH: 119 amino acids
intrEs: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-513-974B-354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 KDVTQI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 KDVTQI 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-513-974B-355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
```

```
Sequence 3508, Application US/09134000C

Patent No. 6617156

Patent No. 6617156

Patent No. 6617156

Patent No. 6617156

Patent No. 6617156

Patent No. 6617156

Patent No. 6617156

Patent Norwarion: Barrencette-Stamm et al APPLICART: Lynn Doucette-Stamm et al APPLICART: Lynn Doucette-Stamm et al APPLICART: Lynn Doucette-Stamm et al TITLE OF INVERTION: BARRENCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVERTION: BARRENCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR PILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SEQ ID NO 3508

LENGTH: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.8%; Score 6; DB 4; Length 128; Best Local Similarity 100.0%; Pred. No. 3.9e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.8%; Score 6; DB 4; Ler
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 45753 DIV2
                                                                                             FILING DATE: 16-MAR. 1995
APPLICATION NUMBER: 7-001177
FILING DATE: 20-JAN-1995
APPLICATION NUMBER: 6-326611
FILING DATE: 28-DEC-1994
APPLICATION NUMBER: 6-270017
FILING DATE: 02-NOV-1994
APPLICATION NUMBER: 6-236357
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-23636
FILING DATE: 30-SEP-1994
APPLICATION NUMBER: 6-1994
APPLICATION NUMBER: 6-189274
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189273
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189273
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189273
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189272
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189272
FILING DATE: 11-AUG-1994
APPLICATION NUMBER: 6-189272
FILING DATE: 11-AUG-1994
ATORNEY/AGENT INPORMATION:
NAME: CONLIN, DAVID G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-461-436B-50
                                                                       APPLICATION NUMBER: 7-057186
                        7-093989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
TELEPHONE: 617-439-4444
TELEPAK: 617-439-4170
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 KDVTQI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 LLKNQP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 KDVTQI 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-134-000C-3508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-134-000C-3508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYO FUJII
TITLE OF INVENTION: G Protein Coupled Receptor Protein,
Production, And Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.8%; Score 6; DB 3; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/513,974
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/JP95/01599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/461,436B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edwards & Angell, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 92
US-09-461-436B-50
; Sequence 50, Application US/09461436B
; Patent No. 6538107
; GENERAL INFORMATION:
APPLICANT: Shuji Hinuma
; APPLICANT: Shuji Hinuma
                      FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 6-189274
PRIOR APPLICATION DATE: J1-AUG-1994
PRIOR APPLICATION NUMBER: JP 6-189273
FILING DATE: J1-AUG-1945
PRIOR APPLICATION NUMBER: JP 6-189272
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: J1-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 101 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 14-Dec-1999
CLASSIFICATION: <Unknown>
APPLICATION NUMBER: JP 6-270017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Reenick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPAN: 617-523-3400
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02209
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 119 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: BOSTON STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 KDVTQI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 KDVTQI 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-513-974B-355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH:
```

ô

. 0

```
Sequence 673, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffals, R.

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev.

TITLE OF INVENTION: and treatment of infection

TITLE OF INVENTION: and treatment of infection

FILE REPERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Glenn, Matthew
APPLICANT: Havukkala, 11kka J.
APPLICANT: Havukkala, 11kka J.
APPLICANT: Lubbers, Mark W.
APPLICANT: Lubbers, Mark W.
APPLICANT: Dekker, James
APPLICANT: Dekker, James
APPLICANT: O'Toole, Paul W.
APPLICANT: O'Toole, Paul W.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: them and methods for using them.
                                                                                                                                                                              , DB 4; Le._
No. 4e+02;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 4; I 100.0%; Pred. No. 4e+02; tive 0; Mismatches 0
                                                                                                                                                                                               Query Match
1.8%; Score 6; DB 4;
Best Local Similarity 100.0%; Pred. No. 4e+C
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 11000.1043UI
CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 372, Application US/09634238 ; Patent No. 6544772
                                                                                                                         ORGANISM: Acinetobacter baumannii
US-09-328-352-4824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Chlamydia pneumoniae
          CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 6; Conservative
                           NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4824
LENGTH: 131
                                                                                                                                                                                                                                                                                                  156 AKIILF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 YISKPE 253
                                                                                                                                                                                                                                                                                                                                                  79 AKIILF 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 YISKPE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-198-452A-673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-634-238-372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 673
                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-481-161-4

Sequence 4, Application US/09481161A

Sequence 4, Application US/09481161A

Sequence 4, Application US/09481161A

Sequence 4, Application US/09481161A

Sequence 4, Application US/09481161A

GENERAL INFORMATION:

APPLICANT: Webb, Bruce

APPLICANT: Webb, Bruce

APPLICANT: Watti, Indu

ITILE OF INVENTION: Materials and Methods Useful to Affect Growth and Development of FILE REFERENCE: P-1023

CURRENT APPLICATION NUMBER: US/09/481,161A

CURRENT FILING DATE: 2000-01-12

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4824, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
                                                                                                                                        Sequence 5393, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR PELICANION NUMBER: US 60/055,778
PRIOR FILING DATE: 1999-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
1.8%; Score 6; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 4; Length 129;
100.0%; Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. ...
Marches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Microplitis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 LRRQIG 110
||||||
86 LLKNQP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 LRRQIG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 YISAHP 24
                                                                                                                    US-09-134-000C-5393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-134-000C-5393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-328-352-4824
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 5393
LENGTH: 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-481-161-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ठे
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
```

.. 0

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Daley, Michael J.
APPLICANT: Daley, Michael J.
APPLICANT: Buckwalter, Brian L.
APPLICANT: Shieh, Hong-Ming
APPLICANT: Shieh, Hong-Ming
APPLICANT: Schieh, Peter
APPLICANT: School, Andrew TITLE OF INVENTION: Stabilization Of Somatotropins And Other
TITLE OF INVENTION: Proteins By Modification Of Cysteine Residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 135;
    100.0%; Pred. No. 4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATE:
FILING DATE: 06-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 2; Ler 100.0%; Pred. No. 4.1e+02; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1937 West Main Street, P.O. Box 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31,278-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/766,142
FILING DATE: 25-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dr. Estelle J. Tsevdos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08459906; Patent No. 6010999; GENERAL INFORMATION:
APPLICANT: Balckwalter, Brian L.,
APPLICANT: Buckwalter, Brian L.
                                                                                                                                                                                                                                   ; Sequence 5, Application US/08383621
; Patent No. 5951972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Tsevdos, Estelle J.
REGISTRATION NUMBER: 31,145
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 203-321-2756
TELEFAX: 203-321-2971
TELEX: 203-710-474-4059
INFORMATION FOR SEQ ID NO: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 135 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-FEB-1
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. Estel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1937 West M
CITY: Stamford
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 PENLKL 257
                                                                      156 AKIILF 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 06904-0060
    Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 PENLKL 36
                                                                                                                17 AKIILF 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-459-906-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-383-621-5
                                                                                                                                                                                                               US-08-383-621-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                                                                                                           ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Mittanck, Cindy A.
APPLICANT: Wu, Yomnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REPERRORS: 38-21(15.036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT APPLICATION NUMBER: US 60/169,513
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 1265
LENGTH: 134
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Mitanck, Cindy A.
APPLICANT: Mitanck, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Younle S.
ITILE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
ITILE PEFERNES: 38-21(15.036) B.
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT PILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
PRIOR FILING DATE: 1999-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
1.8%; Score 6; DB 4; Length 134;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 4; Length 134;
                                                                                          Query Match
1.8%; Score 6; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
; LOCATION: 1...133
; OTHER INFORMATION: Xaa=unknown or other US-09-198-452A-673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1265, Application US/09732210; Patent No. 6573361; GENERAL INFORMATION; APPLICANT: Bunkers, Greg J. APPLICANT: Liang, Jihong APPLICANT: Mittanck, Cindy A.
                                                                                                                                                                                                                                                                                                                                                 ; Sequence 804, Application US/09732210 ; Patent No. 6573361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Pyrobotrys stellata US-09-732-210-804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Euglena gracilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 VTKRQS 228
                                                                                                                                                                                                                                   37 IVKILK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 VTKROS 58
                                                                                                                                                                                       17 IVKILK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-732-210-1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-732-210-1265
                                                                                                                                                                                                                                                                                                     RESULT 99
US-09-732-210-804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                       ò
                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
REFLING DATE: 1997-05-23
RAPLICATION NUMBER: 60/047,583
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
RETLING DATE: 1997-05-23
                                          R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,615

R APPLICATION NUMBER: 60/047,597

R FILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,582

R FILING DATE: 1997-05-23

R PILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,632

R APPLICATION NUMBER: 60/047,601

R APPLICATION NUMBER: 60/047,601

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/043,580

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R APPLICATION NUMBER: 60/047,584
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,500
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,587
R FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,671
R APPLICATION NUMBER: 60/043,674
R APPLICATION NUMBER: 60/043,674
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,669
R FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,314

R FILING DATE: 1997-04-11

R PPLICATION NUMBER: 60/043,569

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-04-11
APPLICATION WUMBER: 60/043,672
ELING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-04-11
APPLICATION UNMBER: 60/048,974
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/056,886
            APPLICATION NUMBER: 60/047,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1997-05-23
APPLICATION UNDBER: 60/647,598
LING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/047,492
                                                                                                                                                                                                                                                                                      EARLIER 1
EARLIER 1
EARLIER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER 1
EARLIER 7
EARLIER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER F
EARLIER E
EARLIER F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEARLIER DEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER /
EARLIER /
EARLIER /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER 1
EARLIER 1
EARLIER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER EARLIER A
                                                                                                                                                                EARLIER
EARLIER
EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER
EARLIER
EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER
EARLIER
EARLIER
EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER
EARLIER
EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER
EARLIER
EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER
EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER
EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER
EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER
EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
APPLICANT: Cady, Susan M.
APPLICANT: Shieh, Hong-Ming
APPLICANT: Shieh, Hong-Ming
APPLICANT: Seddon, Andrew P.
APPLICANT: Seddon, Andrew P.
TITLE OF INVENTION: Stabilization of Somatotropins and Other
TITLE OF INVENTION: Proteins by Modification of Cysteine Residues
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/459,906
FILING DATE: 02-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.8%; Score 6; DB 3; Ler
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: PZ002P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER APPLICATION NUMBER: 60/040,636
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,336
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                    ADDRESSEE: American Cyanamid Company STREET: One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 554, Application US/09149476 Patent No. 6420526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Webster, Darryl L.
REGISTRATION NUMBER: 34,276
REFRENCE/DOCKET NUMBER: 31,2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3247
TELEPHONE: 201-831-3365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acide TOPOLOGY: 1:-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-459-906-5
                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: American (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Jersey
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 PENLKL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 PÉNĽKĽ 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             Wayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-149-476-554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dd
```

```
BARLIER PILING DATE: 1997-08-22
BARLIER PLING DATE: 1997-08-23
BARLIER PILING DATE: 1997-08-23
BARLIER PILING DATE: 1997-08-23
BARLIER PILING DATE: 1997-08-23
BARLIER PILING DATE: 1997-08-23
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-22
BARLIER PILING DATE: 1997-08-23
BARLIER PILING DATE: 1997-08-23
BARLIER PILING DATE: 1997-08-23
BARLIER PILING DATE: 1997-08-23
BARLIER PILING DATE: 1997-08-23
BARLIER PILING DATE: 1997-05-23
BARLIER PILING DATE: 1997-05-23
BARLIER PILING DATE: 1997-05-23
BARLIER PILING DATE: 1997-05-23
BARLIER PILING DATE: 1997-05-23
BARLIER PILING DATE: 1997-05-23
BARLIER PILING DATE: 1997-05-23
BARLIER PILING DATE: 1997-05-23
BARLIER PILING DATE: 1997-05-23
BARLIER PILING DATE: 1997-05-23
BARLIER PILING DATE: 1997-05-23
BARLIER PILING DATE: 1997-05-23
BARLIER PILING DATE: 1997-05-23
```

```
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709,2004001
CURENT APPLICATION NUMBER: US (09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11504
LENGTH: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 1.8%; Score 6; DB 4; Length 136; Best Local Similarity 100.0%; Pred. No. 4.1e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.8%; Score 6; DB 4; Lei
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-08-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-06-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-489-039A-11504
; Sequence 11504, Application US/09489039A
; Patent No. 6610836
; GRNERAL INFORMATION:
; APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 13120, Application US/09489039A; Patent No. 6610836
                                                                 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,881
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,909
FILING DATE: 1997-08-22
                                                                                                                                                                                        APPLICATION NUMBER: 60/056,875
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,862
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/056,887
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,908
APPLICATION NUMBER: 60/056,664
FILING DATE: 1997-08-22
                    FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,876
                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/048,964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 TLIADL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 SLKLLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 SLKLLG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 TLIADL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 105
US-09-489-039A-13120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-489-039A-11504
                                                                                                                                                                                                                                        EARLIER |
EARLIER |
EARLIER |
EARLIER |
EARLIER |
EARLIER |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
         Z1F: >43.04
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIBLE
                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TESTTUT02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 DLKKTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: TESTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-872-783-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
           APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: PREDMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13120
LENGTH: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 73, Application US/09370838
; Sequence 73, Application US/09370838
; Retent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Beed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Roadoh
; APPLICANT: Secriat, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
; TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
; CURRENT APPLICATION NUMBER: US 09/285,323
; CURRENT FILING DATE: 1999-04-02
; BARLIER FILING DATE: 1999-04-02
; WUMBER OF SEQ ID NOS: 289
; SOFTWARE: FRAESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 136;
0. 4.1e+02;
cches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 4; Length 144;
100.0%; Pred. No. 4.3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08872783

Patent No. 5858717

GENERAL INFORMATION:
APPLICANT: Hallman, Jennifer L.
APPLICANT: Lal, Preeti
ITILE OF INVENTION:
HUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 4
100.0%; Pred. No. 4.1
vative 0; Mismatches
                                                                                                                                                                                                                                                                                       ; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13120
                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity الاست
من 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 EDYEKL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 VEYISA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 VEYİSA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 EDYEKL 63
SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-370-838-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 144
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-370-838-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 107
US-08-872-783-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
WANTIER FEBRUARIE FORM:

WANTIER FEBRUARIE FORM:

SOURTIER SIEM COMMANIANE

SOURTIER SIEM COMMANIANE

SOURTIER SIEM COMMANIANE

STIND AND THE BETWEND ACT.

FILING DATE: BETWEND ACT.

FRICKATION NUMBER: U/00/872/83

FRICKATION NUMBER: U/00/873

REFERENCE/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERRING/DOCKET NUMBER: 16,749

RESERVING SYSTEM DOCK NUMBER: 16,749

RESERVING SYSTEM DOCK NUMBER: 16,749

RESERVING SYSTEM DOCK NUMBER: 16,749

RESERVING SYSTEM DOCK NUMBER: 16,749

RESERVING SYSTEM DOCK NUMBER: 16,749

RESERVING SYSTEM DOCK NUMBER: 16,749

RESERVING SYSTEM DOCK NUMBER: 16,749

RESERVING SYSTEM DOCK NUMBER: 16,749

RESERVING SYSTEM DOCK NUMBER: 16,749

RESERVING SYSTEM DOCK NUMBER: 16,749

RESERVING SYSTEM DOCK NUMBER: 16,749

RESERVING SYSTEM DOCK NUMBER: 16,749

RESERVING SYSTEM NUMBER: 16,749

RESERVING SYSTEM NUMBER: 16,740

RESERVING SYSTEM NUMBER: 16,740

RESERVING SYSTEM NUMBER: 16,740

RESERVING SYSTEM NUMBER: 16,740

RESERVING SYSTEM NUMBER: 16,740

RESERVING SYSTEM NUMBER: 16,740

RESERVING SYSTEM NUMBER: 16,740

RESERVING SYSTEM NUMBER: 16,740

RESERVING SYSTEM NUMBER: 16,740

RESERVING SYSTEM NUMBER: 16,740

RESERVING SYSTEM NUMBER: 16,740

RESERVING SYSTEM NUMBER: 16,740

RESERVING SYSTEM NUMBER: 16,740

RESERVING SYSTEM NUMBER: 1
```

. 0

```
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
TAPLICANT: Mittanck, Cindy A.
APPLICANT: Wu, Younie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21 (15036) B
CURRENT APPLICATION NUMBER: US 60/169,513
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR PLING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 532
LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Mittanck, Cindy A.
APPLICANT: Wiltenck, Cindy A.
APPLICANT: Wu, Yomie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21 (15.036)B
CURRENT APPLICATION NUMBER: US 60/169,513
FRIOR APPLICATION NUMBER: US 60/169,513
PRIOR APPLICATION NUMBER: US 60/169,540
PRIOR PRILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR PRILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 531
LENGTH: 162
                                                                                                                                                                                 Gaps
                                                                                                                                                                                 .
0
                                                                                                                           Query Match
1.8%; Score 6; DB 4; Length 160;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 4; Length 161; 100.0%; Pred. No. 4.8e+02; tive 0; Mismatches 0; Indels
                        TYPE: PRT; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4854
                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 532, Application US/09732210
; Patent No. 6573361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 531, Application US/09732210
; Patent No. 6573361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mycoplasma pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Mycoplasma genitalium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 NNILRR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 NNILRR 61
                                                                                                                                                                                                                                 78 LLVTLI 83
                                                                                                                                                                                                                                                                               16 LLVTLI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   US-09-732-210-532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-732-210-532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-732-210-531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-732-210-531
  LENGIH: 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 112
                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENITON: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENITON: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICAM: Marc J. Rubenfield et al.

APPLICAM: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.8%; Score 6; DB 4; Length 155;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.8%; Score 6; DB 4; Length 151; Best Local Similarity 100.0%; Pred. No. 4.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 30905, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 4854, Application US/09134001C
; Patent No. 6380370
                  REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 423: SEQUENCE CHARACTERISTICS: LENGTH: 151 amino acide TYPE: amino acid
                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: No. 6348328e
Gimmi, Edward R
                                                                                                                         TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4854
                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 KVLVAD 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 IALRCG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 IALRCG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 KVLVAD 58
                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-252-991A-30905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-252-991A-30905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-134-001C-4854
                                                                                                                                                                                                                                                                                                                                                     US-08-858-207A-423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 30905
                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                   TELEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
```

```
TITLE OF INVENTION: 186 Human Secreted proteins
                                                                                       EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1998-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
                             FILE REFERENCE: PZ002P1
CURRENT APPLICATION NUMBER: US/09/149,476
                                                                                                                                                                                                                                                                                            FILING DATE: 1997-03-07
APPLICATION UNDRER: 60/040,334
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,336
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
FILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/047,600
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-05-23
APPLICATION WUMBER: 60/047,597
APPLICATION DATE: 1997-05-23
APPLICATION NUMBER: 60/047,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/047, 633
FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,613
FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/047,596
FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 60/043,569
EARLIER FILLING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/047,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/047,617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/047,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60/047,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/047,584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LICATION NUMBER: 60/047,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 60/047,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/047,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/047,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/047,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/043,580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/043,568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/043,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/047,601
                                                                         CURRENT FILING DATE: 1998-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EARLIER
                                                                                                                                                                                                APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19902
LENGTH: 170
                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                    ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                  0; Indels
    1.8%; Score 6; DB 4; Length 162;
100.0%; Pred. No. 4.8e+02;
vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.8%; Score 6; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 4
100.0%; Pred. No. 4.8
rative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19902, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 526, Application US/09149476
Patent No. 6420526
PENERAL INPORMATION:
APPLICANT: ROBEN et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Pseudomonas aeruginosa
Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                         102 NNILRR 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 FKDLLT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 FKDLLT 100
                                                                                                                                57 WILLR 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 EVSKSL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 EVSKSL 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 114
US-09-252-991A-19902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-252-991A-19902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-149-476-526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 163
                                                                                                                                  ПЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

```
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER PILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-23
EARLIER FILING DATE: 1997-08-23
EARLIER FILING DATE: 1997-08-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
                                                                                            EARLIER APPLICATION NUMBER: 60/043,674
EARLIER FILING DATE: 1997-04-11
EARLIER PRINCATION NUMBER: 60/043,669
EARLIER PILING DATE: 1997-04-11
EARLIER PEPLICATION NUMBER: 60/043,312
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,313
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,896
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,630
FILING DATE: 1997-08-22
FILING DATE: 1997-04-11
APPLICATION WUNBER: 60/043,671
ELING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/056,878
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LING DATE: 1997-08-22
PLICATION NUMBER: 60/056,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILLING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,882
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/056,637
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/056,636
FILING DATE: 1997-08-22
PAPLICATION NUMBER: 60/056,874
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/056,911
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,864
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/056,888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LING DATE:
```

```
R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,590

R FILING DATE: 1997-05-23

R PILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILLING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,664
FILLING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,876
FILLING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,576
FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1997-08-22
APPLICATION WUMBER: 60/056,875
APPLICATION WUMBER: 60/056,875
APPLICATION NUMBER: 60/056,862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER FILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-96
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/061,060
FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/047,614
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/056,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/056,887
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/057,669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-09-05
APPLICATION NUMBER: 60/049,610
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,593
FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/056,908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1997-09-05
APPLICATION NUMBER: 60/056,884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/047,501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/056,881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER BEARLIER PEARLIER PEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEARLIER BEAR
```

Gaps .. Length 174; 0: Indels Query Match
1.8%; Score 6; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 0;

.,

195 KVLVAD 200 40 KVLVAD 45 g

US-09-328-352-4965

Sequence 4965, Application US/09328352

Patent No. 6562958

Patent No. 6562958

Patent No. 6562958

Patent No. 6562958

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: BADMANNI FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4965

```
à
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 4; Length 178;
100.0%; Pred. No. 5.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                         Query Match 1.8%; Score 6; DB 4; Length 178; Best Local Similarity 100.0%; Pred. No. 5.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: AATINICIO, PAMELA DENEKE
REFERENCE/DOCKET NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...178
SEQUENCE DESCRIPTION: SEQ ID NO: 5800:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                       ; Sequence 5800, Application US/09107532A; Patent No. 6583275; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 178 amino acids TYPE: amino acid
                  // TYPE: PRT
// ORGANISM: Acinetobacter baumannii
US-09-328-352-4965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 5800:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.4
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 KTQPIV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 KTQPIV 105
                                                                                                                                                                                                   18 VKILKD 23
                                                                                                                                                                                                                                           83 VKILKD 88
                                                                                                                                                                                                                                                                                                                                     US-09-107-532A-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÚS-09-107-532A-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
LENGTH: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQ
                                                                                                                                                                                                     à
                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
```

```
Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 94 Human Secreted Proteins

FILE REFERENCE: PRO29P1

CURRENT PELING DATE: 2001-12-12

PRIOR PELING DATE: EARLIER APPLICATION NUMBER: 09/461,325

PRIOR PELING DATE: EARLIER FILING DATE: 1999-12-14

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.8%; Score 6; DB 4; Length 181; Best Local Similarity 100.0%; Pred. No. 5.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                   APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/461,325A
CURRENT PILING DATE: 1999-12.14
CURRENT PILING DATE: 1999-12.14
EARLIER PEPLICATION NUMBER: PC1/US99/13418
EARLIER PELING DATE: 1999-06-15
EARLIER PILING DATE: 1998-06-16
EARLIER PILING DATE: 1998-06-16
EARLIER PILING DATE: 1998-06-16
EARLIER PILING DATE: 1998-06-16
EARLIER PILING DATE: 1998-06-16
EARLIER PELING DATE: 1998-06-16
EARLIER PILING DATE: 1998-06-16
EARLIER PELING DATE: 1998-06-16
EARLIER PILING DATE: 1998-06-16
EARLIER PELING DATE: 1998-06-16
EARLIER PELING DATE: 1998-06-16
EARLIER PELING DATE: 1998-06-22
EARLIER PILING DATE: 1998-06-22
EARLIER PELING DATE: 1998-06-22
EARLIER PELING DATE: 1998-06-22
EARLIER PELING DATE: 1998-06-22
NUMBER: OF SGO DI NOS: 55.2
                          Sequence 196, Application US/09461325A Patent No. 6475753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 196, Application US/10012542
; Patent No. 6627741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 196
LENGTH: 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-012-542-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 GLLVTL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77 GLLVTL 82
                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-012-542-196
US-09-461-325-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-461-325-196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 196
LENGTH: 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
```

```
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
RIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
NUMBER OF SEQ ID NOS: 14342
LENGTH: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: GATY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,2004001
CURRENT PEPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) Sequence 4452, Application US/09107532A
; Sequence 4452, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
APPLICANT: LYON A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 4; Length 188; 100.0%; Pred. No. 5.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                     Score 6; DB 4; Length 184; Pred. No. 5.4e+02;
                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                         1.8%; Scor.
100.0%; Pred. No. 5...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 8986, Application US/09489039A ; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                       ) ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8986
LENGTH: 188
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100..
--hea 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 GELILD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 GELILD 46
                                                                                                                                                                                                                                                                                                                                                                                                                 18 VKILKD 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 VKILKD 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 124
US-09-107-532A-4452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-489-039A-8986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-489-039A-8986
                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                   Sequence 612, Application US/09198452A

Sequence 612, Application US/09198452A

Patent NO. 6559294

GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevering PTILE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999

CURRENT APPLICATION UNMERR: US/09/198,452A

CURRENT PILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 7656, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
A APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 4; Length 183; 100.0%; Pred. No. 5.4e+02; tive 0; Mismatches 0; Indels
                            1.8%; Score 6; DB 4; Length 181;
100.0%; Pred. No. 5.3e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
1.8%; Score 6; DB 4; Ler
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7656
LENGTH: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 122
US-09-489-039A-12490
; Sequence 12490, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Chlamydia pneumoniae US-09-198-452A-612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; APPLICANT: Gary Breton et. al
    Query Match
Best Local Similarity luv...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 DLLTRH 194
                                                                                                                                                              99 GLLVTL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 DLLTRH 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 VTLIAD 85
                                                                                                                     77 GLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 VTLIAD 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 121
US-09-489-039A-7656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-489-039A-7656
                                                                                                                                                                                                                                RESULT 120
US-09-198-452A-612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            qq
                                                                                                                     à
                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
```

ô

```
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22287, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: AREGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AREGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ·,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.8%; Score 6; DB 4; Length 207; Best Local Similarity 100.0%; Pred. No. 6e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.8%; Score 6; DB 4; Length 190; 100.0%; Pred. No. 5.5e+02; tive 0; Mismatches 0; Indels
CURRENT APPLICATION DATA:

APPLICATION UNDER: 10/09/107,532A
FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION UNBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 1111,2,1997
ATTORNEY/ABENT INFORMATION:

NAME: ATIMICALIO, PAMELA DENEK
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...190
SEQUENCE DESCRIPTION: SEQ ID NO: 4452:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 126
US-08-811-519-24
; Sequence 24, Application US/08811519B
                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 190 amino acids
                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 4452: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 LLRDKS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 LLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 LEKQDK 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 LEKQDK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 125
US-09-252-991A-22287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-252-991A-22287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-107-532A-4452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
```

```
Sequence 3080, Application US/09134001C
PATENT NO. 5380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUE
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
GENERAL INFORMATION:

APPLICANT: PETERBOX, Alexandre
APPLICANT: PETERBOX: ALEXANDRE
TITLE OF INVENTION: CALCIUM INDEPENDENT RECEPTOR OF ALPHA-LATROTOXIN,
TITLE OF INVENTION: CHARACTERIZATION AND USES THEREOF
FILE REFERENCE: 1049-11-007
CURRENT APPLICATION NUMBER: US/08/811,519B
CURRENT FILING DATE: 1997-03-04
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIAL VET: 2.0
SEQ ID NO 24
LENGTH: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 6; DB 4; Length 207;
100.0%; Pred. No. 6e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.8%; Score 6; DB 4; Length 209; Best Local Similarity 100.0%; Pred. No. 6e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 128
US-09-391-741A-10
Sequence 10. Application US/09391741A
Sequence 10. Application US/09391741A
Setent No. 655572
GENERAL INFORMATION:
APPLICANT: Sharma, Yogesh Kumar
TITLE OF INVENTION:
PILE REFERENCE: 0866D
CURRENT APPLICATION NUMBER: US/09/391,741A
CURRENT TILING DATE: 1999-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR PELICATION NUMBER: 60/111,919
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: 60/100,284
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: 09/391,741
PRIOR FILING DATE: 1999-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Staphylococcus epidermidis US-09-134-001C-3080
                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 FLSSFQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 TLIADL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 FLSSFQ 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 TLIADL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 127
US-09-134-001C-3080
                                                                                                                                                                                                                                                                                                                                                   US-08-811-519-24
```

.. 0

```
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                 1.8%; Score 6; DB 4; Length 212;
100.0%; Pred. No. 6.1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 4; Length 214; 100.0%; Pred. No. 6.2e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 4; Length 214; 100.0%; Pred. No. 6.2e+02;
                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09391741A
; Sequence 2, Application US/09391741A
; Patent No. 6555732
; GENERAL INFORMATION:
    APPLICANT: Davick, Jonathan P.
    APPLICANT: Bharma, Yogesh Kumar
; TITLE OF INVENTION: Rac-Like Genes and Methods of Use
; FILE REPRENCE: 0866D
; CURRENT APPLICATION NUMBER: US/09/391,741A
; PRIOR APPLICATION NUMBER: 06/111,919
; PRIOR FILING DATE: 1998-09-08
; PRIOR FILING DATE: 1998-09-14
; PRIOR FILING DATE: 1998-09-14
; PRIOR FILING DATE: 1998-09-08
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-391-741A-16
| Sequence 16, Application US/09391741A
| Patent No. 6555732
| GENERAL INFORMATION:
| APPLICANT: Davick, Jonathan P.
| APPLICANT: Davick, Jonathan P.
| APPLICANT: Davick, Jonathan P.
| APPLICANT: Davick, Jonathan P.
| TITLE NOT INVENTION: RAC-Like Genes and Methods of Use FILE REFERENCE: 0866D
| CURRENT FILING DATE: 1999-09-08
| PRIOR PELING DATE: 1999-09-08
| PRIOR PELING DATE: 1999-09-14
| PRIOR PILING DATE: 1998-12-11
| PRIOR PILING DATE: 1999-09-14
| PRIOR PILING DATE: 1999-09-14
| PRIOR PILING DATE: 1999-09-08
| NUMBER OF SEQ ID NOS: 51
| SEQ ID NO 16
| SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.8'
Best Local Similarity 100.
Matches 6; Conservative
                                                                                           Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 LRRQIG 110
                                                                                                                                                                    105 LRRQIG 110
                                                                                                                                                                                                                 146 LRRQIG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 LRRQIG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Zea mays
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-391-741A-16
                    US-09-391-741A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-391-741A-2
                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                      ò
                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34, Application US/09391741A

Fatent No. 6555732

GENERAL INFORMATION:
APPLICANT: Duvick, Jonathan P.
APPLICANT: Davick, Jonathan P.
TITLE OF INVENTION: Rac-Like Genes and Methods of USE TITLE OF INVENTION: Rac-Like Genes and Methods of USE TITLE REPRENCE: 0866D

CURRENT APPLICATION NUMBER: US/09/391,741A

CURRENT APPLICATION NUMBER: 00/111,919

FRIOR FILING DATE: 1999-00-08

FRIOR FILING DATE: 1998-09-14

FRIOR FILING DATE: 1998-09-14

FRIOR FILING DATE: 1998-09-14

FRIOR FILING DATE: 1998-09-14

FRIOR FILING DATE: 1998-09-08

NUMBER OF SEQ ID NOS: 51

SEQ ID NO 34

LENGTH: 212
                                                                                                                                                                                      Query Match 1.8%; Score 6; DB 4; Length 212; Best Local Similarity 100.0%; Pred. No. 6.1e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 4; Length 212;
100.0%; Pred. No. 6.1e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Divick, Jonathan P.
APPLICANT: Sharma, Yogesh Kumar
TITLE OF INVENTION:
FILE SEPRENCE: 0866D
CURRENT APPLICATION NUMBER: US/09/391,741A
CURRENT APPLICATION NUMBER: US/09/391,741A
CURRENT PILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: 60/11,919
PRIOR APPLICATION NUMBER: 60/11,919
PRIOR FILING DATE: 1998-09-14
PRIOR FILING DATE: 1998-09-14
PRIOR FILING DATE: 1998-09-14
PRIOR FILING DATE: 1998-09-14
PRIOR FILING DATE: 1998-09-18
NUMBER: OF SEQ ID NOS: 51
SOSTWARE: RastSEQ for Windows Version 3.0
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/09391741A; Parent No. 6555732; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                        105 LRRQIG 110
                                                                                                                                                                                                                                                                                                                                      146 LRRQIG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 LRRQIG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 LRRQIG 151
                                                                                           TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 129
US-09-391-741A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 130
US-09-391-741A-34
                                                                                                                                             US-09-391-741A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-391-741A-24
                    SOFTWARE: Fas
SEQ ID NO 10
LENGTH: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 24
LENGTH: 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
```

```
Sequence 6222, Application US/09328352

Patent No. 6562958

Patent No. 6562958

Patent No. 6562958

TITUR OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: BAUGANNI FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: US/09/328,352

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 6222

LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEFE, DANIEL
TILLE OF INVENTION: SOVBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL.-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT APPLICATION NUMBER: 08/924,747
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR APPLICATION NUMBER: 08/924,747
PRIOR FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
                                                                                                                                   APPLICANT: Holland, Ross
APPLICANT: O'Toole, Paul W.
APPLICANT: Reid, Julian R.
APPLICANT: Reid, Timothy
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: them and methods for using them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 4; Length 218; 100.0%; Pred. No. 6.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 4; Length 218; 100.0%; Pred. No. 6.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                           SEQ ID NOS: 422
FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                  FILE REFERENCE: 11000.1043U1
CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSEQ for Windows Version 4.C
SEQ ID NO 341
LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-247-373B-50; Sequence 50, Application US/09247373B; Patent No. 6168954
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Lactobacillus rhamnosus US-09-634-238-341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6222
                         Havukkala, Ilkka J.
Bloksberg, Leonard, N.
                                                                                                                Christensson, Anna C.
                                                               Lubbers, Mark W.
Dekker, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.(
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 6; Conservative
    Glenn, Matthew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 FLEQNY 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 KDLLTR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 KDLLTR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 FLEONY 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 136
US-09-328-352-6222
                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                              APPLICANT:
                                                 APPLICANT:
                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 134
US-09-238-352-6571
US-09-238-352-6571
Sequence 6571, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
    Gaps
    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 214;
    0; Indels
                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Duvick, Jonathan P.
APPLICANT: Bharma, Yagesh Kumar.
TITLE OF INVENTION: Rac-Like Genes and Methods of Use;
FILE REFERENCE: 0866D
CURRENT PILING DATE: 1999-09-08
PRIOR FILING DATE: 1998-1011, 919
PRIOR PLING DATE: 1998-02-11
PRIOR PLING DATE: 1998-02-14
PRIOR PLING DATE: 1998-09-14
PRIOR FILING DATE: 1998-09-14
PRIOR FILING DATE: 1998-09-14
PRIOR FILING DATE: 1998-09-18
PRIOR FILING DATE: 1998-09-18
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; pred. No. b.z.
Matcheg 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.8%; Score 6; DB 4
Best Local Similarity 100.0%; Pred. No. 6.2
Matches 6; Conservative 0; Mismatches
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 135
US-09-634-238-341
Sequence 341, Application US/09634238
Patent No. 6544772
GENERAL INFORMATION:
                                                                                                                                                                                              ; Sequence 26, Application US/09391741A; Patent No. 6555732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Acinetobacter baumannii
  6; Conservative
                                            105 LRRQIG 110
                                                                                       148 LRROIG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 LRRQIG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 LRRQIG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 SGLLVT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 SGLLVT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-328-352-6571
                                                                                                                                                        SULT 133
-09-391-741A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-391-741A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 26
Matches
                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     원
                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
```

```
Sequence 6078, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
                                                                        RESULT 140
US-09-107-532A-5238
; Sequence 5238, Application US/09107532A
; Patent No. 6583775
; GENERAL INFORMATION:
; GENERAL INFORMATION:
the sequence 5238 and David Bush
the sequence 52375
; TILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF INVENTION:
TILE OF TILE OF INVENTION:
TILE OF TILE OF TILE OF TILE OF TILE OF TILE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
1.8%; Score 6; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: U1/12, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ALINICID. Pamela Deneke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...230; SEQUENCE DESCRIPTION: SEQ ID NO: 5238: US-09-107-532A-5238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8277
INFORMATION FOR SEQ ID NO: 5238:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 230 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 LLRDKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 LLRDKS 219
108 EAFHVF 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-543-681A-6078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3. Application US/09134001C
Sequence 3. Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PELING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR SEQ ID NOS: 5674
SEQ ID NO 3053
LENGTH: 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9910, Application US/09489039A; Patent No. 6610836; GENERAL INFORMATION:
APPLICANT: GENERAL INFORMATION:
APPLICANT: GENERAL GENERAL OF THE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.8%; Score 6; DB 4; Length 227; Best Local Similarity 100.0%; Pred. No. 6.5e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.8%; Score 6; DB 4; Length 222; Best Local Similarity 100.0%; Pred. No. 6.4e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                   1.8%; Score 6; DB 3; Length 220; 100.0%; Pred. No. 6.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Klebsiella pneumoniae
   Microsoft Office 97
                                                                                                                                                                                                   Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 EAFHVF 277
                                                                                                                                                                                                                                                                                                                                                                                212 DYEKLL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 IRDLKK 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 DYEKLL 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 IRDLKK 93
                                                                                                                                  ; ORGANISM: SOYBEAN US-09-247-373B-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-489-039A-9910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-489-039A-9910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-134-001C-3053
SOFTWARE: Mic
SEQ ID NO 50
LENGTH: 220
                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
APPLICANT: Demaggio, Anthony J.
APPLICANT: Hoekstra, Merl F.
TITLE OF INVENTION: Materials and Methods Relating to Proteins
TITLE OF INVENTION: that Interact with Casein Kinase I
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/376,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.8%; Score 6; DB 1; Le:
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 6; Conservative 0; Mismatches 0;
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,605
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INPORMATION:
NAME: No. 5728806and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31784
TELECOMMUNICATION INPORMATION:
TELEPHONE: 312/474-6300
TELEPHONE: 312/474-6448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 21.JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: No. 5846764and, Greta E.
RESISTRATION NUMBER: 25.302
REFERENCE/DOCKET NUMBER: 27866/31784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6300 Sears tower,
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/184,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 7, Application US/08376843
; Patent No. 5846764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                      I: 232 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 232 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                   TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312/474-0448
                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-036-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 KYVELS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 KYVELS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-376-843-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-376-843-7
                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709-2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1090-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 10973
LENGTH: 231
                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Demaggio, Anthony J.
APPLICANT: Demaggio, Anthony J.
APPLICANT: Hoekstra, Merl F.
TITLE OF INVENTION: Materials and Methods Relating to Proteins that
TITLE OF INVENTION: Interact with Casein Kinease I
WIDMER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.8%; Score 6; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                        Length 231;
                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60606-6402

CMEDIUM TYPE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,036
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                   Query Match
1.8%; Score 6; DB 4; Ler
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 6; Conservative 0; Mismatches 0;
     CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 60'8
LENGTH: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 142
US-09-489-039A-10973
; Sequence 10973, Application US/09489039A
; Parent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 6060-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: US/08/468,036
06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 7, Application US/08468036
; Patent No. 5728806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                        TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                 105 LRRQIG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 LRRQIG 110
                                                                                                                                                                                                                                                                                                                                                                                                 87 LRRQIG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 LRRQIG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Gary Bro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-489-039A-10973
                                                                                                                                                                                                     US-09-543-681A-6078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-468-036-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 143
```

à

```
Sequence 2870, Application US/0925291A

Sequence 2870, Application US/0925291A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFREENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 29870

LENGTH: 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GONES, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TYPOSINE PHOSPHATASES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS: 34
CORRESPONDENCE ADDRESS: ADDRESSES: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ALLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 4; Length 243;
100.0%; Pred. No. 6.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
APPLICATION NUMBER: PCT/US94/09943
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 11,616
REFERENCE/DOCKET NUMBER: LO461/7003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/09100804
Patent No. 6066472
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100. Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: BOSTON STATE: MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 GLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 GLLVTL 34
US-09-252-991A-29870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-252-991A-29870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-100-804-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 182, Application US/09198452A

Patent No. 6559294

GENERAL INCRMATION:

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preversor and realment of infection

FILE REFERENCE: 9710-003-999 (1003-999)

FILE REFERENCE: 9710-003-999 (1003-999)

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

LENGTH: 242

TYPE: PRT

ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                      Sequence (013, Application US/09134001C
Patent No. 6380370
GENERAL INPORATION:
TELL INPORATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 4; Length 233; 100.0%; Pred. No. 6.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 242;
DB 2; Length 232; 0. 6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.8%; Score 6; DB 4; Ler
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 6; Conservative 0; Mismatches 0;
Query Match
1.8%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 6.6
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: Xaa-unknown or other US-09-198-452A-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 100.
Matches 6; Conservative
                                                                                                   170 KYVELS 175
                                                                                                                                                 113 KYVELS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 NYLIKQ 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 NYLIKO 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 IVKILK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 IVKILK 77
                                                                                                                                                                                                                                RESULT 145
US-09-134-001C-4013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-134-001C-4013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-198-452A-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 4013
LENGTH: 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                      à
```

```
GENERAL INV. 0231/93

GENERAL INV. 0231/93

GENERAL INV. 0231/93

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25583

LENGTH: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AOFIGE 10196.126

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 19444

LENGTH: 255
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                             ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 4; Length 254;
100.0%; Pred. No. 7.2e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.8%; Score 6; DB 4; Length 255; Best Local Similarity 100.0%; Pred. No. 7.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                             Indels
                                           .
                   100.0%; Pred. No. 7.1e+02;
                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-252-991A-19444
; Sequence 19444, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                 Sequence 25583, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-311-731A-141
; Sequence 141, Application US/08311731A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 DKASEE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 GLLVTL 182
                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 DKASEE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 GLLVTL 82
                                                                                      64 EAVAQL 69
                                                                                                                                  45 EAVAQL 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Marc J.
                                                                                                                                                                                                   RESULT 151
US-09-252-991A-25583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-252-991A-19444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-25583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 152
                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                      ð
                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR PAPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT PELLING NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-29
PRIOR APPLICATION NUMBER: US 60/117,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                                                       DB 3; Length 247;
5. 7e+02;
cches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 247;
5. 7e+02;
cches 0; Indels
                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 3
100.0%; Pred. No. 7e+
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 4
100.0%; Pred. No. 7e+
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 7921, Application US/09489039A ; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 8345, Application US/09489039A
; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 247
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                             INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
STRANDEDNESS: single
LELEFAX: 617-720-3500
TELEFAX: 617-720-2441
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8345
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Thea 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.83
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 SSGLLV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 VAQLAQ 208
                                                                                                                                                                                                                                                                                                                                                                                                                                   75 SSGLLV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 VAQLAQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    ; ANTI-SENSE: NO
US-09-100-804-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 150
US-09-489-039A-8345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 149
US-09-489-039A-7921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-489-039A-7921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-489-039A-8345
                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                   à
```

DB 4;

1.8%; Score 6;

Query Match

```
US-09-634-955B-23
                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                   APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NICLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
CORRESPONDENCES: 411
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Meyers, Rachel
APPLICANT: Cook, William James
TITLE OF INVENTION: 32142, 21481, 25964, 21686, NOVEL HUMAN DEHYDROGENASE
TITLE OF INVENTION: MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: 3-beta hydroxysteroid dehydrogenase domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 4; Length 255; 100.0%; Pred. No. 7.2e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
                                                                                                                                                                                               E: WOLF, GREENFIELD & SACKS, P.C. 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELEPHONICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-3441
INFORMATION FOR SEQ ID NO: 141:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/634,955B
CURRENT FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/192,002
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 23
LENGTH: 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-634-955B-23
Sequence 23, Application US/09634955B
Patent No. 6511834
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                          ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                               MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 LVTLIA 207
                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 LVTLIA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                              BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-311-731A-141
                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                 STATE:
```

```
Sequence 4853, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERROCE: GTC99-0391
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4853
LENGTH: 263
                                                                                                                                                                                                                                                        Sequence 25534, Application US/09252991A

Sequence 25534, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANTION: WICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
1.8%; Score 6; DB 4; Length 257;
100.0%; Pred. No. 7.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 4; Length 257; 100.0%; Pred. No. 7.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 4; Length 263;
100.0%; Pred. No. 7.4e+02;
cive 0; Mismatches 0; Indels
             100.0%; Preq. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 23, Application US/09198452A ; Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                    Best Local Similarity 100.0
Matches 6; Conservative
                                                                                              265 KSPNIQ 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 LLVTLI 242
                                                                                                                                             142 KSPNIQ 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 LLVTLI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 QLAQEL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 QLAQEL 65
                                                                                                                                                                                                                                                 US-09-252-991A-25534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-252-991A-25534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-328-352-4853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-328-352-4853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-198-452A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
```

```
US-07-857-224B-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 42, Application US/07857224B
Patent No. 5598784
BARBRAL INFORMATION:
TITLE OF INFORMATION:
TITLE OF INFORMATION:
NUMBER OF SEQUENCE: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: Switzerland
ZIP: (note: this is an international post code) CH-8092
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 4; Length 265; 100.0%; Pred. No. 7.5e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (International) 41 1 632 2830 TELEFAX: (International) 41 1 262 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Saccharomyces cerevisiae
FEATURE: Protein kinase; Table 8 Column 48
FUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS: Hanke, S. K.
AUTHORS: Quinn, A. M.
AUTHORS: Hunter, T.
TITLE: The protein kinase family
JOURNAL: Science
VOLUME: 241
PAGES: 42-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: none TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.(
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 DYEKLL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 DYEKLL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zurich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       none
                                                                                                                                                                                                                                                                                                                       US-09-198-452A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 158
US-07-857-224B-42
                                                                                                                                                                                                                       SEQ ID NO 23
LENGTH: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
```

```
Sequence 31810, Application US/09252991A
Patent No. 6551795
Patent No. 6551795
Patent No. 6551795
Patent No. 6551795
Patent No. 6551795
Patent No. 6551795
Patent No. 6551795
Patent No. MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
PATILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
PATILE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 62, Application US/09101146
Parent No. 6124125
GENERAL INFORMATION:
APPLICANT: Dartmouth College, St. Vincents Institute of
APPLICANT: Medical Research, Kemp et al.
TITLE OF INVENTION: No. 6124125el AMP Activated Protein Kinase
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                       1.8%; Score 6; DB 2; Length 267;
100.0%; Pred. No. 7.58+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.8%; Score 6; DB 4; Length 269; 100.0%; Pred. No. 7.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0 FOR WINDOWS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/101,146
FILING DATE: October 7, 1998
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PN7450
FILING DATE: 8 JAN 1996
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licate
REGISTRATION NUMBER: 32,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Jane Massey Licata, Esq. STREET: 66 E. Main Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31810
Query Match
Best Local Similarity 100..
6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 LVADFL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 LVADFL 107
                                                                                                                        22 KDNLAI 27
                                                                                                                                                                   69 KDNLAI 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marlton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                       US-09-252-991A-31810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-252-991A-31810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 160
US-09-101-146-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
```

```
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-01-08
PRIOR FILING DATE: 1997-08-14
SRIOR FILING DATE: 1997-08-14
SRIOR FILING DATE: 1997-08-14
SRIOR FILING DATE: 1997-08-14
SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NAME ABUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 7494, Application US/09328352; Patent No. 6562958; GENERAL INFORMATION: APPLICANT: APPLICANT: GENERAL INFORMATION: Dreton et al. 1TILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.8%; Score 6; DB 4; Length 274; Best Local Similarity 100.0%; Pred. No. 7.7e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.8%; Score 6; DB 4; Length 279; Best Local Similarity 100.0%; Pred. No. 7.8e+02; Matches 6; Conservative 0; Mismatches 0; Indels
Indels
0
Mismatches
                                                                                                                                                                                                                                           Sequence 3921, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Sequence 4229, Application US/09328352
, Patent No. 6562958
, GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Acinetobacter baumannii
US-09-328-352-4229
  .
0
  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199 ADFLEQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 EDYEKL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 EDYEKL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 ADFLEQ 158
                                                    81 TLIADL 86
                                                                                                         86 TLIADL 91
                                                                                                                                                                                                                         US-09-134-001C-3921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-328-352-4229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-328-352-7494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 165
  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAGENT AND CASE OF THE PROPERTY ON THE REPETING TO STAPHYLOCOCCUS TITLE OF INVENTION:
TITLE OF INVENTION: DOUGETE-Stamm et al TITLE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US 6094,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2004001
CURRENT PELLING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13748
LENGTH: 272
                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 6; DB 4; Length 272; 100.0%; Pred. No. 7.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 4; Length 272; 100.0%; Pred. No. 7.7e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                         Query Match 1.8%; Score 6; DB 3; Length 270; Best Local Similarity 100.0%; Pred. No. 7.6e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 13748, Application US/09489039A; Patent No. 6610836
REFERENCE/DOCKET NUMBER: DC-0050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (856) 810-1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRGANISM: Staphylococcus epidermidis US-09-134-001C-2864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                            TELEFAX: (856) 810-1454
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                               TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 YISKPE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         248 YISKPE 253
                                                                                                                                                                                                                      TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 TLIADL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 TLIADL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-489-039A-13748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-489-039A-13748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-134-001C-2864
                                                                                                                                                                                                                                                 US-09-101-146-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        임
```

δ

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.8%; Score 6; DB 3; Length 283; Best Local Similarity 100.0%; Pred. No. 8e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 6; DB 4; Length 284;
100.0%; Pred. No. 8e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc. STRET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: A Anders Brookes
REGLSTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB369P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 426, Application US/09071035; Patent No. 6448043
                                                             SEQ-4P
                     NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
TELEFAX: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 426:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                              INFORMATION FOR SEQ ID NO: 339: SEQUENCE CHARACTERISTICS:
    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                  LENGTH: 283 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Gil H. C
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 EAVAQL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 EAVAQL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20850
                                                                                                                                                                                                                                                                                                                                US-09-009-913-339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 168
US-09-071-035-426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-071-035-426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

BPPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

SEQ ID NO 3538

LENGTH: 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                    Query Match

1.8%; Score 6; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Ler
5. 7.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZOUNTY SANDABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

COMPUTER: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/009,913

FILING DATE: 21-JAN-1998

CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 339, Application US/09009913
Patent No. 6087485
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
ADDRESSEE: BOZICEVIC & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.8%; Score 6; DB 4
Best Local Similarity 100.0%; Pred. No. 7.9
Matches 6; Conservative 0; Mismatches
              CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 3538, Application US/09540236
; Patent No. 6673910
                                                                                                                                      , ORGANISM: Acinetobacter baumannii
US-09-328-352-7494
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: M. catarrhalis
                                                                                                                                                                                                                                                                                                                            135 DNLAIL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 TDDEQF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 285 Hami
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                   23 DNLAIL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 TODEOF 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAUSA
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 166
US-09-540-236-3538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-540-236-3538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 167
US-09-009-913-339
                                                                            SEQ ID NO 7494
LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
```

à

8

.. 0

```
APPLICANT: The Board of Regents of the University of Oklahoma
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASS, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASS, AND METHODS OF USE THEREOF
FILE REFERENCE: 5820.504
CURRENT APPLICATION NUMBER: US/09/150,133B
CURRENT FILING DATE: 1998-09-09
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Wordperfect 5.1 (saved in ASCII format)
SEQ ID NO 13
LENGTH: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: The Board of Regents of the University of Oklahoma
APPLICANT: The Board of Regents of the University of Oklahoma
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASS, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASS, AND METHODS OF USE THEREOF
TITLE REPERENCE: 5820.4855
CURRENT APPLICATION NUMBER: US/09/150,141B
CURRENT FILING DATE: 1998-09-09
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: BNTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032 CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 4; Length 294; 100.0%; Pred. No. 8.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
1.8%; Score 6; DB 3; Les
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 45
SOFTWARE: Wordperfect 5.1 (saved in ASCII format)
SEQ ID NO 13
LENGTH: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: estrogen sulfotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: estrogen sulfotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 13, Application US/09150133B; Patent No. 6060295; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 13, Application US/09150141B; Patent No. 6071732
                                                                                                                                                                                                                                                                                                                   ORGANISM: Enterococcus faecalis
                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 4481
LENGTH: 294
                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 KLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 KLIEFL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 LVTLIA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 LVTLIA 33
                                                                                                                                                                                                                                                                                                                                                  US-09-134-000C-4481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 172
US-09-150-133-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 173
US-09-150-141-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-150-133-13
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ठ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6438, Application US/09543681A
Patent No. 6605709
GENERAL INCORMATION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709:1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                  APPLICANT: Dean, Frank
APPLICANT: Dean, Frank
APPLICANT: O'Donnell, Michael E.
TITLE OF INVENTION: DNA MOLECULES ENCODING SINGLE STRAND GAP RESPONSE
TITLE OF INVENTION: PROTEINS INVOLVED IN ACTIVATION OF A DNA REPAIR/CELL
TITLE OF INVENTION: CYCLE CHECKPOINT PATHWAY
FILE REPRENCE: 22221/1011
FILE REPRENCE: 22221/1011
CURRENT APPLICATION NUMBER: 60/082,020
PRIOR APPLICATION NUMBER: 60/082,020
PRIOR PILING DATE: 1998-04-16
PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 5-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.8%; Score 6; DB 4; Length 287;
100.0%; Pred. No. 8.1e+02;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

1.8%; Score 6; DB 4; Length 287;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-134-000C-4481
; Sequence 4481, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
                                                                                                                                                                                                           ; Sequence 25, Application US/09292858B; Patent No. 6455681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 EAPQIA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 EAPQIA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 TIFEDY 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 TIFEDY 62
                        79 LUTLIA 84
                                                                            18 LVTLIA 23
                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-543-681A-6438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-543-681A-6438
                                                                                                                                                       RESULT 169
US-09-292-858B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-292-858B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

Gaps

.; 0

Indels

0;

```
100.0%; Pred. No. 8.3e+02; tive 0; Mismatches 0;
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus
                                                                       300 KLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 KLIEFL 305
                                                                                                              206 KLIEFL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 KLIEFL 211
                                                                                                                                                                                                                US-09-374-492-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-785-343-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                       ਨੇ
                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: The Board of Regents of the University of Oklahoma
TITLE OF INVENTION: TYROSYLPROETIN SULFOTRANSFERASES AND METHODS OF USE THEREOF
FILE REFERENCE: 5820.546
CURRENT PRINCATION NUMBER: US/09/374,493
CURRENT FILING DATE: 1999-08-13
EARLIER APPLICATION NUMBER: 09/150,133
EARLIER FILING DATE: 1998-09-09
EARLIER PILING DATE: 1998-01-29
EARLIER PILING DATE: 1998-01-29
EARLIER PILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Wordperfect 8.0 (saved in ASCII format)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: The Board of Regents of the University of Oklahoma

ITLE OF INVENTION: TYROSYLPROETIN SULFOTRANSFERASES AND METHODS OF USE THEREOF

FILE REPERENCE: 5820.347

CURRENT APPLICATION NUMBER: US/09/374,824

CURRENT APPLICATION NUMBER: 09/150,133

EARLIER APPLICATION NUMBER: 09/150,133

EARLIER FILING DATE: 1998-09-09

EARLIER FILING DATE: 1998-01-29

EARLIER FILING DATE: 1998-01-29

EARLIER RILING DATE: 1999-07-23

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Wordperfect 8.0 (saved in ASCII format)
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.8%; Score 6; DB 3; Length 295;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                              1.8%; Score 6; DB 3; Length 295;
100.0%; Pred. No. 8.3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: estrogen sulfotransferase US-09-374-493-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: estrogen sulfotransferase US-09-374-824-13
                                                                                                                                                                                                                                                       RESULT 174
US-09-374-493-13
Sequence 13, Application US/09374493
Patent No. 6204016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 13, Application US/09374824; Patent No. 6207414
                                                                  Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mus musculus
                                                                                                                                         300 KLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 KLIEFL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 KLIEFL 211
                                                                                                                                                                                     206 KLIEFL 211
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 175
US-09-374-824-13
  US-09-150-141-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 13
LENGTH: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 13
LENGTH: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                     Dp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dp
```

```
Sequence 13, Application US/09374492
; Sequence 13, Application US/09374492
; Patent No. 6207432
; GENREAL INFORMATION:
; APPLICANT: The Board of Regents of the University of Oklahoma
; TITLE OF INVENTION: TYROSYLPROETIN SULFOTRANSFERASES AND METHODS OF USE THEREOF
; FILE REFERENCE: 580.545
; CURRENT FILING DATE: 1999-08-13
; EARLIER APPLICATION NUMBER: 09/150,141
; EARLIER PILING DATE: 1998-09-09 99
; EARLIER PILING DATE: 1998-09-09; SARLIER PILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Wordperfect 8.0 (saved in ASCII format)
; SEQ ID NO 13
; LENGTH: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INC. 80.2315.

GENERAL INC. 80.2315.

APPLICANT: The Board of Regents of the University of Oklahoma
APPLICANT: The Board of Regents of the University of Oklahoma
TITLE OF INVENTION: TYROSYLPROFTIN SULFOTRANSFERASES AND METHODS OF USE THEREOF
FILE REFERENCE: 58.2 0.03
CURRENT APPLICATION NUMBER: US/09/785,343
CURRENT FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/012,994
PRIOR APPLICATION NUMBER: FOT/US99/16750
PRIOR APPLICATION NUMBER: PCT/US99/16750
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Wordperfect 8.0 (saved in ASCII format)
LENGTH: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 3; Length 295;
100.0%; Pred. No. 8.3e+02;
trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.8%; Score 6; DB 4; Length 295; Best Local Similarity 100.0%; Pred. No. 8.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: estrogen sulfotransferase US-09-785-343-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: estrogen sulfotransferase US-09-374-492-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 13, Application US/09785343
; Patent No. 6605455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0 Matches 6; Conservative
```

```
US-09-216-294-1
        LENGTH:
                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 3737
LENGTH: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
1.8%; Score 6; DB 4; Length 295;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08923856

Patent No. 5928894

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Tang, Tom
APPLICANT: Shah, Purvi
ITILE OF INVENTION: HUMAN ACTVA-ORF4-LIKE PROTEIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS;
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,856
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF-0380 US TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                          Sequence 3737, Application US/09134000C
Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 31/2 .
300 KLIEFL 305
                                     206 KLIEFL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 TLIADL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 TLIADL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                  RESULT 178
US-09-134-000C-3737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-134-000C-3737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-923-856-1
ð
                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
ö
                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 3; Length 299;
100.0%; Pred. No. 8.4e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                          Query Match 1.8%; Score 6; DB 2; Length 299; Best Local Similarity 100.0%; Pred. No. 8.4e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN ACTVA-ORF4-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09216294

Patent No. 608073

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Tang, Tom
APPLICANT: Corley, Neil C.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
ITLE OF INVENTION: HUMAN ACTVA-ORF4-LIKE F.
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STRRET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SUFTWARE: FastSBO for Windows Version 2.0
SUFRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILLING DALES
ATTORNEY, GAGENT INFORMATION:
NAME: Billings, Lucy J.
REGLETRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0380 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/923,856
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
299 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 299 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100,(
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: PANCNOTO1
CLONE: 223909
                                                                                              PANCNOTO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                         211 EDYEKL 216
                                                                                                                                                                                                                                                                                             244 EDYEKL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 EDYEKL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 EDYEKL 249
                                                                             MEDIAL
LIBRARY: PANAL
223909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94304
                                                                                                                                    US-08-923-856-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
```

```
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-4P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-237-3231
                                                                                                                                                      UMBER: US/09/009,913
21-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09976594; Patent No. 6673549; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 300 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650-327-3231
                                                                                                                                                                               FILING DATE: 21-JAN-1
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-09-009-913-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 EAVAQL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 NIQFEA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 NIQFEA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 EAVAQL 69
USA
                   94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 7
LENGTH: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-976-594-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-976-594-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                      APPLICANT: Lynn A Dougette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.8%; Score 6; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                      CURRENT ASYSTEM: «Unknown»
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORREY/AGENT INFORMATION:
NAME: ALINEILO, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09009913
Patent No. 6087485
GENERAL INFORMATION:
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDE ADDRESS:
ADDRESSEE: BOALCOVIC & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...299
SEQUENCE DESCRIPTION: SEQ ID NO: 4050:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecium
                       ; Sequence 4050, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           ZIP: 02354
COMPUTER READABLE PORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 299 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 4050:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                    CITY: Waltham
                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 KVLVAD 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 KVLVAD 73
        US-09-107-532A-4050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-107-532A-4050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-009-913-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

```
APPLICANT: Furness, Michael
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA.0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT APPLICATION NUMBER: 60/240,409
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.8%; Score 6; DB 3; Length 300;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 4; Length 300; 100.0%; Pred. No. 8.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 3170236CD1
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SUSTWARE: FASTERO for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
```

```
patent No. 651791. Application US/09252991A

Patent No. 651795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEG ID NO 27921

LENGTH: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29243, Application US/09252991A

Sequence 29243, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc Of Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFRENCE: 107196.13

CURRENT APPLICATION NUMBER: US 60/094,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 4; Length 308;
100.0%; Pred. No. 8.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.8%; Score 6; DB 4; Length 308; Best Local Similarity 100.0%; Pred. No. 8.6e+02; Matches 6; Conservative 0; Mismatches 0; Indele
EARLIER APPLICATION NUMBER: 60/089,508
EARLIER FILING DATE: 1998-06-16
EARLIER FILING DATE: 1998-06-16
EARLIER FILING DATE: 1998-06-16
EARLIER FILING DATE: 1998-06-16
EARLIER FILING DATE: 1998-06-16
EARLIER FILING DATE: 1998-06-22
EARLIER FILING DATE: 1998-06-22
EARLIER FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
SOFTWARE: PALCATION VOMBER: 60/090,113
EARLIER FILING DATE: 1998-06-22
SOFTWARE: PALCATION NUMBER: 60/090,113
EARLIER FILING DATE: 1998-06-22
SOFTWARE: PALCATION VOMBER: 60/090,113
EARLIER FILING DATE: 1998-06-22
SOFTWARE: PALCATION VOMBER: 60/090,113
SEQ ID NO 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-325-437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 LRRQIG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 LRRQIG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 ĞLLVTL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 GLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-252-991A-29243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-252-991A-27921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-27921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4994, Application US/09328352

Patent No. 6562958

Patent No. 6562958

Patent No. 6562958

Patent No. 6562958

Patent No. 6562958

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4994

LENGTH: 307
                                                                                                                                        GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27266
LENGTH: 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.8%; Score 6; DB 4; Length 307; Best Local Similarity 100.0%; Pred. No. 8.6e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 6; DB 4; Length 303;
Pred. No. 8.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: PZ029P1
CURRENT APPLICATION NUMBER: US/09/461,325A
CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: PCT/US99/13418
EARLIER APPLICATION NUMBER: 60/089,507
EARLIER APPLICATION NUMBER: 60/089,507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.8%; Score 6; DB 4 ilarity 100.0%; Pred. No. 9.5 Conservative 0; Mismatches
                                                                                   Sequence 27266, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 437, Application US/09461325A
Patent No. 6475753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
.hag 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 YEKLLQ 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 YEKLLÓ 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 LLVTLI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 LLVTLI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                              US-09-252-991A-27266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-27266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-328-352-4994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 186
US-09-461-325-437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               임
```

```
TURRENT APPLICATION NUMBER: US/10/012,542

CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/461,325
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/461,325
PRIOR FILING DATE: BARLIER FILING DATE: 1999-12-14
PRIOR FILING DATE: BARLIER FILING DATE: 1998-06-16
PRIOR PLILING DATE: BARLIER FILING DATE: 1998-06-16
PRIOR PLILING DATE: BARLIER FILING DATE: 1998-06-16
PRIOR PLILING DATE: BARLIER FILING DATE: 1998-06-16
PRIOR PLILING DATE: BARLIER FILING DATE: 1998-06-16
PRIOR PLILING DATE: BARLIER FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 60/090,112
PRIOR PLILING DATE: BARLIER FILING DATE: 1998-06-16
PRIOR PLILING DATE: BARLIER FILING DATE: 1998-06-16
PRIOR PLILING DATE: BARLIER FILING DATE: 1998-06-16
PRIOR PLILING DATE: BARLIER FILING DATE: 1998-06-16
PRIOR PLILING DATE: BARLIER FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
SOFTWARE: PATENTIER FILING DATE: 1998-06-22
SOFTWARE: PATENTIER FILING DATE: 1998-06-22
SOFTWARE: PATENTIER FILING DATE: 1998-06-22
PRIOR FILING DATE: BARLIER FILING DATE: 1998-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 4; Length 308; 100.0%; Pred. No. 8.6e+02; tive 0; Mismatches 0; Indels
                               GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: PZ02991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 37
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
ses 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 GLLVTL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 LSSFOK 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 LSSFOK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 GLLVTL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Vitis sp
US-09-655-908-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-252-991A-22411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-012-542-437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 192
US-09-655-908-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Mic
SEQ ID NO 12
LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7093, Application US/09328352

Patent No. 5652958

GENERAL INCORMATION:
TOTALE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REPRENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEO ID NO 7093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 190
US-09-128-352-7158
Sequence 7159, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GENTY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPREDENCE: GTC99-03PA
FILE REPREDENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 4; Length 308; 100.0%; Pred. No. 8.6e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                            1.8%; Score 6; DB 4; Length 308; 100.0%; Pred. No. 8.6e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 4; Length 308; 100.0%; Pred. No. 8.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7158
LENGTH: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 437, Application US/10012542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Acinetobacter baumannii
US-09-328-352-7158
                                                                                                  ORGANISM: Pseudomonas aeruginosa
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.(
Matches 6; Conservative
                                                                                                                                                                                                      Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 SLKLLG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 SLKLLG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 LYSSGL 155
                                                                                                                                                                                                                                                                                   75 SSGLLV 80
                                                                                                                                                                                                                                                                                                                      22 SSGLLV 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 LYSSGL 78
                                                                                                                         US-09-252-991A-29243
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 189
US-09-328-352-7093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-328-352-7093
                          SEQ ID NO 29243
LENGTH: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 191
US-10-012-542-437
                                                                               TYPE: PRT
                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \stackrel{>}{\circ}
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 4; Length 309;
100.0%; Pred. No. 8.6e+02;
tive 0; Mismatches 0; Indels
Sequence 12, Application US/09655908
Patent No. 6645747
Patent No. 6645747
Patent No. 645747
TYLE APPLICANT: Hallahan, David L.
TITLE OF INVENTION: cise-Premyltransferases from Plants
FILE REPERANCE: BC1019 US NA
CURRENT APPLICATION NUMBER: US/09/655,908
PRIOR APPLICATION NUMBER: 60/155,046
PRIOR FILING DATE: 1999-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 22411, Application US/09252991A ; Patent No. 6551795 ; GENERAL INFORMATION; ; APPLICANT: Marc J. Rubenfield et al.
```

```
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT APPLICATION NUMBER: US/09/252,991A PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR PILING DATE: 1998-02-18 PRIOR PILING DATE: 1998-02-18 PRIOR PILING DATE: 1998-07-17 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER: US EQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8342, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
NUCLRIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION:
PILE REPREDICATION:
CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT PILING DATE: 1090-01-27

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Perrino, Fred W
TITLE OF INVENTION: Mammalian Genes Encoding 3'-5' Exonuclease
FILE REPERENCE: wak200/48001/4-018
CURRENT APPLICATION NUMBER: US/09/634,137
CURRENT FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: US 60/148,018
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 314
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 1.8%; Score 6; DB 4; Length 313; Best Local Similarity 100.0%; Pred. No. 8.7e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 4; Length 314;
100.0%; Pred. No. 8.7e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 30, Application US/09634137
; Patent No. 6632665
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100...
6. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CRGANISM: Mus musculus
US-09-634-137-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 IADLQL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 TEAVAQ 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 IADLOL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 TEAVAQ 68
                                                                                                                                                                                                                                                                                                                                                                             US-09-252-991A-22411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-489-039A-8342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-634-137-30
                                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                            APPLICANT: Rubin, Gerry M.
APPLICANT: Therrien, Marc
APPLICANT: Therrien, Marc
APPLICANT: Chang, Henry C.
APPLICANT: Karing, Henry C.
APPLICANT: Wassarman, David A.
TITLE OF INVENTION: A No. 5700675e1 Protein Kinase Required for Ras
TITLE OF INVENTION: Signal Transduction
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 268 BUSH STREET, SUITE 3200
                                                 Gaps
                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.8%; Score 6; DB 1; Length 315;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
1.8%; Score 6; DB 4; Length 314;
100.0%; Pred. No. 8.7e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/571,758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: B96-010
TELECOMONIOTATION INFORMATION.
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 12:
SEGUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08909984A
Patent No. 5747275
GENERAL INFORMATION:
APPLICANT: Rubin, Gerry M.
APPLICANT: Therrien, Marc
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Felix D.
                                                                                                                                                                                                                                               ; Sequence 12, Application US/08571758; Patent No. 5700675; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,6
                       Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                   102 DNLAIL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                         23 DNLAIL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 KDNLAI 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 KDNLAI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 197
US-08-909-984A-12
                                                                                                                                                                                                                          US-08-571-758-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-571-758-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
    Query Match
                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Therrien, Marc
APPLICANT: Therrien, Marc
APPLICANT: Therrien, Marc
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Felix D.
APPLICANT: Wassarman, David A.
TITLE OF INVENTION: A No. 5747288el Protein Kinase Required for Ras
TITLE OF INVENTION: A Signal Transduction
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
APPLICANT: Wassarman, David A.
TITLE OF INVENTION: A No. 5747275el Protein Kinase Required for Ras
TITLE OF INVENTION: Signal Transduction
UNDER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 1; Length 315; 100.0%; Pred. No. 8.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                        ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPITER: IP C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,984A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,983
FILING DATE: 12-JUN-1997
                                                                                                            ADDRESSEE: SIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Prec. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET VIMBER: B96-010
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4341
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08909983; Patent No. 5747288; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 315 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 KDNLAI 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 KDNLAI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-909-984A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 198
US-08-909-983-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
```

```
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.8%; Score 6; DB 1; Length 315; Best Local Similarity 100.0%; Pred. No. 8.8e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROW ISO9660

COMPUTER: PC
COMPATING SYSTEM: «UNKNOWN»
SOSTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Atiniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 5596, Application US/09107532A; Patent No. 6583275; GENERAL INFORMATION:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/571,758
                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 317 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 5596:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                         not relevant
                                                                                                                                                                                                                                                                                                             315 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: not relevant MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 KDNLAI 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 KDNLAI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-107-532A-5596
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-909-983-12
                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

ORIGINAL SOURCE:

```
Sequence 18724, Application US/09252991A
Parent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: MUBBER: US/09/252,991A
CURRENT APPLICATION WUBBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
SEQ ID NO 18724
LENGTH: 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cone, Roger D
APPLICANT: Roselli-Rehfuss, Linda
APPLICANT: Roselli-Rehfuss, Linda
APPLICANT: Robbins, Linda
APPLICANT: Robbins, Linda
TITLE OF INVENTION: Mammalian Melanocyte Stimulating Hormone
TITLE OF INVENTION: Receptors and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.8%; Score 6; DB 4; Length 322; Best Local Similarity 100.0%; Pred. No. 8.9e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                               1.8%; Score 6; DB 4; Length 322;
100.0%; Pred. No. 8.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,812A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 4, Application US/08044812A; Patent No. 5837521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                               Query Match
Best Local Similarity 100.1
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESSEE: Allegrett
                             ORGANISM: Homosapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 KVLVAD 200
                                                                                                                                                                                                                                                                                  207 SSGLLV 212
                                                                                                                                                                                                                           75 SSGLLV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 KVLVAD 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               US-09-252-991A-18724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-252-991A-18724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-044-812A-4
                                                          US-09-848-294-4
  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANTON: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENITION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENITION NUMBER: US 09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TONKS, Nicholas K.

TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el

TITLE OF INVENTION: Protein Tyrosine Phosphotase Which Localizes to Focal
TITLE OF INVENTION: Adhesions and Uses Therefor
TITLE OF INVENTION: Adhesions and Uses Therefor
TITLE OF INVENTION: Adhesions and Uses Therefor
TITLE OF INVENTION: Adhesions and Uses Therefor
GURRENT APPLICATION NUMBER: 08/09/84,294
CURRENT FILING DATE: 1999-01-5-03
PRIOR APPLICATION NUMBER: 08/107,420
PRIOR APPLICATION NUMBER: 08/107,420
PRIOR APPLICATION NUMBER: 08/107,420
PRIOR FILING DATE: 1991-03-01
PRIOR PELING DATE: 1991-03-01
PRIOR FILING DATE: 1991-03-01
PRIOR FILING DATE: 1991-03-01
PRIOR FILING DATE: 1990-03-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE FASTESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                        ..
o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                           Query Match

1.8%; Score 6; DB 4; Length 317;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 320;
5. 8.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
1.8%; Score 6; DB 4
Best Local Similarity 100.0%; Pred. No. 8.9
Matches 6; Conservative 0; Mismatches
                                   NAME/KEY: misc_feature;
; LOCATION: (B) LOCATION 1...317
; SEQUENCE DESCRIPTION: SEQ ID NO: 5596:
US-09-107-532A-5596
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 4204, Application US/09134001C; Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-848-294-4; Sequence 4, Application US/09848294; Patent No. 6479640
                                                                                                                                                                                                                                                                                                          119 ISAHPH 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 ISAHPH 124
                                                                                                                                                                                                                                                                                                                                                              41 ISAHPH 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 ISAHPH 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-134-001C-4204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 4
LENGTH: 322
                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cone, Roger D
APPLICANT: Roselli-Rehfuss, Linda
APPLICANT: Mountjoy, Kathleen G
APPLICANT: Robbins, Linda S
TITLE OF INVENTION: Mammalian Melanocyte Stimulating Hormone
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 323;
0. 9e+02;
cches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,637
FILING DATE: 07-JUN-1995
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US/08/044,812
FILING DATE: 04-APR-1993
CLASSIFICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLICATION: ASSISTANCE APPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18: Allegretti & Witcoff, Ltd.
10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.8%; Score 6; DB 2
Best Local Similarity 100.0%; Pred. No. 9e+
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: ATTORNEY AGENT INFORMATION:
NAME: No. 5994087nan, Kevin E
REGISTRATION NUMBER: 35,303
REGISTRATION NUMBER: 92,835
                                                                                        92,835
No. 5837521nan, Kevin E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08475637 Patent No. 5994087
                                 REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1000
TELEFAX: 910-221-5317
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 92,8:
TELECOMOUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELERA: 312-715-1234
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                 : 323 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 323 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-044-812A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 KEILCG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 KEILCG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Cone, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-475-637-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-475-637-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
```

1.8%; Score 6; DB 2; Length 323;

Query Match

. 0

```
APPLICANT: Cone, Roger D
APPLICANT: Cone, Roger D
APPLICANT: Boston, Bruce A
APPLICANT: Boston, Bruce A
APPLICANT: Boston, Bruce A
APPLICANT: Government of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of 
                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                Gaps
                                                ó
100.0%; Pred. No. 9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McDonnell Boehnen Hulbert & Berghoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 3;
100.0%; Pred. No. 9e+02
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,281A
FILING DATE: 04-SEP-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/08706281A Patent No. 6100048 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09191359; Patent No. 6261838
GENERAL INFORMATION:
APPLICANT: Cone, Roger D; APPLICANT: Rosell-Refiss, Linda APPLICANT: Robbins, Linda S; APPLICANT: Robbins, Linda S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 300 South Wacker Drive
Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6100048nan, Kevin E
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
Best Local Similarity 100. Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 323 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                      311 KEILCG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 KEILCG 316
                                                                                                                 50 KEILCG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 KEILCG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                            US-08-706-281A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-706-281A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: II COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-191-359-4
                                                                                                                                                                                                                                                                                                        RESULT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 206
                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

```
Boston, Bruce A
Kesterton, Robert A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/09353099; Patent No. 6476187
GENERAL INFORMATION:
          FILING DATE: 12-Jun-1998
                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 323 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cone, Roger D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lu, Dongsi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fan, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 300 Sc
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 KEILCG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 KEILCG 55
                                                                                                                                                                                                                                                                                                                                               US-09-097-231-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 208
US-09-353-099-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/09097231
Patent No. 6278038
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
Low, Malcolm J
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
  Mammalian Melanocyte Stimulating Hormone
Receptors and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 3; Length 323;
100.0%; Pred. No. 9e+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Mononell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1,0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                 3: Allegretti & Witcoff, Ltd.
10 South Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,231
                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/475,637
FILING DATE: 07-UN-1995
APPLICATION NUMBER: US/08/044,812
FILING DATE: 04-ARR-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6.561838nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/191,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / TOPOLOGY: linear
// MOLECULE TYPE: protein
US-09-191-359-4
                                                                                                                                                                           ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegrett
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                  STREET: 10 South
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 KEILCG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 KEILCG 55
                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 207
US-09-097-231-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
```

```
Chen, Wenbiao
TITLE OF INVENTION: Methods and Reagents for Discovering and
Using Mammalian Melanocortin Receptor Agonists and Antagon
To Modulate Feeding Behavior in Animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 1.8%; Score 6; DB 3; L
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 6; Conservative 0; Mismatches 0
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6278038nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886-C
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-913-0001
TELEFAX: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,099
FILING DATE: 14-Sep-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 96,886
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/706,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 04-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: No. 6476187nan, Kevin B
REGISTRATION NUMBER: 35,303
```

g

à

```
Sequence 2, Application US/09709066
Patent No. 6633123
GENERAL INFORMATION
APPLICANT: Van der Ploeg, Leonardus H.T.
APPLICANT: Chen, Howard Y.
APPLICANT: Chen, Airu S.
TITLE OF INVENTION: NON-HUMAN TECEPTOR DEFICIENT CELLS
TITLE OF INVENTION: COMPOUNDS WHICH REGULATE BODY WEIGHT
FILE REFERENCE: 20561Y
FILE REFERENCE: 20561Y
CURRENT APPLICATION UNDEER: US/09/709,066
CURRENT APPLICATION UNDEER: 120/09/109,066
CURRENT SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INCORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Monath, Roadoh
APPLICANT: Monath, Roadoh
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LOME CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.475c1
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT APPLICATION NUMBER: US/09/370,838
EARLIER FILING DATE: 1999-08-09
EARLIER FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 4; Length 324;
100.0%; Pred. No. 9e+02;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.8%; Score 6; DB 4; Length 323; Best Local Similarity 100.0%; Pred. No. 9e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 10843, Application US/09489039A
; Patent No. 6610836
; GRNEMATION:
; APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-05-370-838-45; Sequence 45, Application US/09370838; Patent No. 6444425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 KEILCG 316
       120 SLKLLG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 KEILCG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 LYSSGL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 LYSSGL 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 213
US-09-489-039A-10843
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER SOFTWARE: FABLUSEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-370-838-45
                                                                                                   US-09-709-066-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-709-066-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 212
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26419, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICANT: MARC 10196.136
TITLE OF INVENTION:
APPLICANT: MARC 110196.136
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICANTON MUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26419
LENGTH: 323
                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-134-000C-5535

Sequence 5535, Application US/09134000C

Sequence 5535, Application US/09134000C

Sequence 5535, Application US/09134000C

GENERAL INPORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT RAPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1999-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.8%; Score 6; DB 4; Length 323;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
1.8%; Score 6; DB 4; Length 323;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                             Query Match 1.8%; Score 6; DB 4; Length 323; Best Local Similarity 100.0%; Pred. No. 9e+02; Matches 6; Conservative 0; Mismatches 0; Indels
             TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-353-099-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecalis
TYPE: amino acid
                                                                                                                                                                                                                                                                                           311 KEILCG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 KVLVAD 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 KVLVAD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 SLKLLG 233
                                                                                                                                                                                                                                                   50 KEILCG 55
                                                                                                                                                                                                                                                                                                                                                                          RESULT 209
US-09-252-991A-26419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-252-991A-26419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-134-000C-5535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 5535
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
```

g

```
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 216
                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 10843

LENGTH: 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREDMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: 2709, 2004001
CURRENT PELLON NUMBER: US/09/489, 039A
PRIOR PILLING DATE: 1900-01-27
PRIOR PELLOATION NUMBER: US 60/117,747
PRIOR PILLING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TOHDA, Hideki
APPLICANT: TOHDA, Hideki
APPLICANT: TOHDA, Hideki
APPLICANT: TOHDA, WAS
APPLICANT: HAMA, YUKO
APPLICANT: NUMAGAI, Hiromicho
TITLE OF INVENTION: USABLE IN SCHIZOSACCHAROMYCES POMBE, EXPRESSION VECTORS
TITLE OF INVENTION: HAVING THE SAME, AND USE THEREOF
TITLE OF INVENTION: HAVING THE SAME, AND USE THEREOF
TITLE OF INVENTION: HAVING THE SAME, AND USE THEREOF
TITLE OF INVENTION: HAVING THE SAME, AND USE THEREOF
THE REFERENCE: 0059-1142-0PCT
CURRENT APPLICATION NUMBER: US/09/331,581
EARLIER APPLICATION NUMBER: DCT/JP98/04929
EARLIER PILING DATE: 1998-10-31
EARLIER PILING DATE: 1998-10-31
EARLIER PILING DATE: 1998-10-31
EARLIER PILING DATE: 1997-10-31
NUMBER: OF SEQ ID NOS: 24
SOFTWARE: PRECENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                   1.8%; Score 6; DB 4; Length 331;
100.0%; Pred. No. 9.2e+02;
live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.8%; Score 6; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Sequence 9330, Application US/09489039A
, Patent No. 6610836
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Schwanniomyces occidentalis
US-09-331-581-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 23, Application US/09331581; Patent No. 6130070
                                                                                                                                                                                                                                                                                                                               ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 HEPLAK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 HEPLAK 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 SNQFRD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 SNOFRD 169
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        US-09-489-039A-10843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-489-039A-9330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-331-581-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 23
LENGTH: 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
Sequence 5285, Application US/09543681A
Patent No. 6605709
Patent No. 6605709
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-1002-001
CURRENT APPLICATION NUMBER: US/09/543, 681A
CURRENT APPLICATION NUMBER: US 60/128, 706
PRICR PRICR APPLICATION NUMBER: US 60/128, 706
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 5285
ILENGTH: 334
                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCCOCCUS PAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 5207
LENGTH: 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                 1.8%; Score 6; DB 4; Length 332; 100.0%; Pred. No. 9.2e+02; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.8%; Score 6; DB 4; Length 333; 100.0%; Pred. No. 9.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 4; Length 334; 100.0%; Pred. No. 9.2e+02; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                         Sequence 5207, Application US/09134000C Patent No. 6617156
LENGTH: 332
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Enterococcus faecalis
                                                                                              Query Match
Best Local Similarity 100..
These 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 6; Conserve
                                                                                                                                                                                                                  290 IVEILL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 GELILD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 ISAHPH 124
                                                                                                                                                                                                                                                            16 IVEILL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 ISAHPH 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 GELILD 43
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                     US-09-489-039A-9330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 217
US-09-543-681A-5285
                                                                                                                                                                                                                                                                                                                                                          US-09-134-000C-5207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-134-000C-5207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-543-681A-5285
```

```
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/08326119A ; Patent No. 6018021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: LIVNAT, SHMUEL
REGISTRATION NUMBER: 33,949
REFERENCE DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 822-0168
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-09-057-762-2
                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                 257 LMMNLL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 KLLGEL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 KLLGEL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                      18 LMMNLL 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.C.
USA
                                                                                              US-09-107-532A-6417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-326-119A-2
                                                                                                                                                                                                                                                                                                                                  US-09-057-762-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                RESULT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 221
                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6417, Application US/09107532A
Sequence 6417, Application US/09107532A
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FABCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                  Sequence 6, Application US/09674826B
Patent No. 6638735
GENERAL INFORMATION
APPLICANT: Corporation
APPLICANT: Korea Institute of Science and Technology
TITLE OF INVENTION: Plasmid for gene expression in Pichia ciferri and
TITLE OF INVENTION: transformation method using the same
FILE REFERENCE: PCT-981031
CURRENT FILING DATE: 2000-11-07
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 6: SEQ ID NOS: 18
LENGTH: 334
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
1.8%; Score 6; DB 4; Length 334;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-7un-1998
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
ATTORNEY/AGENT INFORMATION:
NAME: ATAIGEIO, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 336 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 6417: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Pichia ciferrii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 PLAKII 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 PLAKII 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 219
US-09-107-532A-6417
            US-09-674-826B-6
                                                                                                                                                                                                                                                                                                                                               US-09-674-826B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
Gaps
                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09057762
| Patent No. 5879909
| GENERAL INFORMATION:
| APPLICANT: FREL, ANDRAS
| TITLE OF INVENTION: HUMAN TRANSALDOLASE: AN AUTOANTIGEN WITH
| TITLE OF INVENTION: A FUNCTION IN METABOLISM
| NUMBER OF SEQUENCES: 24
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: WASHISON & FOERSTER
| STREET: WASHINGTON
| CITY: WASHINGTON | CONTINUED NO. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                    Query Match

1.8%; Score 6; DB 4; Length 336;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 6; DB 2; Length 337;
100.0%; Pred, No. 9.36+02;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/057,762
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...336
SEQUENCE DESCRIPTION: SEQ ID NO: 6417:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280932000100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/326,119
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20006-1812
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
```

GENERAL INFORMATION:

```
GENERAL INFORMATION:
APPLICANT: Freed, Bllen
APPLICANT: Ruggieri, Rosamaria
TITLE OF INVENTION: Interaction of raf-1 and 14-3-3 Proteins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.8%; Score 6; DB 4; Length 338;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
FILING DATE: 14-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: 60/143,401
PRIOR PILING DATE: 1999-07-12
PRIOR FILING DATE: 1999-07-12
PRIOR PLING DATE: 1999-07-12
PRIOR PLING DATE: 1999-07-12
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR APPLICATION NUMBER: 60/146,650
PRIOR PLING DATE: 1999-07-30
PRIOR PLING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR PLING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/172,959
PRIOR FILING DATE: 1999-12-21
PRIOR PLING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
                                                                                                                                                                                                                                                                                                     APPLICANT: Lee, Jian Ming
APPLICANT: Sakai, Halime
APPLICANT: Weng, Zude
APPLICANT: Caimi, Perry G
APPLICANT: Anderson, Shawn
TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
CITY: Palo Alto
STATE: CA
COUNTRY: US"
ZIP
                                                                       Sequence 150, Application US/09614912
Patent No. 6677502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 5, Application US/08276151; Patent No. 5597719
                                                                                                                                                           Allen, Steve
Rafalski, Antoni
Orozco, Buddy
Miao, Gou-Hau
Famodu, Omolayo O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 DNLAIL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 DNLAIL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                         US-09-614-912-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-614-912-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 150
LENGTH: 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 224
US-08-276-151-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-198-452A-642

Sequence 642, Application US/09198452A

Patent No. 655294

GENERAL INFORMATION:

APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: and treatment of infection

TITLE OF INVENTION: and treatment of infection

FILE REPERBENCE: 9710-003-999

CURRENT APPLICATION WUMBER: US/09/198,452A

CURRENT APPLICATION WUMBER: 1998-11-24
APPLICANT: PERL, ANDRAS
TITLE OF INVENTION: HUMAN TRANSALDOLASE: AN AUTOANTIGEN WITH
TITLE OF INVENTION: A FUNCTION IN METABOLISM
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORRSTER
STREET: 2000 Pennsylvania Avenue N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.8%; Score 6; DB 4; Length 338; Best Local Similarity 100.0%; Pred. No. 9.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
COMPATING SYSTEM:
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
GURSTHENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,119A
FILING DATE: US/08/326,119A
FILING DATE: US/08/326,119A
ATTORNEY/AGENT INFORMATION:
NAME: LIVNAT, SHAUEL
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 280932000100
TELESTANCE/LOCKET NUMBER: 280932000100
TELESTANCE/LOCKET NUMBER: 280932000100
TELESTANCE/LOCKET NUMBER: 280932000100
TELESTANCE/LOCKET NUMBER: 280932000100
TELESTANCE/LOCKET NUMBER: 280932000100
TELESTANCE/LOCKET NUMBER: 280932000100
TELESTANCE/LOCKET NUMBER: 280932000100
TELESTANCE/LOCKET NUMBER: 280932000100
TELESTANCE/LOCKET NUMBER: 280932000100
TELESTANCE/LOCKET NUMBER: 280932000100
TELESTANCE/LOCKET NUMBER: 280932000100
TELESTANCE/LOCKET NUMBER: 280932000100
TELESTANCE/LOCKET NUMBER: 280932000100
TELESTANCE/LOCKET NUMBER: 280932000100
TELESTANCE/LOCKET NUMBER: 33,949
REPERBORICE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 6; DB 3; Ler
Pred. No. 9.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
1.8%; Score 6; DB 3
Best Local Similarity 100.0%; Pred. No. 9.3
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 KLLGEL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 KLLGEL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 YLIKQI 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 YLIKÓI 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-198-452A-642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-326-119A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 642
LENGTH: 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
```

ö

0; Gaps

```
1.8%; Score 6; DB 2; Length 346;
100.0%; Pred. No. 9.5e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                              CITY: .....
STATE: D.C.
COUNTRY: USA
ZIP: ZOOD5-2477
ZIP: ZOOD5-2477
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/476,254
FILING DATE: 06-JUN-1995
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Weber, J. Mark
APPLICANT: Meber, J. Mark
APPLICANT: Luu, B. Mainh
TITLE OF INVENTION: Method for Strain Improvement of
TITLE OF INVENTION: Brythromycin Producing Bacterium
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson Avenue, 2 Prudential Plaza
                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: WATSON COLE STEVENS DAVIS, P.L.L.C. STREET: 1400 K STREET NW CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 06-JUN-1995

CLASSIFTCATION: 435

ATTORNEY, AGENT INFORMATION:
NAME: POULOS III, JAMES A.
REGISTRATION NUMBER: 31,714

REFERENCE/DOCKET NUMBER: JAP30319C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 628-6088

TELEPHONE: 202 628-8034

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    Sequence 10, Application US/08476254
Patent No. 5846231
GENERAL INFORMATION:
APPLICANT: WEINER, RONALD M.
APPLICANT: FUQUA, WILLIAM C.
TITLE OF INVENTION: MAINE MELA GENE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 10, Application US/09153599A ; Patent No. 6420177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S. colwelliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 346 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide HYPOTHETICAL: NO
                206 YDTIFE 211
                                                           267 YDTIFE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 YDTIFE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 YDTIFE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-153-599A-10
                                                                                                                                                    US-08-476-254-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-476-254-10
                                                                                                                                 RESULT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 227
                                                      ΩD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.8%; Score 6; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRIE: D.C.
COUNTRY: USA
ZIP: 20005-247
ZIP: 20005-247
ZIP: 20005-247
COMPUTER READABLE FORM:
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION 1995
CLASSIFICATION: 435
ATTORNEY/ASTRI INFORMATION:
NAME: POULOS III, JAMES A.
REFERENCE/DOCKET NUMBER: 31,714
REFERENCE/DOCKET NUMBER: 34,714
TELECHOMM: 202 628-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 628-008
TELEFRAX: 202 628-018
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TEMPTATION FOR SEQ ID NO: 2:
TEMPTATION FOR SEQ ID NO: 2:
TEMPTATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: WATSON COLE STEVENS DAVIS, P.L.L.C. STREET: 1400 K STREET NW CITX: WASHINGTON
CLASSIFICATION: 530
ATTOKNEY/AGENT INFORMATION:
NAME: TOrchia, Ph.D., Timothy E
REGISTRATION NUMBER: 36,700
TELEPRENGE/DOCKET NUMBER: ONYX-005/00US
TELEPROMUTICATION INFORMATION:
TELEPROM: (415) 843-5481
TELEPROM: (415) 847-6663
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
1.8%; Score 6; DB 1
Best Local Similarity 100.0%; Pred. No. 9.5
Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08476254
Patent No. 584651
GENERAL INFORMATION:
APPLICANT: WEINER, RONALD M.
APPLICANT: FUQUA, WILLIAM C.
TITLE OF INVENTION: MARINE MEIA GENE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                : 346 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                C-terminal
                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
CRGANISM: HOMO sapiens
US-08-276-151-5
                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 KDNLAI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 KDNLAI 27
                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 225
US-08-476-254-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-476-254-2
```

0; Gaps

```
FILING DATE: 08-NOV-1993
                                                                                                                                                                                                                                                                                   206 YDTIFE 211
                                                                                                                                                                                                                                                                                                                     267 YDTIFE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 PQIALR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 PQIALR 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                US-09-252-991A-31854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-31854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-489-039A-7292
                                                                                                                                               LENGTH: 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-489-039A-7292
                                                                                                                                                                                                        Query Match
                                                                                                                           SEQ ID NO:7
                                                                                                                                                                 5474933-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 231
                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٥:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
1.8%; Score 6; DB 4; Length 346;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6; Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #PELICANT: EINER, RONALD M.; FUQUA JR., WILLIAM C.
#TITLE OF INVENTION: MARINE MELA GENE
#INVERSOR SEQUENCES: 9
CURRENT APPLICATION DATA:
#PELICATION NUMBER: US 08/148,945
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
#PELICATION NUMBER: 974,837
FILING DATE: 10-NOV-1992
#PELICATION NUMBER: 974,837
#PELICATION NUMBER: 974,837
#PELICATION NUMBER: 21-NOV-1992
#PELICATION NUMBER: 21-NOV-1992
#PELICATION NUMBER: 21-NOV-1992
#PELICATION NUMBER: 21-NOV-1992
#PELICATION NUMBER: 21-NOV-1992
                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/153,599A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATECT NO. 5474933

PAPELICANT: EINER, RONALD M.; FUQUA JR., WILLIAM C. TITLE OF INVENTION: MARINE MELA GENE

'NUMBER OF SEQUENCES: 9

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/148,945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 6
100.0%; Pred. No. 9.5
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                             FER2159P0041US
                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAGINET, Lisa V.
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: FER21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                346 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 10u..
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           206 YDTIFE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267 YDTIFE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 YDTIFE 272
                      Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 YDTIFE 211
                                        U.S.A.
Chicago
                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:2:
; LENGTH: 346
                                                          60601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-153-599A-10
                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 228
5474933-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5474933-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5474933-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΩ
```

```
Sequence 31854, Application US/09252991A
Sequence 31854, Application US/09252991A
GENERAL INFORMATION
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/4,788
PRIOR APPLICATION NUMBER: US/0/094,190
PRIOR PELICATION NUMBER: US/0/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEG ID NO 31854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7292
LENGTH: 351
                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 4; Length 347;
100.0%; Pred. No. 9.6e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                  Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
1.8%; Score 6; DB 4; Length 351;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                               1.8%; Score 6; DB 6; Le. 100.0%; Pred. No. 9.5e+02; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 7292, Application US/09489039A; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Klebsiella pneumoniae
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 974,837
FILING DATE: 10-NOV-1992
APPLICATION NUMBER: 45,804
FILING DATE: 21-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                        Best Local Similarity 100.0
Matches 6; Conservative
```

```
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-03.
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIAN OF 1997-08-15
SOFTWARE: PATENTIAN OF 1997-08-15
SOFTWARE: PATENTIAN OF 1997-08-15
SOFTWARE: PATENTIAN OF 1997-08-15
SOFTWARE: PATENTIAN OF 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
0
                                                                                                                                                                               DB 4; Length 355;
                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Matthew
APPLICANT: Mathlur, Preete
TITLE OF INVENTION: HUMAN GROWTH-RELATED CDC10 HOMOLOG
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8%; Score 6; DB 4; Ler
100.0%; Pred. No. 9.8e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,182
                                                                                                                                                                          1.8%; Score 6; DB 4;
100.0%; Pred. No. 9.86
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4914, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application US/08978182
; Patent No. 5849556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                               ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Enterococcus faecalis
    1999-01-29
                    NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 9887
LENGTH: 355
                                                                                                                                                 Query Match
Best Local Similarity 100.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                               231 LLGELI 236
                                                                                                                                                                                                                                                                                                          282 LLGELI 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 GLLVTL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 GLLVTL 82
PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                            US-09-134-000C-4914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-134-000C-4914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-978-182-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                        RESULT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Griffais, R.
APPLICANT: Griffais, R.
TILLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REPERENCE: 9710-003-99
CURRENT APPLICATION NUMBER: US/09/198,452A
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03-03-04
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.8%; Score 6; DB 4; Length 352;
100.0%; Pred. No. 9.7e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 6; DB 4; Length 353;
100.0%; Pred. No. 9.7e+02;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 9887, Application US/09489039A ; Patent No. 6610836
                                                                                                                                                          ; Sequence 702, Application US/09198452A ; Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5230, Application US/09328352; Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5230
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 6; Conservative
                                      343 LIADLQ 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 EKLLQS 219
         82 LIADLO 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 EKLLOS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 TLIADL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 TLIADL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-489-039A-9887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 233
US-09-328-352-5230
                                                                                                                                    US-09-198-452A-702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-198-452A-702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 5230
LENGTH: 353
                                                                                                                 RESULT 232
                                         В
      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
```

ð

```
; OTHER INFORMATION: NAD-dependent epimerase/dehydratase domain US-09-634-955B-21
                                                                                                                                                                                                                  1.8%; Score 6; DB 2; Length 357; 100.0%; Pred. No. 9.8e+02; ttive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 4; Length 359;
100.0%; Pred. No. 9.9e+02;
tive 0; Mismatches 0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: MNI-134
CURRENT APPLICATION NUMBER: US/09/634,955B
CURRENT FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: 60/192,002
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 21
LENGTH: 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21741
                                LENGTH: 357 amino acide
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 578115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                      Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 6; Conservative
            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                    215 KLLQSE 220
                                                                                                                                                                                                                                                                                                                                         198 KLLQSE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 KLLGEL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 KLLGEL 297
                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-634-955B-21
                                                                                                                                                                          US-09-205-681-4
                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                  ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.8%; Score 6; DB 2; Length 357; Best Local Similarity 100.0%; Pred. No. 9.8e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Yue, Henry
APPLICANT: Yue, Henry
APPLICANT: Kaser, Matthew
APPLICANT: Kaser, Matthew
APPLICANT: Mathur, Preete
TITLE
TITLE OF INVENTION: HUMAN GROWTH-RELATED CDC10 HOMOLOG
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FasteSEG for Windows Version 2.0
CURRENT APPLICATION DAIN:
APPLICATION NUMBER: US/09/205,681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                           FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0426 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRONS: 650-845-055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0426 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/978,182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09205681
Patent No. 5952214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 650-855-0555
FILING DATE: Herewith
                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 KLLOSE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 KULQSE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: GenBa
; CLONE: 578115
US-08-978-182-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-205-681-4
```

```
TESCUE 239

Sequence 21741, Application US/09252991A

Sequence 21741, Application US/09252991A

Sequence 21741, Application US/09252991A

Sequence 21741, Application US/09252991A

Sequence 21741, Application US/09252991A

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 21741

LENGTH: 359
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                    Sequence 21, Application US/09634955B
Patent No. 6511834
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel
APPLICANT: Cook, William James
TITLE OF INVENTION: 32142, 21481, 25964, 21686, NOVEL HUMAN DEHYDROGENASE
TITLE OF INVENTION: MOLECULES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
                                                       Gaps
                                                       .
0
Query Match 1.8%; Score 6; DB 4; Length 359; Best Local Similarity 100.0%; Pred. No. 9.9e+02; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 6; DB 2; Length 362;
100.0%; Pred. No. 9.98+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,897
                                                                                                                                                                                                                                                                                   APPLICANT: King, Mary-Claire
APPLICANT: Lynch, Eric D.
APPLICANT: Lev. Ming
APPLICANT: Morrow, Jan E.
APPLICANT: Welcsh, Piri L.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE FREHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILSBOROUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UW97-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 6, Application US/09323735; Patent No. 6197932; GENERAL INFORMATION: APPLICANT: King, Mary-Claire; APPLICANT: Lynch, Eric D. APPLICANT: Lee, Ming; APPLICANT: Morrow, Jan E.
                                                                                                                                                                                                      US-09-080-897-6; Sequence 6, Application US/09080897; Patent No. 5985774; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: UW TELECOMMUNICATION INFORMATION: TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CALIFORNIA
                                                                                 197 LVADFL 202
                                                                                                                         272 LVADFL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 EİVKİL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 EIVKIL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-09-080-897-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-323-735-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 241
                                                                                                                     g
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09594669
Fatent No. 6311424
GENERAL INFORMATION:
TOTALE APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman.
TITLE OF INVENTION: No. 6331424el motor proteins and methods for ITILE OF INVENTION: Their use
FILE REFERENCE: 1042
CURRENT APPLICATION NUMBER: US/09/594,669
CURRENT FILING DATE: 1999-04-20
FRIOR APPLICATION NUMBER: US 09/295,612
FRIOR FILING DATE: 1999-04-20
FRIOR APPLICATION NUMBER: US 09/314,464
FRIOR FILING DATE: 1999-04-20
FRIOR FILING DATE: 1999-04-20
FRIOR FILING DATE: 1999-04-20
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
FRIOR FILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 3; Length 362;
100.0%; Pred. No. 9.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/323,735
                                                                                                                                                                                          ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 75 DENIES DRIVE CITY: HILLSBOROUGH STATE: CALLFORNIA
APPLICANT: Welcsh, Piri L.
APPLICANT: Leon, Pedro E.
TILLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UW97-001
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/080,897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSWAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UW97
TELECOMMUNICATION INFORMATION:
TELECHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I: 362 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100:
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: BII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 EIVKIL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 EIVKIL 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                         USA

// TYPE: PRT
// ORGANISM: Human
US-09-594-669-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                     94010
                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-323-735-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-594-669-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
```

1.8%; Score 6; DB 4; Length 362;

Query Match

```
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREDMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1099-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13446
LENGTH: 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5920, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FARCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 6; DB 4; Length 363; 100.0%; Pred. No. 1e+03; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
FILING DATE: 10-MAY 1998
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                      . Sequence 13446, Application US/09489039A
; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 370 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (781)893-8277 INFORMATION FOR SEQ ID NO: 5920:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.00
Lahes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                     172 EQFADE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 LAILEK 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 LAILEK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                          JS-09-489-039A-13446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-489-039A-13446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-107-532A-5920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APLICANT:
APLICANT:
APLICANT:
APLICANT:
APLICANT:
APLICANTON WOUGHEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION:
APLICANTON NUMBER:
US/09/252,991A
CURRENT APPLICATION NUMBER:
US/09/252,991A
CURRENT PILING DATE:
1999-02-18
PRIOR PILING DATE:
1998-02-18
PRIOR APPLICATION NUMBER:
US/06/094,190
PRIOR FILING DATE:
1998-07-27
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUMBER:
NUM
                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: No. 6638754el motor proteins and methods for
TITLE OF INVENTION: their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
1.8%; Score 6; DB 4; Length 362;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
100.0%; Pred. No. 9.9e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.8%; Score 6; DB 4; Length 363; Best Local Similarity 100.0%; Pred. No. 1e+03; Matches 6; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 1042A

CURRENT APPLICATION NUMBER: US/10/112,432

CURRENT FILING DATE: 2002-03-29

PRIOR APPLICATION NUMBER: 09/724,215

PRIOR FILING DATE: 2000-11-28

PRIOR FILING DATE: 1999-04-20

PRIOR APPLICATION NUMBER: 09/295,612

PRIOR APPLICATION NUMBER: 09/314,464

PRIOR FILING DATE: 1999-05-18

PRIOR FILING DATE: 1999-05-18

PRIOR FILING DATE: 2000-66-15

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FASTEEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 27806, Application US/09252991A; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/10112432; Patent No. 6538784; GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                      6; Conservative
   Best Local Similarity
                                                                                                     294 LLKNQP 299
                                                                                                                                                                 128 LLKNOP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 LLKNQP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 LLKNOP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 EQFADE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 244
US-09-252-991A-27806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-27806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 27806
LENGTH: 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 362
                                                                                                                                                                                                                                                                                                       -10-112-432-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-112-432-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                     ò
```

```
٥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08746789A
Retent No. 5789200
GENERAL INFORMATION
APPLICANT: Ismail Kola, Martin J. Tymms, Christine DeBouck
TITLE OF INVENTION: A No. 5789200el Human ETS Family Member, ELF3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: AnithKline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                            Length 370;
                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 6; DB 1; Length 371;
100.0%; Pred. No. 1e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486
COMPUTER: IBM 486
COMPUTER: IBM 486
SOFTWARE: MICROSOFF WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,789A
FILING DATE: No. 5789200ember 15, 1996
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
REFIRENCE DOCKET NUMBER:
ATTORNEY/ABORT INFORMATION:
NAME: William T. Han ATTORNEY/BOCKET NUMBER: ATTORNEY/BOCKET NUMBER: ATTORNEY/BOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEBRONE: 610 270 5219
TELECOMMUNICATION INFORMATION:
TELEBRONE: 610 270 4026
INFORMATION FOR SEQ 1D NO: 2:
LENGTH.
                                                                                                                                                                                                              Query Match 1.8%; Score 6; DB 4; L
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 6; Conservative 0; Mismatches 0
                                                                                                 NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...370

SEQUENCE DESCRIPTION: SEQ ID NO: 5920:

US-09-107-532A-5920
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                     244 IMTKYI 249
                                                                                                                                                                                                                                                                                                                                             145 IMTKYI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 EAVAQL 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 EAVAQL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 61
INFORMATION FOR
                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 247
US-08-746-789A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-746-789A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                         Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   d
```

; Sequence 5, Application US/09570593 ; Patent No. 6566063

RESULT 248 US-09-570-593-5

```
Sequence 6429, Application US/09543681A

Parent No. 6605709

GREERLI INFORMATION:
APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT APPLICATION NUMBER: US 60/128,706

PRIOR PILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 6429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USCOLA 489-039A-8389

Sequence 8389; Application US/09489039A

Sequence 8389; Application US/09489039A

Sequence 8389; Application US/09489039A

Sequence 8389; Application US/09489039A

GENERAL INFORMATION:

TITLE OF INVENTION: PNEUMONIAR FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: PNEUMONIAR FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT PEPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

LENGTH: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
          APPLICANT: Kaufman, Joerg
APPLICANT: Kaufman, Joerg
APPLICANT: Xin, Hong
APPLICANT: Xin, Hong
TITLE OF INVENTION: EXPRESSION OF ETS-DOMAIN PROTEINS IN
TITLE OF INVENTION: CANCER
FILE REFERENCE: 2300-1556
CURRENT APPLICATION NUMBER: US/09/570,593
CURRENT FILING DATE: 2000-05-12
PRIOR PILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FREEEE FREEEEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 6; DB 4; Length 371;
100.0%; Pred. No. 1e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 6; DB 4; Length 371;
100.0%; Pred. No. 1e+03;
tive 0; Mismatches 0; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                          TYPE: PRT; ORGANISM: Homo sapiens
US-09-570-593-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 EAVAOL 314
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 EAVAQL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 EAFHVF 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 EAFHVF 205
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-543-681A-6429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-543-681A-6429
                                                                                                                                                                                                                                                                                             371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 371
                                                                                                                                                                                                                                                                       SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                             LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8389
```

0; Gaps Query Match 1.8%; Score 6; DB 4; Length 373; Best Local Similarity 100.0%; Pred. No. 1e+03; Matches 6; Conservative 0; Mismatches 0; Indels

0

22 KDNLAI 27 |||||| 210 KDNLAI 215 g

ð

Search completed: April 12, 2004, 10:37:51 Job time : 29 secs